

## (12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
17 July 2003 (17.07.2003)

PCT

(10) International Publication Number  
**WO 03/058201 A2**

- (51) International Patent Classification<sup>7</sup>: **G01N**
- (21) International Application Number: PCT/US02/41825
- (22) International Filing Date:  
31 December 2002 (31.12.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
60/345,317 31 December 2001 (31.12.2001) US
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**  
— *without international search report and to be republished upon receipt of that report*
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



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(54) Title: METHODS FOR IDENTIFYING MARKER GENES FOR CANCER

(57) Abstract: The invention describes a method of identifying tissue-specific tumor markers and diagnostic and therapeutic methods and compositions of using the same. More specifically, the invention presents a method for a rational search of diagnostic and prognostic cancer markers and therapeutic targets among the genes negatively regulated by tumor suppressor genes.

## METHODS FOR IDENTIFYING MARKER GENES FOR CANCER

### Field of the Invention

5           The invention relates generally to the field of cancer. More specifically, the invention details methods for the identification of markers specific for one or several types of cancer, depending on tissue origin. Such markers are useful in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic intervention.

10

### Background of the Invention

          An effective cure of any given cancer will greatly depend on the development of new diagnostic assays based on identification of reliable serological and histological markers and on designing new therapeutic strategies and  
15   pharmaceuticals for effective elimination of cancer cells in the diseased individual. Tumor suppressor genes normally function to inhibit division or survival of genetically damaged cells and thus function to prevent the development of tumors. Mutations in tumor suppressor genes cause the cell to ignore one or more of the components of a network of inhibitory signals, removing the inhibitory mechanisms  
20   from the cell cycle, and resulting in a higher rate of uncontrolled growth, *i.e.*, cancer. Tumor suppressor genes are defined by the impact of their absence and thus tend to be recessive. Thus, neoplasia is the result of the loss of function of these genes. The loss or inactivation of a normal tumor suppressor gene may be acquired somatically in a single clone of cells or be constitutionally present throughout the body, including the  
25   germ line.

          There are numerous tumor suppressors known to those of skill in the art, including, for example, p53; the retinoblastoma gene, commonly referred to as Rb1; the adenomatous polyposis of the colon gene (APC); familial breast/ovarian cancer gene 1 (BRCA1); familial breast/ovarian cancer gene 2 (BRCA2); CDH1  
30   cadherin 1 (epithelial cadherin or E-cadherin) gene; cyclin-dependent kinase inhibitor 1C gene (CDKN1C, also known as p57, KIP2 or BWS); cyclin-dependent kinase inhibitor 2A gene (CDKN2A also known as p16 MTS1 (multiple tumor suppressor 1), TP16 or INK4); familial cylindromatosis gene (CYLD; formerly known as EAC



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(epithelioma adenoides cysticum)); E1A-binding protein gene (p300); multiple exostosis type 1 gene (EXT1); multiple exostosis type 2 gene (EXT2); homolog of *Drosophila* mothers against decapentaplegic 4 gene (MADH4; formerly referred to as DPC4 (deleted in pancreatic carcinoma 4) or SMAD4 (SMA- and MAD-related protein 4)); mitogen-activated protein kinase kinase 4 (MAP2K4; also referred to as JNKK1, MEK4, MKK4, or PRKMK4; formerly known as SEK1 or SERK1); multiple endocrine neoplasia type 1 gene (MEN1); homolog of *E. coli* MutL gene (MLH1 also known as HNPCC (hereditary non-polyposis colorectal cancer) or HNPCC2; formerly referred to as COCA2 (colorectal cancer 2) and FCC2); homolog of *E. coli* MutS 2 gene (MSH2 also called HNPCC (hereditary non-polyposis colorectal cancer) or HNPCC1 and formerly known as COCA1 (colorectal cancer 1) and FCC1); neurofibromatosis type 1 gene (NF1); neurofibromatosis type 2 gene (NF2); protein kinase A type 1, alpha, regulatory subunit gene (PRKAR1A, formerly known as PRKAR1 or TSE1 (tissue-specific extinguisher 1)); homolog of *Drosophila* patched gene (PTCH; also called BCNS); phosphatase and tensin homolog gene (PTEN, also called MMAC1 (mutated in multiple advanced cancers 1), formerly known as BZS (Bannayan-Zonana syndrome) and MHAM1 (multiple hamartoma 1)); succinate dehydrogenase cytochrome B small subunit gene (SDHD; also called SDH4); Swi/Snf5 matrix-associated actin-dependent regulator of chromatin gene (SMARCB1, also referred to as BAF47, HSNFS, SNF5/INI1, SNF5L1, STH1P, and SNR1); serine/threonine kinase 11 gene (STK11 also known as LKB1 and PJS); tuberous sclerosis type 1 gene (TSC1 also known as KIAA023); tuberous sclerosis type 2 gene (TSC2, previously referred to as TSC4); von Hippel-Lindau syndrome gene (VHL); and Wilms tumor 1 gene (WT1, formerly referred to as GUD (genitourinary dysplasia), WAGR (Wilms tumor, aniridia, genitourinary abnormalities, and mental retardation), or WIT-2), DAP-kinase, FHIT, Werner syndrome gene, and Bloom syndrome gene.

The p53 tumor suppressor gene is an exemplary tumor suppressor in its mode of action. It encodes a nuclear transcription factor that accumulates in cells in response to a variety of stresses, thereby inducing growth arrest or apoptosis (Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996). p53 or the pathway mediated by p53 are inactivated in the majority of human tumors, including advanced prostate cancer (Steele *et al.*, *Br J Surg.*, 85(11):1460-1467 (1998); Ozen and Pathak, *Anticancer Res.*, 20(3B):1905-1912 (2000).

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One of the functions of the p53 protein in the cell is that it binds DNA stimulating the expression of p21-waf1 that interacts with a cell division-stimulating protein (cdk2). When p21 is complexed with cdk2, the cell cannot pass to the S stage of cell division (G1 check point). Mutant p53 can no longer bind DNA in an effective way, and as a consequence the p21-waf1 protein is not made available to act as the 'stop signal' for cell division. Thus, cells divide uncontrollably and form tumors. Thus, inactivation of p53 is associated with the loss of this cell cycle checkpoint control and with the consequent resistance to anti-cancer treatment, genomic instability, and enhanced angiogenesis, leading to rapid tumor progression (Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996); Cordon-Cardo *et al.*, *Semin. Surg. Oncol.*, 13:319-327 (1997).

Many p53-mediated effects are achieved through the activity of p53-responsive genes that are either up- or down-regulated by p53. In fact, the activity of p53-responsive genes account, in part, for p53-mediated checkpoint control [upregulation of p21-waf1, 14-3-3  $\square$  (G2 checkpoint)], apoptosis (upregulation of bax, PUMA, and genes determining enhanced reactive oxygen species metabolism), suppression of angiogenesis (upregulation of thrombospondins 1 and 2, and downregulation of VEGF) and p53 feedback regulation (upregulation of mdm2) (see Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996) for references). Much like p53, the other tumor suppressors listed above also mediate their effects through the activity of responsive genes that are either up- or down-regulated by the tumor suppressor, directly or indirectly. Genes that have altered expression in tumors may serve as targets for development of anti-cancer drugs, or cancer markers or both. However, the relationship between changes in gene expression, resulting from tumor suppressor deficiency, and tumor progression is not sufficiently understood. It also remains unclear why the germline loss of tumor suppressor gene function leads to development of certain specific types of cancer and not others. This implies that in each specific tissue the changes in gene expression imposed by the loss of tumor suppressor gene are unique. Taking into account a need for tissue-specific markers of cancer, the inventors have devised a method for the identification of such tissue-specific markers by exploiting the tumor suppressor regulation of genes in cancer cells.

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### Summary of the Invention

The invention relates to methods for diagnosing and prognosing cancer by utilizing general as well as tissue-specific genetic markers, methods for identifying these markers, and the markers identified by such methods.

5           The invention provides a method of identifying tissue-specific and general tumor markers and diagnostic and therapeutic methods and compositions of using the same. Diagnostic markers may be screening markers (secreted polypeptides), histological markers (using which it is possible to distinguish tumor tissue from benign tissue within histological samples) or staging markers  
10 (determining the stage of a cancer by detection of the presence of specific cancer cells in blood (micrometastases) by RT-PCR on identified cancer-type-specific markers on the whole blood RNA).

          The invention provides a method of identifying a diagnostic marker for a cancer comprising: a) obtaining a first cell from a first cell type of the cancer, the  
15 cell comprising a defective tumor suppressor expression; b) obtaining a second cell of the first cell type, wherein the second cell comprises a wild-type tumor suppressor expression; c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and d) selecting at least one gene of step c) as a diagnostic marker for the cancer.

20           In the diagnostic and therapeutic methods for using such a marker(s), the invention provides a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected  
25 from the group consisting of a) polypeptides encoded by the polynucleotides listed in Table 5 or in Table 6; and b) polypeptides which are at least 70% homologous to the polypeptides of a) at the amino acid sequence level. In one embodiment of the diagnostic methods, the level of a polypeptide-encoding polynucleotide is determined, rather than the polypeptide itself. In such methods, the invention contemplates any of  
30 the polynucleotides in Table 6, polynucleotides having sequences that differ from the polynucleotides in a) without changing the polypeptide encoded thereby, and polynucleotides that are at least 70% homologous to the polynucleotides of a) at the nucleic acid sequence level.

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In the case of at least p53 and possibly other tumor suppressors, the invention further provides a method of determining the p53 status within the tumor (*i.e.*, whether the cancer cell is a p53<sup>-</sup> or a p53<sup>+</sup> tumor cell.), which is important for prognosis and treatment selection.

5           The invention also provides a method for monitoring the activity of p53 suppressive drugs, or drugs that suppress other tumor suppressors described herein, by measuring any of the markers identified herein the polypeptides of which are secreted, such as PSA or pancreatitis-associated protein. In this aspect, the invention provides a method of measuring the responsiveness of a subject to a cancer  
10 treatment comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of the polypeptide in a sample taken from the subject after treatment, a decrease in the level indicating responsiveness of the subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of a) polypeptides encoded by the  
15 polynucleotides listed in Table 5 and Table 6; and b) polypeptides which are at least 70% homologous to the polypeptides of a).

In a related aspect, the invention provides a method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject  
20 before treatment, and comparing it with the level of the polynucleotide in a sample taken from the subject after treatment, a decrease in the level indicating responsiveness of the subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of: a) the polynucleotides listed in Table 6; b) polynucleotides having sequences that differ from the polynucleotides in a), without  
25 changing the polypeptide encoded thereby; and c) polynucleotides which are at least 70% homologous to the polynucleotides of a).

According to another aspect of the invention, a method is provided of screening for drugs useful in the treatment of cancer. A cell which harbors a tumor suppressor mutation or defective expression is contacted with a test substance.  
30 Expression of a transcript or its translation product is monitored. The transcript is a tissue-specific tumor marker of the invention. A test substance is identified as a potential drug for treating cancer if it decreases expression of a marker identified as one that is up-regulated as a result of loss of tumor suppressor function. Alternatively,

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the test substance is identified as a potential drug if it increases the expression of a marker identified as one that is down regulated as a result of loss of tumor suppressor function.

For example, the invention provides a method for screening for  
5 compounds that modulate the activity of a tumor suppressor gene comprising a) obtaining a cell comprising a defective tumor suppressor expression; b) measuring the level of expression of a marker of Table 5 or 6 in the cell; c) contacting the cell with a test compound; and d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after the contacting  
10 step as compared to the level of expression before the contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.

Another aspect of the invention concerns a method of determining p53 inactivation in prostate cells of an individual comprising determining the levels of serum PSA, wherein elevated serum PSA levels in said individual are indicative of  
15 p53 inactivation in said prostate cells.

Yet another aspect of the invention a method of monitoring the effect of a p53-based cancer therapy on a prostate cancer patient, the prostate cancer cells of said patient having a p53 loss of function mutation, said method comprising determining the levels of serum PSA of said patient before and after said therapy,  
20 wherein a decrease in the serum PSA levels after provision of said therapy is indicative of said therapy overcoming the deleterious effects of said p53 mutation.

In addition, the invention also contemplates a method of detection of p53 inactivation in other tissues. For example, from observations of pancreatitis associated protein, the inactivation of p53 in pancreatic carcinoma may be  
25 determined. Similar observations may be made about other preferred markers disclosed in this application.

Numerous other aspects and advantages of the invention will be apparent upon consideration of the following drawings and detailed description.

30

### **Brief Description of the Drawings**

The following drawings form part of the present specification and are included to further illustrate aspects of the invention. The invention may be better

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understood by reference to the drawings in combination with the detailed description of the preferred embodiments presented herein.

Figure 1: Inactivation of p53 pathway in LNCaP cells by GSE56 correlates with increased secretion of PSA. Quantitation of PSA protein in culture medium conditioned by the indicated cells, performed by the Microparticle Enzyme Immunoassay method using IMx operation system (Abbott Diagnostics, Abbott Park, IL, USA) binding to DNA for repression (Kley *et al.*, *Nucleic Acids Res.*, 20:4083-4087 (1992); Sun *et al.*, *J. Biol. Chem.*, 274:11535-11540 (1999); Xu *et al.*, *Oncogene*, 19:5123-5133 (2000).

Figure 2: Opposite regulatory effect of p53 on PSA and p21 promoters. Chloramphenicol acetyltransferase (CAT)-reporter constructs were used to estimate p53 influence on PSA and p21 promoter elements. A panel of reporter constructs: pBasic-CAT (CAT gene under minimal thymidine kinase promoter), pWAF1-CAT (p53-binding site from p21/Waf1 gene upstream of the minimal thymidine kinase promoter); p407ECAT plasmid, containing 1.6 kb enhancer (-5322 to -3740) and 418 bp promoter (-407 to +11) elements from PSA gene followed by promoterless CAT (Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788 (1997); Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150 (1997) were transfected into LNCaP cells in combination with different amounts of pLp53SN, containing human wild type p53, pLGSE56SN expressing GSE56 or empty pLXSN vector using Lipofectamin Plus reagent (Gibco BRL). Bars reflect relative CAT activity in lysates of LNCaP cells transiently transfected with either PSA-CAT (upper panel) or p21-CAT (lower panel) constructs in combination with the indicated plasmids. Results are normalized according to transfection efficiency and CAT expression in control cells transfected with insert-free vector. wt, plasmid expressing wild type human p53 cDNA; GSE, plasmid. (1) and (2) indicate plasmid concentration in micrograms. The experiment was repeated three times and showed similar results with variations in relative CAT activity values less than 20 percent.

Figure 3: Trichostatin A (TSA) treatment eliminates the effect p53 has on PSA promoter activity. Bars show relative CAT activity in lysates of LNCaP cells transiently transfected with the indicated plasmid DNAs. TSA (100 nM) was added 5 h and CAT activity was measured 40 h post-transfection. Values reflect average of three independent experiments normalized according to transfection efficiency and CAT expression in control cells transfected with insert-free vector with no TSA.

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156Pro mutants had no detectable effect on PSA. Thus, the dominant negative activity of tumor-derived p53 mutants is well correlated with the increased production of PSA by LNCaP cells, suggesting that similar events occur during tumor progression.

Figure 4: Effect of tumor-derived p53 mutants on the levels of p21 protein expression and on PSA secretion by LNCaP cells. LNCaP cells were transduced with insert-free retrovirus or retroviruses expressing indicated p53 mutants. A panel of constructs expressing p53 mutants (pPS-p53<sup>135Val</sup>, pPS-p53<sup>141Ala</sup>, pPS-p53<sup>156Pro</sup>, pPS-p53<sup>175His</sup>) was prepared in Mo- MuLV-based retroviral vector pPS-Hygro, expressing the p53 cDNA under the control of LTR and the hygromycin resistance gene under the control of SV40 promoter (Ossovskaya *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314 (1996). Expression of p53 and p21 proteins was detected in the lysates of untreated LNCaP cell populations by Western immunoblotting with appropriate antibodies. Before loading, samples were normalized according to protein amounts confirmed by membrane staining and probing with anti-actin antibodies. 24-hour medium was collected from the same cell cultures and amounts of PSA protein were measured by Microparticle Enzyme Immunoassay, using IMx operation system (Abbott Diagnostics, Abbott Park, IL, USA).

Figure 5 contains the sequences of the genes listed in Tables 5 and 6, in order of the sequence ID number (SEQ ID NO). Note that the GenBank accession Number of the mouse EST printed on the chip is given in the tables; the name of the corresponding human consensus sequence [mRNA] (obtained by bioinformatic analysis) and the GenBank ID(s) of the sequence closest to the consensus sequence, where available, was added into Tables 5 and 6. Figure 5 contains the human consensus sequence of each gene, where available, or the mouse consensus sequence, if the human sequence was unavailable, or the mouse EST sequence, if neither human nor mouse consensus sequence was available. The sequence identifier (SEQ ID NO), and corresponding Genbank accession number, are denoted before each sequence.

This application contains six Excel tables (Table 1-6 discussed herein). These tables are attached to this application as printed tables and also on a diskette.

### Detailed Description of the Preferred Embodiments

The invention deals with methods of obtaining genetic markers for diagnosis and prognosis of cancer and methods for the use of these markers.

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A preferred embodiment of the diagnostic aspect concerns a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of: polypeptides encoded by the human polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 or 6, and homologs of said polypeptides having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may be taken from a bodily fluid, such as blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine. The sample may also originate from a tissue, such as brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta, uterus, ovary, endometrium, testicle, lymph node, skin, head or neck, esophagus, bone marrow, and blood or blood cells.

General protocols for the detection of cancer markers can be found in "Tumor Marker Protocols", Hanausek & Walaszek (Eds.), Humana Press, 1998. Methods of determining the level of a polypeptide in a sample are well known in the art (see, for example: Coligan et al, Unit 9, Current Protocols in Immunology, Wiley Interscience, 1994) and include, *inter alia*: immunohistochemistry (Microscopy, Immunohistochemistry and Antigen Retrieval Methods: For Light and Electron Microscopy, M.A. Hayat (Author), Kluwer Academic Publishers, 2002; Brown C.: "Antigen retrieval methods for immunohistochemistry", *Toxicol Pathol* 1998; 26(6): 830-1; ELISA (Onorato et al., "Immunohistochemical and ELISA assays for biomarkers of oxidative stress in aging and disease", *Ann NY Acad Sci* 1998 20; 854: 277-90), western blotting (Laemmli UK: "Cleavage of structural proteins during the assembly of the head of a bacteriophage T4", *Nature* 1970;227: 680-685; Egger & Bienz, "Protein (western) blotting", *Mol Biotechnol* 1994; 1(3): 289-305), antibody microarray hybridization (Huang, "detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13) and Targeted molecular imaging, which can be carried out on the whole body with imaging agents such as antibodies against the marker polypeptides (which may be membrane-bound proteins), the marker polypeptides themselves, receptors and contrast agents. The



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visualizations techniques include single photon and positron emission tomography, magnetic resonance imaging (MRI), computed tomography or ultrasonography (Thomas, Targeted Molecular Imaging in Oncology, Kim et al (Eds)., Springer Verlag, 2001). Any other known methods of polypeptide detection are also envisaged

5 in connection with the invention. Optimization of protein detection procedures for diagnosis is well known in the art and described herein below. Specifically, diagnostic assays using the above methods may be carried out essentially as follows: Immunohistochemistry for diagnosis may be carried out essentially as described in Diagnostic Immunohistochemistry, David J., MD Dabbs, Churchill Livingstone, 1<sup>st</sup>

10 Ed, 2002; Quantitative Immunohistochemistry: Theoretical Background and its Application in Biology and Surgical Pathology, Fritz et al., Gustav Fischer, 1992. Western blotting-based diagnosis may be carried out essentially as described in Brys et al., "p53 protein detection by the Western blotting technique in normal and neoplastic specimens of human endometrium", *Cancer Letters* 2000; 148 (197-205);

15 Rochon et al., "Western blot assay for prostate-specific membrane antigen in serum of prostate cancer patients" *Prostate* 1994; 25(4): 219-23; Dalmau et al., "Detection of the anti-Hu antibody in the serum of patients with small cell lung cancer-- a quantitative western blot analysis", *Ann Neurol* 1990; 27(5): 544-52; Joyce et al., "Detection of altered H-ras proteins in human tumors using western blot analysis",

20 *Lab Invest* 1989; 61(2): 212-8. ELISA based diagnosis may be carried out essentially as described in D'ambrosio et al., "An enzyme-linked immunosorbent assay (ELISA) for the detection and quantitation of the tumor marker 1-methylinosine in human urine", *Clin Chim Acta* 1991; 199(2): 119-28; Attalah et al., "A dipstick, dot-ELISA assay for the rapid and early detection of bladder cancer", *Cancer Detect Prev* 1991;

25 15(6): 495-9; Erdile et al., "Whole cell ELISA for detection of tumor antigen expression in tumor samples", *Journal of Immunological Methods* 2001; 258: 47-53. Antibody microarray-based diagnosis may be carried out essentially as described in Huang, "detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13. Targeted molecular imaging-based

30 diagnosis may be carried out essentially as described in Thomas, Targeted Molecular Imaging in Oncology, Kim et al (Eds)., Springer Verlag, 2001; Shahbazi-Gahrouei et al., "In vitro studies of gadolinium-DTPA conjugated with monoclonal antibodies as cancer-specific magnetic resonanace imaging contrast agents", *Australas Phys Eng Sci Med* 2002; 25(1): 31-8; Tiefenauer et al., "Antibody-magnetite nanoparticles: in

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vitro characterization of a potential tumor-specific contrast agent for magnetic resonance imaging", *Bioconjug Chem* 1993; 4(5): 347-52; Cerdan et al., "Monoclonal antibody-coated magnetite particles as contrast agents in magnetic resonance imaging of tumors", *Magn Reson Med* 1989; 12(2): 151-63. In addition, polypeptides may be  
5 detected and a diagnostic assay performed using Mass Spectrometry, essentially as described in Bergquist et al., "peptide mapping of proteins in human body fluids using electrospray ionization fourier transform ion cyclotron resonance mass spectrometry", *Mass Spectrometry Reviews*, 2002; 21:2-15 and Gelpi, "Biomedical and biochemical applications of liquid-chromatography-mass spectrometry", *Journal of*  
10 *Chromatography A*, 1995; 703: 59-80.

An additional embodiment of the diagnostic aspect of the invention provides for a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide-encoding polynucleotide, wherein a higher level of the polynucleotide compared to the level of  
15 the polynucleotide in a subject free of cancer is indicative of cancer, and wherein the polynucleotide is selected from the group consisting of human polynucleotides or the human orthologs of mouse polynucleotides listed in Tables 5 and 6, preferably in Table 6, polynucleotides having sequences that differ from these polynucleotides without changing the polypeptide encoded thereby, and homologs thereof having at  
20 least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may originate from a tissue or a bodily fluid, as described above.

Methods of determining the level of a polynucleotide in a sample are  
25 well known in the art and include, *inter alia*: RT-PCR analysis, in-situ hybridization and northern blotting; polynucleotide detection may also be performed by hybridizing a sample with a microarray imprinted with markers. Any other known methods of polynucleotide detection are also envisaged in connection with the invention. Optimization of polynucleotide detection procedures for diagnosis is well known in  
30 the art and described herein below. Specifically, diagnostic assays using the above methods are well known in the art (see, for example: Sidransky, "Nucleic Acid-Based methods for the Detection of Cancer", *Science*, 1997; 278: 1054-1058) and may be carried out essentially as follows: RT-PCR for diagnosis may be carried out essentially as described in Bernard & Wittwer, "Real-Time PCR Technology for

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Cancer Diagnostics", *Clinical Chemistry* 2002; 48(8): 1178-85; Raj et al., "Utilization of Polymerase Chain Reaction Technology in the Detection of Solid Tumors", *Cancer* 1998; 82(8): 1419-1442; Zippelius & Pantel, "RT-PCR-based detection of occult disseminated tumor cells in peripheral blood and bone marrow of patients with solid tumors. An overview", *Ann NY Acad Sci* 2000; 906:110-23. In-situ hybridization for diagnosis may be carried out essentially as described in "Introduction to Fluorescence In Situ Hybridization: Principles and Clinical Applications", Andreeff & Pinkel (Editors), John Wiley & Sons Inc., 1999; Cheung et al., "Interphase cytogenetic study of endometrial sarcoma by chromosome in situ hybridization, modern Pathology 1996; 9:910-918. Northern blotting for diagnosis may be carried out essentially as described in Trayhurn, "Northern blotting", *Proc Nutr Soc* 1996; 55(1B): 583-9; Shifman & Stein, "A reliable and sensitive method for non-radioactive Northern blot analysis of nerve growth factor mRNA from brain tissues", *Journal of Neuroscience Methods* 1995; 59: 205-208; Pacheco et al., "Prognostic significance of the combined expression of matrix metalloproteinase-9, urokinase type plasminogen activator and its receptor in breast cancer as measured by Northern blot analysis", *Int J Biol Markers* 2001; 16(1): 62-8. Polynucleotide microarray-based diagnosis can be carried out essentially as described in Ring & Boss, "Microarrays and molecular markers for tumor classification", *Genome Biol* 2002; 3(5): comment2005; Lacroix et al., "A low-density DNA microarray for analysis of markers in breast cancer", *Int J Biol Markers* 2002; 17(1): 5-23. In addition, polynucleotide microarray hybridization for diagnosis may be carried out essentially as described in the following review concerning micorarrays in the diagnosis of various cancers: Schmidt & Begley, "Cancer diagnosis and microarrays", *The International Journal of Biochemistry and Cell Biology*, 2003; 35: 119-124. Diagnostic assays using tissue microarrays are also possible and may be performed essentially as described in Ginestier et al., "Distinct and comlementary information provided by use of tissue and DNA microarrays in the study of breast tumor markers", *Am J Pathol* 2002; 161(4): 1223-33; Fejzo & Slamon, "Frozen tumor tissue microarray technology for analysis of tumor RNA, DNA and proteins", *Am J Pathol* 2001; 159(5): 1645-50.

An example of detection of polynucleotides in bodily fluid is that of "staging" markers, which determine the stage of a cancer by detection of the presence of specific cancer cells in the blood (micrometastases) by RT-PCR of identified cancer-type-specific markers expression on the whole blood RNA (provided these

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markers are not normally expressed in blood cells) such detection and diagnosis can be carried out essentially as described in Luke & Kaul, "Detection of Breast Cancer Cells in Blood Using Immunomagnetic Bead Selection and Reverse Transcription-Polymerase Chain Reaction", *Mol Diagn* 1998; 3(3): 149-155; Ghossein et al.,

5 "Molecular Detection of Micrometastases and Circulating Tumor Cells in Solid Tumors", *Clinical Cancer Research* 1999; 5: 1950-1960; Mellado et al., "Detection of circulating neoplastic cells by reverse-transcriptase polymerase chain reaction in malignant melanoma: association with clinical stages and prognosis", *J Clin Oncol* 1996; 14(7): 2091-7.

10 Any of the diagnostic methods as described above can also be used together, simultaneously or not, and can thus provide a stronger diagnostic tool and validate or strengthen the results of a particular diagnosis. For combinations of different diagnostic methods see, *inter alia*: Hoshi et al., "Enzyme-linked immunosorbent assay detection of prostate-specific antigen messenger ribonucleic

15 acid in prostate cancer", *Urology* 1999; 53 (1): 228-235; Zhong-Ping et al., "Quantitation of ERCC-2 Gene Expression in Human Tumor Cell Lines by Reverse Transcription-Polymerase Chain Reaction in Comparison to Northern Blot Analysis", *Analytical Biochemistry* 1997; 244: 50-54; Hatta et al., "Polymerase chain reaction and immunohistochemistry frequently detect occult melanoma cells in regional lymph

20 nodes of melanoma patients", *J Clin Pathol* 1998; 51(8): 597-601.

Any one of the diagnostic methods of the invention as recited above may also be employed to examine the status of a tumor suppressor gene or a biological pathway in which a tumor suppressor gene is involved, or to examine the effectiveness of a modulator of the activity of a tumor suppressor gene, such as a

25 drug. The tumor suppressor gene in question may preferably be any one of p53, Rb1 and PTEN, as well as any other tumor suppressor gene deemed suitable. A list of tumor suppressor genes is provided above.

A preferred embodiment of the prognostic aspect of the invention concerns a method of measuring the responsiveness of a subject to a cancer treatment

30 comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of said polypeptide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of: polypeptides encoded by the human

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polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 or 6, and homologs of said polypeptides having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

As mentioned herein, the sample may be taken from a bodily fluid, as described above; the level of the polypeptide in the sample can be determined as described above.

In addition, the prognostic aspect of the invention comprises further a method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject before treatment, and comparing it with the level of said polynucleotide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of: human polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 and 6, preferably in Table 6, polynucleotides having sequences that differ from these polynucleotides without changing the polypeptide encoded thereby, and homologs thereof having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may originate from a tissue, preferably blood or bone marrow cells, or a bodily fluid, as described above.

The level of the polynucleotide in the sample is determined by the methods disclosed above, preferably by RT-PCR analysis. Any other polynucleotide detection methods disclosed herein may also be employed.

In accordance with the prognostic aspect of the invention, the treatment in conjunction with which the above methods of measuring the responsiveness of a subject to a cancer treatment may be employed include, *inter alia*, radiotherapy or administration of a chemotherapeutic drug such as etoposide, 5-FU (5-fluorouracil), cis-platinum, doxorubicin, a vinca alkaloid, vincristine, vinblastine, vinorelbine, taxol, cyclophosphamide, ifosfamide, chlorambucil, busulfan, mechlorethamine, mitomycin, dacarbazine, carboplatinum, thiotepa, daunorubicin, idarubicin, mitoxantrone, bleomycin, esperamicin A1, dactinomycin, plicamycin, carmustine, lomustine, tauromustine, streptozocin, melphalan, dactinomycin, procarbazine, dexamethasone, prednisone, 2-chlorodeoxyadenosine, cytarabine, docetaxel, fludarabine, gemcitabine, herceptin, hydroxyurea, irinotecan, methotrexate,

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oxaliplatin, rituxin, semustine, tomudex and topotecan, and chemotherapeutically active analogs of these drugs.

5 In a further embodiment of the prognostic aspect of the invention, the methods disclosed herein may also be indicative of the status of a tumor suppressor gene, as described above. Where a tumor suppressor gene or a pathway in which such gene is involved is defective or abnormal, this information may also serve in prognosis of both disease progression and treatment responsiveness of a patient, regardless of whether said treatment is directed to the tumor suppressor in question.

10 In an additional embodiment, the diagnostic and prognostic methods of the invention may also be carried out essentially as described herein wherein the method comprises determining the level of at least two polypeptides or polypeptide-encoding polynucleotides in a sample taken from a subject. Methods of determining the level of polypeptides and polynucleotides are described above.

15 Different combinations of polypeptides or polynucleotides of the cancer markers may be employed in different diagnostic or prognostic methods for various cancers.

For bodily fluid sample based diagnosis or prognosis, at least one polypeptide or combination of at least two polypeptides encoded by the human polynucleotide or human orthologs of the polynucleotides, of Table 3 and 5, preferably of Table 5, more preferably of the highlighted genes of Table 5, may be employed as markers.

20 For tissue sample based diagnosis or prognosis at least one polypeptide or combination of at least two polypeptides encoded by the human polynucleotide or human orthologs of the polynucleotides, of Table 2 and 6, preferably of Table 6, or the polynucleotides themselves may be employed as markers.

For the diagnosis or prognosis of a cancer of a specific tissue, the markers comprise at least one, preferably at least 2, human polypeptides or polynucleotides, or human orthologs of the mouse polypeptides or polynucleotides, or homologs thereof, listed in Table 2 and Table 6. For the tissues breast, placenta/uterus, kidney, bladder, lung, brain, colon, intestine, stomach, liver, pancreas and spleen the above described polypeptides and polynucleotides are listed in Table 2 and Table 6 as follows:

For the diagnosis or prognosis of a cancer of the breast, the markers listed in Table 2 sheet 1 and Table 6, preferably in Table 6 under the heading "breast";

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For the diagnosis or prognosis of a cancer of the uterus, the markers listed in Table 2 sheet 2 and Table 6, preferably in Table 6 under the heading "placenta/uterus";

For the diagnosis or prognosis of a cancer of the kidney, the markers listed in Table 2 sheet 3 and Table 6, preferably in Table 6 under the heading "kidney";

For the diagnosis or prognosis of a cancer of the bladder, the markers listed in Table 2 sheet 4 and Table 6, preferably in Table 6 under the heading "bladder";

For the diagnosis or prognosis of a cancer of the lung, the markers listed in Table 2 sheet 5 and Table 6, preferably in Table 6 under the heading "lung";

For the diagnosis or prognosis of a cancer of the brain, the markers listed in Table 2 sheet 6 and Table 6, preferably in Table 6 under the heading "brain";

For the diagnosis or prognosis of a cancer of the colon, the markers listed in Table 2 sheet 7 and Table 6, preferably in Table 6 under the heading "colon";

For the diagnosis or prognosis of a cancer of the intestine, the markers listed in Table 2 sheet 8 and Table 6, preferably in Table 6 under the heading "intestine";

For the diagnosis or prognosis of a cancer of the stomach, the markers listed in Table 2 sheet 9 and Table 6, preferably in Table 6 under the heading "stomach";

For the diagnosis or prognosis of a cancer of the liver, the markers listed in Table 2 sheet 10 and Table 6, preferably in Table 6 under the heading "liver";

For the diagnosis or prognosis of a cancer of the pancreas, the markers listed in Table 2 sheet 11 and Table 6, preferably in Table 6 under the heading "pancreas";

For the diagnosis or prognosis of a cancer of the spleen, the markers listed in Table 2 sheet 12 and Table 6, preferably in Table 6 under the heading "spleen."

The invention further comprises a method of identifying a diagnostic marker for a cancer comprising:

(a) obtaining a first cell from a first cell type of said cancer, said cell comprising a defective tumor suppressor expression;

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(b) obtaining a second cell of the first cell type, wherein said second cell comprises a wild-type tumor suppressor expression;

(c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and

5 (d) selecting at least one gene of step (c) as a diagnostic marker for a cancer.

In a related aspect, the invention further comprises a method of identifying a tissue-specific diagnostic marker for a cancer comprising a) obtaining a first cell from a second cell type of the cancer, the cell comprising a defective tumor  
10 suppressor expression; b) obtaining a second cell of the second cell type, wherein the second cell comprises a wild-type tumor suppressor expression; c) identifying genes having an increased level of expression in the first cell of the second cell type as compared to the second cell of the second cell type; d) comparing the genes having an increased expression in the first cell type with the genes having an increased  
15 expression in the second cell type; e) identifying genes having an increased expression in the first cell type but not in the second cell type; and f) selecting at least one gene of step (e) as a diagnostic marker of a cancer of the first cell type.

The identification step of both methods (steps (c) or e) above, respectively) may be performed using a microarray; in addition, the tumor suppressor  
20 in question may be p53, Rb1 and PTEN as well as any other tumor suppressor gene deemed suitable. A list of possible tumor suppressor genes is provided herein.

In certain embodiments, the diagnostic marker is a secreted product of the first cell type. In certain embodiments, the selected gene is not expressed in other tissue irrespective of its status. In other embodiments, the diagnostic marker is a  
25 membrane bound marker that localizes to the cell membrane of the first cell type. In specific embodiments, the tumor suppressor is selected from the group consisting of p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1.

30 An additional embodiment of the invention concerns a method for screening for compounds that modulate the activity of a tumor suppressor gene comprising: a) obtaining a cell comprising a defective tumor suppressor expression;



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- b) measuring the level of expression of a marker of Table 5 or 6 in the cell; c) contacting the cell with a test compound; and d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after the contacting step as compared to the level of expression before the contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.

The tumor suppressor in question may be selected from the tumor suppressor group consisting of, *inter alia*, p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1. The test compound may be a small chemical molecule. The measuring of steps b) and d) may comprise monitoring the level of mRNA of the marker or the level of the polypeptide of the marker, according to methods well known in the art and described herein. In addition, the change in the level of expression in step d) may be a reduction in the level of expression, in which case compounds identified according to said method may be employed in the treatment of cancer, possibly as anti-cancer drugs.

The term "small chemical molecule" is used interchangeably with "chemical compound", and is understood to refer to chemical moieties of any particular type which are not necessarily, but may be, naturally occurring and typically have a molecular weight of less than 2000 daltons, more preferably less than 1000 daltons.

Another aspect of the invention provides a microarray composition for measuring tissue-specific gene expression comprising at least 4 polynucleotides from tables 5 and 6. The invention further contemplates a method of diagnosing a cancer comprising contacting a cell sample nucleic acid with a microarray described herein under conditions suitable for hybridization; providing hybridization conditions suitable for hybrid formation between said cell sample nucleic acid and a polynucleotide of said microarray; detecting said hybridization; and diagnosing a cancer based on the results of detecting said hybridization.

Further in this aspect, an antibody microarray is provided. Said microarray comprises at least 4 antibodies directed against polypeptides corresponding to the polynucleotides given in Tables 5 and 6. The invention further

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contemplates a method of diagnosing a cancer comprising contacting a bodily fluid sample with the antibody microarray described herein, and detecting hybridization between the antibodies present on the array and at least one polypeptide present in the bodily fluid, the results of said detection enabling a diagnosis or a prognosis of a cancer.

The invention further contemplates a vector comprising a polynucleotide having a sequence of a tissue specific tumor marker identified according to the invention. Also contemplated is a cell transformed or transfected with such a vector.

Another aspect of the invention is directed to a method of treating cancer in a patient, wherein said treatment is effected through the decrease in expression of a tumor marker gene. In preferred embodiments, a polynucleotide is administered to cancer cells of a patient. The polynucleotide comprises an antisense sequence of said tissue-specific tumor marker in those embodiments where the tissue-specific tumor marker is up-regulated as a result of loss of function of the tumor suppressor, whereas the polynucleotide comprises a sense coding sequence of said tissue-specific tumor marker in those embodiments where the tissue specific marker is down-regulated as a result of loss of function of the tumor suppressor. In specific embodiments, the cancer cells of the patient harbor a mutant tumor suppressor gene selected from the group consisting of p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1.

By "homolog/homology", as related to polynucleotides and polypeptides and used herein, is meant at least about 70%, preferably at least about 75% homology, advantageously at least about 80% homology, more advantageously at least about 90% homology, even more advantageously at least about 95%, e.g., at least about 97%, about 98%, about 99% or even about 100% homology. The invention also comprehends that these polynucleotides and polypeptides can be used in the same fashion as the herein or aforementioned polynucleotides and polypeptides.

Alternatively or additionally, "homology", with respect to sequences, can refer to the number of positions with identical nucleotides or amino acid residues, divided by the number of nucleotides or amino acid residues in the shorter of the two sequences, wherein alignment of the two sequences can be determined in accordance

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with the Wilbur and Lipman algorithm ((1983) Proc. Natl. Acad. Sci. USA 80:726), for instance, using a window size of 20 nucleotides, a word length of 4 nucleotides, and a gap penalty of 4, and computer-assisted analysis and interpretation of the sequence data, including alignment can be conveniently performed using  
5 commercially available programs (e.g., Intelligenetics™ Suite, Intelligenetics Inc., CA). When RNA sequences are said to be similar, or to have a degree of sequence identity or homology with DNA sequences, thymidine (T) in the DNA sequence is considered equal to uracil (U) in the RNA sequence. RNA sequences within the scope of the invention can be derived from DNA sequences or their complements, by  
10 substituting thymidine (T) in the DNA sequence with uracil (U).

Additionally or alternatively, amino acid sequence similarity or homology can be determined, for instance, using the BlastP program (Altschul *et al.*, Nucl. Acids Res. 25:3389-3402) and available at NCBI. The following references provide algorithms for comparing the relative identity or homology of amino acid  
15 residues of two polypeptides, and additionally, or alternatively, with respect to the foregoing, the teachings in these references can be used for determining percent homology: Smith *et al.*, (1981) Adv. Appl. Math. 2:482-489; Smith *et al.*, (1983) Nucl. Acids Res. 11:2205-2220; Devereux *et al.*, (1984) Nucl. Acids Res. 12:387-395; Feng *et al.*, (1987) J. Molec. Evol. 25:351-360; Higgins *et al.*, (1989) CABIOS  
20 5:151-153; and Thompson *et al.*, (1994) Nucl. Acids Res. 22:4673-4680.

The term “polynucleotide” refers to any molecule which comprises two or more of the bases guanine, cytosine, thymine, adenine, uracil or inosine, inter alia, or chemical analogs thereof, includes “oligonucleotides” and encompasses  
25 “nucleic acids”. Preferably, a polynucleotide has from about 75 to 10,000 nucleotides, more preferably from about 100 to 3,500 nucleotides. An oligonucleotide refers generally to a chain of nucleotides extending from 2-75 nucleotides.

By the term “polypeptide” is meant a molecule composed of amino acids and the term includes peptides, polypeptides, proteins and peptidomimetics; dominant polypeptide fragments are also considered to be polypeptides.

30 The term “amino acid” refers to any one of the 20 naturally occurring amino acids, and also amino acids which have been chemically modified or synthetic amino acids.

The invention provides methods for the identification of marker gene targets for both diagnostic and therapeutic applications in any given cancer type. In

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certain embodiments, these methods use a combination of recently developed powerful functional gene cloning methodologies with cDNA array-based gene expression profiling and rationally designed experimental models. Diagnostic and therapeutic value of the identified genes may then be evaluated using specific inhibitors and antibodies according to methods well known to those of skill in the art.

By identifying those genes that are specifically upregulated (or indeed downregulated) in cancer cells as a result of tumor suppressor regulation, the invention provides markers of advanced stages of cancer. More specifically, the invention relates to identifying potential targets of tumor suppressor regulation associated with early and advanced stages of the disease by performing micro-array hybridization and analyses using model cancer cell line(s) or primary normal cell cultures that retain wild-type tumor suppressor activity and engineering a variant of such a cell line or primary cells in which the tumor suppressor is inactivated. Alternatively, the tissue pairs for comparison will be normal animal tissues and the same cancer-free tissues from genetically modified animals in which a tumor suppressor gene of interest was knocked out.

The methods of the invention generally provide a systematic approach for the search of cancer markers or targets for therapeutic intervention among the genes normally under negative control of tumor suppressor proteins. Many such genes are transcriptionally activated in tissues following the wild-type activity loss of the most common tumor suppressor genes, such as p53, PTEN, RB, and p16/p19 and this regulation is conserved in normal and tumor cells from the same origin. The methods of the invention may be performed by comparing gene expression profiles in the isogenic pairs of cell lines or tissues differing in their tumor suppressor gene status or tissue pairs derived from normal and genetically modified mice, with inactivated tumor suppressors, i.e. p53 <sup>-/-</sup> mice, p16/p19 <sup>-/-</sup> mice, and mice with targeted expression of, e.g., SV40 large T antigen that simultaneously inactivates both RB and p53 function (TRAMP mice).

In an exemplary model for the invention, the inventors created an isogenic pair of LNCaP prostate tumor cell lines differing in their p53 status and applied cDNA microarray analysis to identify differentially expressed genes. These investigations revealed that the baseline expression of several known tumor markers is significantly elevated in LNCaP cells that lack functional p53 protein compared to the same cells that express wt p53. These genes include e.g., COX2, tumor-specific

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heparin-binding growth factor midkine (which possesses angiogenic and anti-apoptotic properties) (Ikematsu *et al.*, *Br J Cancer*, 83(6):701-706 (2000), tumor tissue associated hyaluronan receptor CD44 and PSA (prostate specific antigen). COX2 inhibitors are currently in clinical trials against prostate cancer. Midkine was immunohistochemically shown to be expressed in 86.3% of prostate cancer specimens examined, with metastatic lesions generally showing higher expression than the corresponding primaries; normal prostate tissues were negative or showed only weak staining. Midkine was also detected in 12 of 15 latent cancers (80%) and in 12 of 16 cases of PIN (75%) (Konishi *et al.*, *Oncology*; 57(3):253-257 (1999).

PSA is the major prostate cancer diagnostic marker currently used commercially. In the invention, it was shown that the PSA promoter is directly suppressed by wt p53, thus PSA up-regulation in prostate cancer is indicative of the loss of wt p53 function. The list of genes the expression of which was changed following wt p53 suppression in LNCaP cells is attached in Table 1. Having determined that it is thus possible to identify the differential expression of genes that are regulated by suppression of the wild-type tumor suppressor, the inventors further demonstrate large-scale microarray-based comparison of gene-expression profiles in the tissue pairs derived from normal and p53-/- mice.

Poly A RNA was extracted from spleen, pancreas, liver, stomach, intestine, colon, lung, brain, bladder, kidney, placenta/uterus and mammary glands of normal and p53-deficient mice and used for fluorescently-labeled probes for microarray hybridizations. The differential (against common control) gene expression levels were normalized between p53-/- tissues and their corresponding normal counterparts. (Table 2). These data were then sorted according to their expression levels in one particular tissue from maximally up-regulated genes to maximally down-regulated genes, thereby identifying genes with maximal differential tissue-specific expression in p53-deficient mice.

Of the identified genes, the tumor makers will be those that are found to be up-regulated in p53-/-tissues. Table 3 lists such genes; the table combines the p53-dependent differential expression data with the tissue specificity of gene expression data. Differential expression of the genes may be determined using any technique well known to those of skill in the art. Such techniques include determining differential expression using cDNA or oligonucleotide microarrays as described herein below, as well as differential display techniques well known to those

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of skill in the art. Gene subtraction techniques also may be used. Also contemplated for determining differential expression of genes is SAGE (Velculescu *et al.*, *Science*, 270:484-487 (1995); Zhang *et al.*, *Science*, 276:1268-1272 (1997).

For effective selection of cancer diagnostic markers, the following  
5 criteria were applied:

(1) genes that are up-regulated in a certain p53-/- tissue and are normally expressed predominantly in that tissue are useful for diagnosis both in tissues and in bodily fluids. Table 5 is derived from Table 3 and contains a list of the preferred genes which can serve as markers of this type (the highlighted genes are  
10 highly preferred).

(2) genes that are normally expressed at certain levels in one or several tissues but are up-regulated in one or numerous p53-/- tissues as compared to the same tissue having normal p53 status are useful for diagnosis primarily in tissues. Table 6 is derived from Table 2 and contains a list of the preferred markers of this  
15 type, sorted according to the tissue in which they are preferred for diagnosis. Both tables are prioritized, so that, for example, under the heading "pancreas" in Table 6 or in sheet 11 of Table 2, the first marker listed, pancreatitis associated protein, is the most preferred marker for pancreatic cancer.

Table 3 contains 445 genes identified as being up-regulated in p53-/-  
20 tissues, which can serve as tissue specific cancer markers and for bodily-fluid cancer diagnosis, depending on their level of expression in normal tissues, which tissues they are normally expressed in, and whether they are secreted.

The genes identified according to the invention will prove useful in diagnostic and prognostic application as well as act as drug targets for therapeutic  
25 intervention of the diseased state. Negative regulation by tumor suppressor genes and tissue specificity of expression are two essential characteristics of prospective tumor markers/drug targets. However, in order to be suitable for diagnostic assays, the gene products ideally, but not necessarily, also need to be secreted into blood, urine, saliva or any other accessible body fluids for detection. Alternatively, the gene products are  
30 such that they are expressed at the cell surface and are therefore amenable to detection using ordinary techniques known to those of skill in the art, *e.g.*, detection of cell surface expression of the gene products using antibodies or ligand/receptor interactions. Membrane-bound and cytosolic RNA may be distinguished based on the fact that mRNA of genes, encoding secreted or membrane proteins is bound to

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membrane-associated polysomes and may be separated from other mRNAs by sedimentation equilibrium or sedimentation velocity (Diehn *et al.*, *Nat. Genet.*, 25:58-62, 2000). RNA from membrane or cytosolic fraction of cells will be isolated using standard protocol and used for synthesis of fluorescently labeled probe from  
5 each fraction. Isolation of membrane-bound polysomes from cell lines preferably is carried out according to published protocol (Diehn *et al.*, *Nat. Genet.*, 25:58-62 (2000). See also U.S. Patent No. 6,403,316.

In summary, the inventors defined genes characterized in regard to tissue-specificity of the normal expression of these genes and induction/reduction in  
10 various p53-deficient tissues. The above-articulated method, while exemplified in terms of p53 regulation, may be performed with any tumor suppressor known to those of skill in the art to identify tissue-specific markers of cancers. In addition to p53, tumor suppressors such as Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2;  
15 PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL; WT1, are exemplary tumor suppressors that may be employed to identify tissue-specific tumor marker genes according to the invention. This is by no means an exhaustive list and those of skill in the art will be aware of other tumor suppressors that may be used in the methods herein. Those of skill in the art will readily be able to obtain the  
20 sequences for these tumor suppressor genes from Genbank.

### **I. Diagnostic Methods of Using Identified Markers**

In the genetic diagnostic applications of the invention, one of skill in  
25 the art would detect variations in the expression of one or more of the tissue-specific tumor markers. This may comprise determining the mRNA level of the gene(s) or determining specific alterations in the expressed gene product(s). The cancers that may be diagnosed according to the invention include cancers of the brain (glioblastomas, medulloblastoma, astrocytoma, oligodendroglioma, ependymomas),  
30 lung, liver, spleen, kidney, pancreas, intestine, blood cells, lymph node, colon, breast, endometrium, stomach, prostate, testicle, ovary, skin, head or neck, esophagus, bone marrow, blood or other tissue.

The biological sample can be any tissue or fluid. Various embodiments include cells of the skin, muscle, fascia, brain, prostate, breast, endometrium, lung,

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head or neck, pancreas, small intestine, blood cells, liver, testes, ovaries, colon, skin, stomach, esophagus, spleen, lymph node, bone marrow or kidney. Other embodiments include fluid samples such as peripheral blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool or urine.

Nucleic acids can be isolated from cells contained in the biological sample, according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be whole RNA. It may be used for Northern blotting analysis or may be converted to a complementary DNA (cDNA). In one embodiment, the RNA is whole cell RNA; in another, it is poly-A RNA. cDNA may be used for preparation of probes for microarray hybridization or may be amplified in PCR reaction (RT-PCR).

In situ hybridization using a labeled nucleic acid probe is performed essentially as known in the art and incorporated herein by reference.

Depending on the format, the specific nucleic acid of interest is identified in the sample directly using amplification or by hybridization to a labeled (radioactively or fluorescently) nucleic acid probe. Next, the identified amplified product is detected. In certain applications, the detection may be performed by visual means (e.g., ethidium bromide staining of a gel). Alternatively, the detection may involve indirect identification of the product via chemiluminescence, radioactive scintigraphy of radiolabel or fluorescent label or even via a system using electrical or thermal impulse signals (Affymax Technology; Bellus, 1994).

#### A. Microarray Analyses

In certain preferred embodiments, DNA-based arrays provide a convenient way to explore the expression of a single polymorphic gene or a large number of genes for a variety of applications. The tissue-specific tumor marker nucleic acids identified by the invention may be presented in a DNA microarray for the analysis and expression of these genes in various cancer cell types. Microarray chips are well known to those of skill in the art (see, e.g., U.S. Patent Nos. 6,308,170; 6,183,698; 6,306,643; 6,297,018; 6,287,850; 6,291,183, each incorporated herein by reference). These are exemplary patents that disclose nucleic acid microarrays and those of skill in the art are aware of numerous other methods and compositions for producing microarrays.



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In addition, protein and antibody microarrays are well known in the art (see, for example: Ekins R.P., *J Pharm Biomed Anal* 1989. 7: 155; Ekins R.P. and Chu F.W., *Clin Chem* 1991. 37: 1955; Ekins R.P. and Chu F.W., *Trends in Biotechnology*, 1999, 17, 217-218). Antibody microarrays directed against a combination of the diagnostic markers disclosed herein will be very useful for the diagnosis of cancer markers in bodily fluids.

The invention provides for a composition comprising a plurality of polynucleotides identified according to the methods of the invention. As used herein, the term "polynucleotide probe" refers to any nucleic acid sequences identified according to the invention as a marker for a given cancer. Preferably, the polynucleotide fragment is at least 9 nucleotides; more preferably, it is at least 20 nucleotides. Such a composition can be employed for the diagnosis and treatment of neoplastic disorder.

The composition is particularly useful as hybridizable array elements in a microarray for monitoring the expression of a plurality of target polynucleotides. The microarray comprises a substrate and the hybridizable array elements. The microarray is used, for example, in the diagnosis and treatment of a cancer.

The term "microarray" refers to an ordered arrangement of hybridizable array elements. The array elements are arranged so that there are preferably at least two or more different array elements, more preferably at least 100 array elements, and most preferably at least 1,000 array elements, on a 1 cm<sup>2</sup> substrate surface. The hybridization signal from each of the array elements is individually distinguishable. In a preferred embodiment, the array elements comprise polynucleotide probes. In another preferred embodiment, the array elements comprise antibodies.

The term "probe" refers to a polynucleotide sequence capable of hybridizing with a target sequence to form a polynucleotide probe/target complex. A "target polynucleotide" refers to a chain of nucleotides to which a polynucleotide probe can hybridize by base pairing. In some instances, the sequences will be complementary (no mismatches) when aligned. In other instances, there may be up to a 10% mismatch.

Alternatively, the term "probe" may refer to a polypeptide probe that can hybridize to an antibody.

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A “plurality” refers preferably to a group of at least 15 or more members, more preferably to a group of at least about 100, and even more preferably to a group of at least about 1,000, members. The maximum number of members is unlimited, but is at least about 100,000 members.

5           The term “gene” or “genes” refers to a polynucleotide sequence(s) of a gene, which may be the partial or complete sequence of the gene and may comprise regulatory region(s), untranslated region(s), or coding regions.

          The polynucleotide or antibody microarray can be used for large-scale genetic or gene expression analysis of a large number of target polynucleotides or  
10   polypeptides respectively. The microarray can also be used in the diagnosis of diseases and in the monitoring of treatments. Further, the microarray can be employed to investigate an individual’s predisposition to a disease. Furthermore, the microarray can be employed to investigate cellular responses to infection, drug treatment, and the like.

15           When the composition of the invention is employed as hybridizable array elements in a microarray, the array elements are organized in an ordered fashion so that each element is present at a distinguishable, and preferably specified, location on the substrate. In the preferred embodiments, because the array elements are at specified locations on the substrate, the hybridization patterns and intensities (which  
20   together create a unique expression profile) can be interpreted in terms of expression levels of particular genes and can be correlated with a particular disease or condition or treatment.

          The composition comprising a plurality of polynucleotide probes can also be used to purify a subpopulation of mRNAs, cDNAs, genomic fragments and  
25   the like, in a sample. Typically, samples will include target polynucleotides of interest and other nucleic acids which may enhance the hybridization background; therefore, it may be advantageous to remove these nucleic acids from the sample. One method for removing the additional nucleic acids is by hybridizing the sample containing target polynucleotides with immobilized polynucleotide probes under hybridizing  
30   conditions. Those nucleic acids that do not hybridize to the polynucleotide probes are removed and may be subjected to analysis or discarded. At a later point, the immobilized target polynucleotide probes can be released in the form of purified target polynucleotides.

#### 1.     **Microarray Production**

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The nucleic acid probes can be genomic DNA or cDNA or mRNA, or any RNA-like or DNA-like material, such as peptide nucleic acids, branched DNAs, and the like. The probes can be sense or antisense polynucleotide probes. Where target polynucleotides are double-stranded, the probes may be either sense or antisense strands. Where the target polynucleotides are single-stranded, the probes are complementary single strands.

In one embodiment, the probes are cDNAs. The size of the DNA sequence of interest may vary and is preferably from 100 to 10,000 nucleotides, more preferably from 150 to 3,500 nucleotides.

The probes can be prepared by a variety of synthetic or enzymatic schemes, which are well known in the art. The probes can be synthesized, in whole or in part, using chemical methods well known in the art (Caruthers *et al.*, *Nucleic Acids Res., Symp. Ser.*, 215-233 (1980). Alternatively, the probes can be generated, in whole or in part, enzymatically.

Nucleotide analogs can be incorporated into the probes by methods well known in the art. The only requirement is that the incorporated nucleotide analog must serve to base pair with target polynucleotide sequences. For example, certain guanine nucleotides can be substituted with hypoxanthine, which base pairs with cytosine residues. However, these base pairs are less stable than those between guanine and cytosine. Alternatively, adenine nucleotides can be substituted with 2,6-diaminopurine, which can form stronger base pairs than those between adenine and thymidine.

Additionally, the probes can include nucleotides that have been derivatized chemically or enzymatically. Typical chemical modifications include derivatization with acyl, alkyl, aryl or amino groups.

The polynucleotide probes can be immobilized on a substrate. Preferred substrates are any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which the polynucleotide probes are bound. Preferably, the substrates are optically transparent.

Complementary DNA (cDNA) can be arranged and then immobilized on a substrate. The probes can be immobilized by covalent means such as by chemical bonding procedures or UV. In one such method, a cDNA is bound to a glass surface

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which has been modified to contain epoxide or aldehyde groups. In another case, a cDNA probe is placed on a polylysine coated surface and then UV cross-linked (Shalon *et al.*, PCT publication WO95/35505, herein incorporated by reference). In yet another method, a DNA is actively transported from a solution to a given position  
5 on a substrate by electrical means (Heller *et al.*, U.S. Pat. No. 5,605,662). Alternatively, individual DNA clones can be gridded on a filter. Cells are lysed, proteins and cellular components degraded, and the DNA coupled to the filter by UV cross-linking.

Furthermore, the probes do not have to be directly bound to the  
10 substrate, but rather can be bound to the substrate through a linker group. The linker groups are typically about 6 to 50 atoms long to provide exposure to the attached probe. Preferred linker groups include ethylene glycol oligomers, diamines, diacids and the like. Reactive groups on the substrate surface react with one of the terminal portions of the linker to bind the linker to the substrate. The other terminal portion of  
15 the linker is then functionalized for binding the probe.

The probes can be attached to a substrate by dispensing reagents for probe synthesis on the substrate surface or by dispensing preformed DNA fragments or clones on the substrate surface. Typical dispensers include a micropipette delivering solution to the substrate with a robotic system to control the position of the  
20 micropipette with respect to the substrate. There can be a multiplicity of dispensers so that reagents can be delivered to the reaction regions simultaneously.

Alternatively, as mentioned above, antibody microarrays can be produced. The production of such microarrays is essentially as described in Schweitzer & Kingsmore, "Measuring proteins on microarrays", *Curr Opin*  
25 *Biotechnol* 2002; 13(1): 14-9; Avseenko *et al.*, "Immobilization of proteins in immunochemical microarrays fabricated by electrospray deposition", *Anal Chem* 2001 15; 73(24): 6047-52; Huang, "Detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13. In general, protein microarrays may be produced essentially as described in Schena *et*  
30 *al.*, Parallel human genome analysis: Microarray-based expression monitoring of 1000 genes. *Proc. Natl. Sci. USA* (1996) 93, 10614-10619; U.S. Patent Nos. 6,291,170 and 5,807,522 (see above); US patent No. 6,037,186 (Stimpson, inventor) "Parallel production of high density arrays"; PCT publications WO 99/13313 (Genovations Inc [US], applicant) "Method of making high density arrays"; WO 02/05945 (Max-

Delbruck-center for molecular medicine [Germany], applicant) "Method for producing microarray chips with nucleic acids, proteins or other test substrates".

## 2. Sample Preparation for Genetic Analysis

In order to conduct sample analysis, a sample containing target  
5 polynucleotides or polypeptides is provided. The samples can be any sample containing target polynucleotides or polypeptides and obtained from any bodily fluid (blood, sperm, urine, saliva, phlegm, gastric juices, etc. as described herein), cultured cells, biopsies, or other tissue preparations. The samples being analyzed using the microarrays will likely be samples from individuals suspected of suffering from a  
10 given cancer. In one embodiment, the microarrays used are those that contain tumor markers specific for that cancer or antibodies against those markers.

DNA or RNA can be isolated from the sample according to any of a number of methods well known to those of skill in the art. For example, methods of purification of nucleic acids are described in Tijssen Laboratory Techniques in  
15 Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, Elsevier, New York N.Y. 1993. In one case, total RNA is isolated using the TRIZOL reagent (Life Technologies, Gaithersburg Md.), and mRNA is isolated using oligo d(T) column chromatography or glass beads. Alternatively, when target polynucleotides are derived from an mRNA, the target  
20 polynucleotides can be a cDNA reverse-transcribed from an mRNA, an RNA transcribed from that cDNA, a DNA amplified from that cDNA, an RNA transcribed from the amplified DNA, and the like. When the target polynucleotide is derived from DNA, the target polynucleotide can be DNA amplified from DNA or RNA reverse transcribed from DNA. In yet another alternative, the targets are target  
25 polynucleotides prepared by more than one method.

When target polynucleotides are amplified, it is desirable to amplify the nucleic acid sample and maintain the relative abundances of the original sample, including low abundance transcripts. Total mRNA can be amplified by reverse transcription using a reverse transcriptase and a primer consisting of oligo d(T) and a  
30 sequence encoding the phage T7 promoter to provide a single-stranded DNA template. The second DNA strand is polymerized using a DNA polymerase and a RNase which assists in breaking up the DNA/RNA hybrid. After synthesis of the double-stranded DNA, T7 RNA polymerase can be added, and RNA transcribed from

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the second DNA strand template (Van Gelder *et al.* U.S. Pat. No. 5,545,522). RNA can be amplified *in vitro*, *in situ* or *in vivo* (See Eberwine, U.S. Pat. No. 5,514,545).

Quantitation controls may be included within the sample to assure that amplification and labeling procedures do not change the true distribution of target polynucleotides in a sample. For this purpose, a sample is spiked with a known amount of a control target polynucleotide and the composition of probes includes reference probes which specifically hybridize with the control target polynucleotides. After hybridization and processing, the hybridization signals obtained should accurately the amounts of control target polynucleotide added to the sample.

Prior to hybridization, it may be desirable to fragment the nucleic acid target polynucleotides. Fragmentation improves hybridization by minimizing secondary structure and cross-hybridization to other nucleic acid target polynucleotides in the sample or noncomplementary polynucleotide probes. Fragmentation can be performed by mechanical or chemical means.

Antibodies against the relevant cancer marker polypeptides and appropriate for attachment to an antibody microarray can be prepared according to methods known in the art (Coligan et al, Unit 9, Current Protocols in Immunology, Wiley Interscience, 1994; Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1988). Additional information regarding all types of antibodies, including humanized antibodies, human antibodies and antibody fragments can be found in WO 01/05998).

Polypeptides can be prepared for hybridization to an antibody microarray from a sample, such as a bodily fluid sample, according to methods known in the art . It may be desirable to purify the proteins from the sample or alternatively, to remove certain impurities which may be present in the sample and interfere with hybridization. Protein purification is practiced as is known in the art as described in, for example, Marshak et al., "Strategies for Protein Purification and Characterization. A laboratory course manual." CSHL Press (1996).

The target polynucleotides or polypeptides may be labeled with one or more labeling moieties to allow for detection of hybridized probe/target complexes. The labeling moieties can include compositions that can be detected by spectroscopic, photochemical, biochemical, bioelectronic, immunochemical, electrical, optical or chemical means. The labeling moieties include radioisotopes, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$  or  $^{35}\text{S}$ , chemiluminescent compounds, labeled binding proteins, heavy metal atoms,

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spectroscopic markers, such as fluorescent markers and dyes, magnetic labels, linked enzymes, mass spectrometry tags, spin labels, electron transfer donors and acceptors, and the like.

Exemplary dyes include quinoline dyes, triarylmethane dyes, phthaleins, azo dyes, cyanine dyes, and the like. Preferably, fluorescent markers absorb light above about 300 nm, preferably above 400 nm, and usually emit light at wavelengths at least greater than 10 nm above the wavelength of the light absorbed. Preferred fluorescent markers include fluorescein, phycoerythrin, rhodamine, lissamine, and C3 and C5 available from Amersham Pharmacia Biotech (Piscataway N.J.).

Nucleic acid labeling can be carried out during an amplification reaction, such as polymerase chain reactions and *in vitro* transcription reactions, or by nick translation or 5' or 3'-end-labeling reactions. When the label may be incorporated after or without an amplification step, the label is incorporated by using terminal transferase or by phosphorylating the 5' end of the target polynucleotide using, e.g., a kinase and then incubating overnight with a labeled oligonucleotide in the presence of T4 RNA ligase. Alternatively, the labeling moiety can be incorporated after hybridization once a probe/target complex has formed.

Polypeptide labeling can be conducted using a variety of techniques well known in the art, and the choice of the technique(s) can be tailored to the polypeptide in question according to criteria known to one of skill in the art. Specifically, polypeptides can be fluorescently labeled with compounds such as FITC or rhodamin, essentially as described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York (1988), in particular pages 353-356, or with other fluorescent compounds such as Nile red or 2-methoxy-2,4-diphenyl-3(2H)furanone (Daban: *Electrophoresis* 2001; 22(5): 874-80). Polypeptides can also be labeled with a detectable protein such as GFP (detection based on fluorescence) or the vitamin biotin (detection with streptavidin). Polypeptides can also be radioactively labeled with the isotope S<sup>35</sup>. Additional methods are widely known in the art.

### 3. Use of Gene Sequences for Diagnostic Purposes

In certain embodiments, the tissue-specific tumor markers identified herein may be used for the diagnosis of advanced stages of cancer in the given tissue for which the markers are specific. The polynucleotide sequences encoding the tissue specific tumor marker or the polypeptide encoded thereby, where appropriate, may be

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used in in-situ hybridization or RT-PCR assays of fluids or tissues from biopsies to detect abnormal gene expression. Such methods may be qualitative or quantitative in nature and may include Southern or Northern analysis, dot blot or other membrane-based technologies; PCR technologies; chip based technologies (for  
5 nucleic acid detection) and dip stick, pin, ELISA and protein-chip technologies (for the detection of polypeptides). All of these techniques are well known in the art and are the basis of many commercially available diagnostic kits.

In addition, such assays may be useful in evaluating the efficacy of a particular therapeutic treatment regime in animal studies, in clinical trials, or in  
10 monitoring the treatment of an individual patient. Such monitoring may generally employ a combination of body fluids or cell extracts taken from normal subjects, either animal or human, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained for normal subjects with a dilution series of a tissue-specific tumor marker gene product  
15 run in the same experiment where a known amount of purified gene product is used. Standard values obtained from normal samples may be compared with values obtained from samples from cachectic subjects affected by abnormal gene expression in tumor cells. Deviation between standard and subject values establishes the presence of disease.

20 Generally, the tissue-specific tumor markers are chosen based on the specificity of their expression in tumors as well as on the high correlation of the reactivity of corresponding antibodies with tumor specimens in ELISA and tissue arrays may be used for development of serological screening procedure. For example, in the context of prostate-specific tumor markers, a large scale analysis of serum and  
25 sperm samples obtained from normal donors of different age (before and after 60), patients with different grades and types of prostate carcinoma, androgen dependent and androgen independent, with local, recurrent and metastatic disease, patients with tumors of other than prostate origin, as well as patients with noncancerous diseases of prostate may be tested by ELISA on the presence and concentration of the potential  
30 candidate polypeptide(s). Then statistical analyses may be performed to evaluate whether the prostate samples express candidate(s) at different levels based on different parameters (histopathological type, Gleason score, tumor size, disease or PSA recurrence).



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Once disease is established, a therapeutic agent is administered; and a treatment profile is generated. Such assays may be repeated on a regular basis to evaluate whether the values in the profile progress toward or return to the normal or standard pattern. Successive treatment profiles may be used to show the efficacy of treatment over a period of several days or several months.

PCR as described in U.S. Patent Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides specific for the tissue-specific tumor marker genes. Such oligomers are generally chemically synthesized, but they may be generated enzymatically or produced from a recombinant source as described herein above. Oligomers generally comprise two nucleotide sequences, one with sense orientation and one with antisense orientation, employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences. Methods of performing RT-PCR are standard in the art and the method may be carried out using commercially available kits.

Additionally, methods to quantitate the expression of a particular molecule include radiolabeling (Melby *et al.*, *J Immunol Methods*, 159: 235-244 (1993) or biotinylating (Duplaa *et al.*, *Anal Biochem*, 229-236 (1993) nucleotides, coamplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated. Quantitation of multiple samples may be speeded up by running the assay in an ELISA-like format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation. For example, the presence of abnormal levels of a tissue-specific tumor marker in extracts of biopsied tissues will be indicative of the onset of a cancer. A definitive diagnosis of this type may allow health professionals to begin aggressive treatment and prevent further worsening of the condition. Similarly, further assays can be used to monitor the progress of a patient during treatment.

#### **4. Hybridization and Detection in Microarrays**

Hybridization causes a denatured probe and a denatured complementary target to form a stable nucleic acid duplex through base pairing. Hybridization methods are well known to those skilled in the art (See, e.g., Ausubel, *Short Protocols in Molecular Biology*, John Wiley & Sons, New York N.Y., units 2.8-2.11, 3.18-3.19 and 4-6-4.9, 1997). Conditions can be selected for hybridization

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where an exactly complementary target and probes can hybridize, i.e., each base pair must interact with its complementary base pair. Alternatively, conditions can be selected where a target and probes have mismatches but are still able to hybridize. Suitable conditions can be selected, for example, by varying the concentrations of salt  
5 in the prehybridization, hybridization and wash solutions, by varying the hybridization and wash temperatures, or by varying the polarity of the prehybridization, hybridization or wash solutions.

Hybridization can be performed at low stringency with buffers, such as 6 x SSPE with 0.005% Triton X-100 at 37°C, which permits hybridization between  
10 target and probes that contain some mismatches to form target polynucleotide/probe complexes. Subsequent washes are performed at higher stringency with buffers, such as 0.5 x SSPE with 0.005% Triton X-100 at 50°C, to retain hybridization of only those target/probe complexes that contain exactly complementary sequences. Alternatively, hybridization can be performed with buffers, such as 5 x SSC/0.2% SDS at 60°C and  
15 washes are performed in 2 x SSC/0.2% SDS and then in 0.1x SSC. Background signals can be reduced by the use of detergent, such as sodium dodecyl sulfate, Sarcosyl or Triton X-100, or a blocking agent, such as salmon sperm DNA.

After hybridization, the microarray is washed to remove nonhybridized nucleic acids, and complex formation between the hybridizable array elements and the  
20 target polynucleotides is detected. Methods for detecting complex formation are well known to those skilled in the art. In a preferred embodiment, the target polynucleotides are labeled with a fluorescent label, and measurement of levels and patterns of fluorescence indicative of complex formation is accomplished by fluorescence microscopy, preferably confocal fluorescence microscopy. An argon ion  
25 laser excites the fluorescent label, emissions are directed to a photomultiplier, and the amount of emitted light is detected and quantitated. The detected signal should be proportional to the amount of probe/target polynucleotide complex at each position of the microarray. The fluorescence microscope can be associated with a computer-driven scanner device to generate a quantitative two-dimensional image of  
30 hybridization intensity. The scanned image is examined to determine the abundance/expression level of each hybridized target polynucleotide.

Typically, microarray fluorescence intensities can be normalized to take into account variations in hybridization intensities when more than one microarray is used under similar test conditions. In a preferred embodiment,

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individual probe/target hybridization intensities are normalized using the intensities derived from internal normalization controls contained on each microarray.

Protein or antibody microarray hybridization is carried out essentially as described in Ekins et al. J Pharm Biomed Anal 1989. 7: 155; Ekins and Chu, Clin Chem 1991. 37: 1955; Ekins and Chu, Trends in Biotechnology, 1999, 17, 217-218; 5 MacBeath and Schreiber, Science 2000; 289(5485): p. 1760-1763.

## 5. Microarray Expression Profiles

This section describes an expression profile using the polynucleotides of the invention. The expression profile can be used to detect changes in the 10 expression of genes implicated in disease.

The expression profile includes a plurality of detectable complexes. Each complex is formed by hybridization of one or more polynucleotides of the invention to one or more complementary target polynucleotides. At least one of the polynucleotides of the invention, and preferably a plurality thereof, is hybridized to a 15 complementary target polynucleotide forming at least one, and preferably a plurality, of complexes. A complex is detected by incorporating at least one labeling moiety in the complex as described above. The expression profiles provide "snapshots" that can show unique expression patterns that are characteristic of the presence or absence of a disease or condition.

20 After performing hybridization experiments and interpreting detected signals from a microarray, particular probes can be identified and selected based on their expression patterns. Such probe sequences can be used to clone a full-length sequence for the gene or to produce a polypeptide.

The composition comprising a plurality of probes can be used as 25 hybridizable elements in a microarray. Such a microarray can be employed in several applications including diagnostics, prognostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics, pharmacogenomics, and the like.

## 6. Preferred microarrays of the invention

30 The invention provides for microarrays for measuring gene expression characteristic of a cancer of a tissue, comprising at least 4 polypeptide encoding polynucleotides or at least 4 antibodies which bind specifically to the polypeptides encoded by these polynucleotides, as listed in Table 2 and according to the following:

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A microarray for measuring gene expression characteristic of breast cancer comprising markers listed in Table 2 sheet 1; A microarray for measuring gene expression characteristic of uterine cancer comprising markers listed in Table 2 sheet 2; A microarray for measuring gene expression characteristic of kidney cancer comprising markers listed in Table 2 sheet 3; A microarray for measuring gene expression characteristic of bladder cancer comprising markers listed in Table 2 sheet 4; A microarray for measuring gene expression characteristic of lung cancer comprising markers listed in Table 2 sheet 5; A microarray for measuring gene expression characteristic of brain cancer comprising markers listed in Table 2 sheet 6; A microarray for measuring gene expression characteristic of colon cancer comprising markers listed in Table 2 sheet 7; A microarray for measuring gene expression characteristic of intestinal cancer comprising markers listed in Table 2 sheet 8; A microarray for measuring gene expression characteristic of stomach cancer comprising markers listed in Table 2 sheet 9; A microarray for measuring gene expression characteristic of liver cancer comprising markers listed in Table 2 sheet 10; A microarray for measuring gene expression characteristic of pancreatic cancer comprising markers listed in Table 2 sheet 11; and A microarray for measuring gene expression characteristic of spleen cancer comprising markers listed in Table 2 sheet 12.

20

#### **B. Immunodiagnosis and polypeptide detection**

In certain embodiments, antibodies may be used in characterizing the tissue-specific tumor marker content of healthy and diseased tissues, through techniques such as ELISAs, immunohistochemical detection and Western blotting. This may provide a screen for the presence or absence of malignancy or as a predictor of future cancer. Once the tissue-specific tumor marker is identified, one of skill in the art may produce antibodies against that marker using techniques well known to those of skill in the art

The use of such antibodies in an ELISA assay is contemplated. For example, such antibodies are immobilized onto a selected surface, preferably a surface exhibiting a protein affinity such as the wells of a polystyrene microtiter plate. After washing to remove incompletely adsorbed material, it is desirable to bind or coat the assay plate wells with a non-specific protein that is known to be antigenically

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neutral with regard to the test antisera such as bovine serum albumin (BSA), casein or solutions of powdered milk. This allows for blocking of non-specific adsorption sites on the immobilizing surface and thus reduces the background caused by non-specific binding of antigen onto the surface.

5           After binding of antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the biological sample to be tested in a manner conducive to immune complex (antigen/antibody) formation.

          Following formation of specific immunocomplexes between the test  
10   sample and the bound antibody, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for the tumor marker that differs from the first antibody. Appropriate conditions preferably include diluting the sample with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline  
15   (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from about 2 to about 4 hr, at temperatures preferably on the order of about 25°C to about 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing  
20   with a solution such as PBS/Tween, or borate buffer.

          For convenient detection purposes, the second antibody may preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the second antibody-bound surface with a urease or  
25   peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (e.g., incubation for 2 hr at room temperature in a PBS-containing solution such as PBS/Tween).

          After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified  
30   by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline)-6-sulfonic acid (ABTS) and hydrogen peroxide, in the case of peroxidase as the enzyme label. Quantitation is then achieved by measuring the degree of color generation, e.g., using a visible spectrum spectrophotometer.

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The preceding format may be altered by first binding the sample to the assay plate. Then, primary antibody is incubated with the assay plate, followed by detecting of bound primary antibody using a labeled second antibody with specificity for the primary antibody.

5           Immunoblotting and immunohistochemical techniques using antibodies directed against the tumor markers also are contemplated by the invention. The antibodies may be used as high-affinity primary reagents for the identification of proteins immobilized onto a solid support matrix, such as nitrocellulose, nylon or combinations thereof. In conjunction with immunoprecipitation, followed by gel  
10   electrophoresis, these may be used as a single step reagent for use in detecting antigens against which secondary reagents used in the detection of the antigen cause an adverse background. Immunologically-based detection methods for use in conjunction with Western blotting include enzymatically-, radiolabel-, or fluorescently-tagged secondary antibodies against the toxin moiety are considered to  
15   be of particular use in this regard.

Flow cytometry methods also may be used in conjunction with the invention. Methods of performing flow cytometry are discussed in Zhang *et al.*, *J. Immunology*, 157:3980-3987 (1996) and Pepper *et al.*, *Leuk. Res.*, 22(5):439-444 (1998). Generally, the cells, preferably blood cells, are permeabilized to allow the  
20   antibody to enter and exit the cell. If the gene in question encodes a cell surface protein, the step of permeabilization is not needed. After permeabilization, the cells are incubated with an antibody. In preferred embodiments, the antibody is a monoclonal antibody. It is more preferred that the monoclonal antibody be labeled with a fluorescent marker. If the antibody is not labeled with a fluorescent marker, a  
25   second antibody that is immunoreactive with the first antibody and contains a fluorescent marker. After sufficient washing to ensure that excess or non-bound antibodies are removed, the cells are ready for flow cytometry. If the marker is an enzyme, the reaction monitoring its specific enzymatic activity either in situ or in body fluids may be performed.

30           Determining the level of a polypeptide in a sample for the purposes of diagnosis may also be carried out in the form of enzymatic activity testing, when the polypeptide being examined offers such an option.

In addition, whole body image analysis following injection of labeled antibodies against cell surface marker proteins is a diagnostic possibility, as described

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above; the detected concentrations of such antibodies are indicative of the sites of tumor/ metastases growth as well as their number and the tumor size.

### C. Carcinogenicity Testing

5           The tissue specific tumor marker genes identified using the methods of the invention can form the basis of a carcinogenicity test. Test agents are evaluated to see if their effects on human cells mimic the effects of loss of the tumor suppressor. Thus the agents are in essence being evaluated for the ability to induce a tumor suppressor mutation, or a mutation in another gene which is in the same regulatory  
10       pathway, or a non-genetic effect which mimics tumor suppressor loss. Test agents which are found to have at least some of the same constellation of effects as tumor suppressor loss on the regulation of the genes identified herein to be tumor suppressor-regulated, are identified as potential carcinogens. Any single gene identified can be used, as can at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100,  
15       125, or 150 or more genes identified herein.

          The invention also contemplates the use of the tissue-specific tumor markers identified herein in the screening of compounds for activity in either stimulating tumor suppressor activity, overcoming the lack of a tumor suppressor, or blocking the effect of a mutant tumor suppressor molecule. It is contemplated that any  
20       agent which decreases the expression of a tissue specific tumor marker that was up-regulated upon tumor suppressor inactivation may serve as an anti-tumor agent. Screening assays for such agents are well known to those of skill in the art. U.S. Patent No. 6,262,242 is incorporated herein by reference as providing a general teaching of such screening assays and others relating to the diagnostic and therapeutic  
25       uses of tumor related genes.

## II. Therapeutic Methods of Using Identified Markers

          The genes identified by the invention herein as down-regulated by the loss of a tumor suppressor may prove effective against a given cancer when delivered  
30       therapeutically to the cancer cells. Antisense constructs of the genes identified herein as up-regulated as a result of loss of tumor suppressor can be delivered therapeutically to cancer cells. Other therapeutic possibilities include siRNA or small molecules or antibodies inhibiting the target protein function and/or expression. The goal of such therapy is to retard the growth rate of the cancer cells. Expression of the sense

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molecules and their translation products or expression of the antisense mRNA molecules has the effect of inhibiting the growth rate of cancer cells or inducing apoptosis. Sense nucleic acid molecules are preferably delivered in constructs wherein a promoter is operatively linked to the coding sequence at the 5'-end and initiates transcription of the coding sequence. Anti-sense constructs contain a promoter operatively linked to the coding sequence at the 3'-end such that upon initiation of transcription at the promoter an RNA molecule is transcribed which is the complementary strand from the native mRNA molecule of the gene.

Delivery of nucleic acid molecules can be accomplished by many means known in the art. Gene delivery vehicles are available for delivery of polynucleotides to cells, tissue, or to a mammal for expression. For example, a polynucleotide sequence of the invention can be administered either locally or systemically in an expression construct or vector. There are a number of ways in which expression vectors may be introduced into cells. In certain embodiments of the invention, the expression construct comprises a virus or engineered construct derived from a viral genome. In other embodiments, non-viral delivery is contemplated. The ability of certain viruses to enter cells via receptor-mediated endocytosis, to integrate into host cell genomes and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, *In: Vectors: A survey of molecular cloning vectors and their uses* Rodriguez R L, Denhardt D T, eds. Stoneham: Butterworth, pp. 467-492, 1988; Nicolas *et al.*, *In: Vectors: A survey of molecular cloning vectors and their uses*, Rodriguez & Denhardt (eds.), Stoneham: Butterworth, pp. 493-513, 1988; Baichwal *et al.*, *In: Gene Transfer*, Kucherlapati ed., New York, Plenum Press, pp. 117-148, 1986; Temin, *In: Gene Transfer*, Kucherlapati (ed.), New York: Plenum Press, pp. 149-188, 1986). The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, parvovirus, paramyxovirus, parvovirus, picornavirus, poxvirus, togavirus viral vector. See generally, Jolly, *Cancer Gene Therapy* 1:51-64 (1994); Kimura, *Human Gene Therapy* 5:845-852 (1994), Connelly, *Human Gene Therapy* 6:185-193 (1995), and Kaplitt, *Nature Genetics* 6:148-153 (1994).

Several non-viral methods for the transfer of expression constructs into cultured bacterial cells are contemplated by the invention. This section provides a discussion of methods and compositions of non-viral gene transfer. DNA constructs of the invention are generally delivered to a cell and, in certain situations, the nucleic



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acid or the protein to be transferred may be transferred using non-viral methods. The non-viral methods include calcium phosphate precipitation (Graham *et al.*, *Virology*, 52:456-467, 1973; Chen *et al.*, *Mol. Cell. Biol.*, 7:2745-2752, 1987; Rippe *et al.*, *Mol. Cell Biol.*, 10:689-695, 1990) DEAE-dextran (Gopal, *Mol. Cell Biol.*, 5:1188-1190, 5 1985), electroporation (Tur-Kaspa *et al.*, *Mol. Cell Biol.*, 6:716-718, 1986; Potter *et al.*, *Proc. Nat. Acad. Sci. USA*, 81:7161-7165, 1984), direct microinjection (Harland and Weintraub, *J. Cell Biol.*, 101:1094-1099, 1985.), DNA-loaded liposomes (Nicolau and Sene, *Biochim. Biophys. Acta*, 721:185-190, 1982; Fraley *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 76:3348-3352, 1979; Felgner, *Sci Am.* 276(6):102-6, 1997; Felgner, *Hum* 10 *Gene Ther.* 7(15):1791-3, 1996), cell sonication (Fechheimer *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 84:8463-8467, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, *Proc. Natl. Acad. Sci USA*, 87:9568-9572, 1990), conjugation (Gavigan *et al.* In: *Mycobacteria Protocols*, Tanya Parish and Neil G. Stoker (eds). pp. 119-128 1998. Humana Press, Twtowa, NJ) and receptor-mediated 15 transfection (Wu *et al.*, *J. Biol. Chem.*, 262:4429-4432, 1987; Wu *et al.*, *Biochemistry*, 27:887-892, 1988; Wu *et al.*, *Adv. Drug Delivery Rev.*, 12:159-167, 1993).

The expression construct also may be entrapped in a liposome. Liposomes that can act as gene delivery vehicles are described in U.S. Pat. No. 5,422,120, PCT Patent Publication Nos. WO 95/13796, WO 94/23697, and WO 20 91/144445, and EP No. 524,968. The addition of DNA to cationic liposomes causes a topological transition from liposomes to optically birefringent liquid-crystalline condensed globules (Radler *et al.*, *Science*, 275(5301):810-4, 1997). These DNA-lipid complexes are potential non-viral vehicles for use in gene delivery.

Also contemplated in the invention are various commercial approaches 25 involving "lipofection" technology. In certain embodiments of the invention, the liposome may be complexed with a hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and to promote cell entry of liposome-encapsulated DNA (Kaneda *et al.*, *Science*, 243:375-378, 1989). In other embodiments, the liposome may be complexed or employed in conjunction with 30 nuclear nonhistone chromosomal proteins (HMG-1) (Kato *et al.*, *J. Biol. Chem.*, 266:3361-3364, 1991).

Receptor-mediated gene targeting vehicles generally consist of two components: a cell receptor-specific ligand and a DNA-binding agent. Several ligands have been used for receptor-mediated gene transfer. The most extensively

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characterized ligands are asialoorosomucoid (ASOR) (Wu *et al.*, 1987, *supra*) and transferrin (Wagner *et al.*, *Proc. Natl. Acad. Sci. USA*, 87(9):3410-3414, 1990). Recently, a synthetic neoglycoprotein, which recognizes the same receptor as ASOR, has been used as a gene delivery vehicle (Ferkol *et al.*, *FASEB J.*, 7:1081-1091, 1993; 5 Perales *et al.*, *Proc. Natl. Acad. Sci. USA*, 91:4086-4090, 1994) and epidermal growth factor (EGF) has also been used to deliver genes to squamous carcinoma cells (Myers, EPO 0273085).

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method 10 depends on the ability to accelerate DNA coated microprojectiles to a high velocity, allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, *Nature*, 327:70-73, 1987). Exemplary naked DNA introduction methods are described in PCT Patent Publication No. WO 90/11092 and U.S. Pat. No. 5,580,859. Several devices for accelerating small particles have been developed. One such 15 device relies on a high-voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:9568-9572, 1990). The microprojectiles used to date have consisted of biologically inert substances such as tungsten or gold beads.

20

### Example 1

#### Validation of the methods of the invention in LNCAP cells

The present Example demonstrates the methods of identifying tissue-specific tumor markers that are negatively regulated by a tumor suppressor. In the 25 present Example, it was demonstrated for the first time that the expression of PSA is negatively regulated by p53.

Prostate cancer, the most frequently diagnosed malignancy in men in western countries (*Cancer*, 71(Suppl.): 880-886, 1993), is often characterized by 30 elevated prostate-specific antigen (PSA) secretion that is broadly used as a blood-borne diagnostic marker of the disease. PSA is synthesized exclusively in prostate epithelia by normal, hyperplastic and malignant cells, and its levels are seen to rise several-fold above background in the blood as a result of benign prostatic

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hyperplasia. The levels of PSA in the serum of individuals at end-stage metastatic prostate carcinoma may be more than a hundred times higher than normal levels of the marker (Kim and Logothetis, *Urol. Clin. North Am.*, 26:281-290 1999; Abate-Shen and Shen, *Genes Dev.*, 14:2410-2434, 2000). Expression of the PSA gene was demonstrated to be directly regulated by binding of androgen receptor (AR) (Young *et al.*, *Cancer Res.*, 51:3748-3752 1991; Montgomery *et al.*, *Prostate*, 21:63-73, 1992; Trapman and Cleutjens, *Semin. Cancer Biol.*, 8:29-36 1997) to three androgen responsive elements (AREs) identified within the 5.8 kb PSA promoter (Schoor *et al.*, *Urology*, 162:2040-2045 1996; Cleutjens *et al.*, *Mol. Endocrinol.*, 11:148-161, 1997; Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788, 1997; Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150, 1997). However, detailed analyses of PSA promoter activity in androgen-dependent and androgen-independent prostate carcinoma cell lines indicated that the control of transcription of the PSA gene is not limited to androgen regulation (Yeung *et al.*, *J. Biol. Chem.*, 275:40846-40855 2000).

The present Example provides evidence showing the involvement of p53 tumor suppressor in regulation of PSA promoter. Micro-array hybridization and analyses were performed using LNCaP cells. This cell line originally isolated from lymph node metastases of prostate adenocarcinoma, retains wild type p53, androgen dependence and expression of a variety of prostate-specific markers, all known as properties of a relatively early stage of prostate cancer progression. Inactivation of p53 function by a dominant negative mutant in these cells imitates an important step in tumor progression and allows analysis of the genetic basis for altered tumor cell phenotype associated with p53 suppression.

A variant of LNCaP cells with inactivated p53, LN-56 (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000), was generated by transduction of retroviral construct expressing the potent dominant negative p53 mutant, GSE56 (Ossovskaya *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314, 1996). GSE56-mediated inactivation of p53 resulted in resistance to apoptosis and increased tumorigenicity of LN-56 cells (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000), suggesting that p53 is at least partially functional in LNCaP cells. Moreover, both steady-state and inducible expression level of p53-responsive gene p21/waf1 were reduced in LN-56 cells.

PSA was among the genes that showed the most pronounced differential expression in LNCaP versus LN-56 cells. PSA was expressed four times higher in LN-56 than in LNCaP cells. To determine whether differences in mRNA

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expression correlated with PSA protein expression, the amount of secreted PSA in the medium from LNCaP and LN-56 cells was determined. This revealed that the latter cells produced 6-8 times more PSA as compared to LNCaP (Figure 1). These observations suggested that expression of PSA gene is likely to be under the negative regulatory control of p53 and that elevated expression of PSA in advanced prostate cancer may be indicative for p53 suppression.

To determine whether p53 directly affects transcription from the PSA promoter, a CAT assay was performed in the LNCaP cells transfected with the reporter constructs containing the CAT gene under the control of the proximal PSA promoter (nucleotides -407 to +11) linked to the PSA enhancer element (nucleotides -5322 to -3740). This construct was previously shown to imitate the endogenous PSA gene regulation (Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788, 1997; Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150, 1997). Since PSA transcription is also known to be androgen dependent, for these studies, LNCaP cells that retain androgen dependence were used. To increase the wild type p53 activity, different amounts of wild type p53 expression plasmid were cotransfected with the PSA-reporter vector. To inhibit endogenous p53 function, cotransfection with the GSE56-expressing plasmid was employed (Ossovskaya *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314, 1996). Another reporter construct containing the CAT reporter gene under the control of p53-responsive promoter carrying the p53-binding site from p21/Waf1 gene was used to monitor the p53 activity in transfected cells.

Introduction of different amounts of wild type p53-expressing plasmid into LNCaP cells resulted in dose-dependent changes of CAT activity driven from both p21- and PSA-derived promoter elements, though in opposite directions: while the p21 promoter construct was activated, expression of the PSA reporter was suppressed by p53. When GSE56 was co-transfected with either of the reporter constructs, an inverted picture was observed (Figure 2).

Sequence analysis does not reveal any canonical p53 binding sites within or in the vicinity of the PSA promoter region and in the first intron of the PSA gene. It is noteworthy that most of the known p53-repressed genes also do not possess such sites in their promoter regions and do not necessarily require p53.

Since it has previously been shown that negative regulation of transcription by p53 may involve p53-mediated recruitment of histone deacetylases (HDAC) (Murphy *et al.*, *Genes Dev.*, 13:2490 -2501 1999), the inventors set out to

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determine whether this would be also true for the PSA promoter. Following co-transfection of PSA-CAT reporter and wild type p53-expressing plasmids, the LNCaP cells were treated with the HDAC inhibitor trichostatin A (TSA) for 24 h and the lysates of transfected cells were tested for CAT activity. These experiments demonstrated that TSA completely abrogated the p53-mediated repression of PSA promoter driven transcriptional activity. At the same time, TSA had no effect on p53-mediated transactivation as determined in a similar experiment employing the p21 promoter-driven CAT reporter construct (Figure 3). Thus, the PSA gene can be added to a growing list of genes that are negatively regulated by p53 through HDAC-mediated transcriptional repression.

Use of a potent dominant negative p53 inhibitor, GSE56, allowed the determination of the p53 dependence of PSA expression. However, this mutant form does not naturally occur in human tumors. In order to more adequately imitate events naturally occurring in the course of tumor progression, the effect of four tumor-derived p53 mutants (135Val, 141Ala, 156Pro and 175His), two of which are frequent types of p53 mutants in prostate cancer (141Ala and 175His), on expression of PSA was determined. LNCaP cells were transduced with retroviruses expressing the above p53 mutant variants and the level of PSA was measured in the medium conditioned by each type of the transduced cell populations. In parallel, the potential suppressive effect of the introduced p53 mutants on the activity of endogenous p53 in LNCaP cells was estimated by monitoring the p53-dependent p21 induction in response to doxorubicin treatment (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000). As seen in Figure 4, only one of the tested mutants, 175His, displayed a strong dominant negative activity against the wild type p53 reflected by the lack of p21 induction by DNA damage. Val135 mutant showed marginal p53 suppression, while the two remaining mutants did not interfere with p53-mediated p21 induction at all. Remarkably, this pattern of anti-p53 activity was exactly mirrored in the pattern of PSA expression: compared to control, 175His expressing cells produced 9-11 times more PSA, whereas in 135Val cells its level was slightly increased and 141Ala, 156Pro.

The list of genes whose expression was changed following wild type p53 suppression in LNCaP cells is attached as Table 1.

In conclusion, this Example demonstrate that the transcription of PSA gene in the prostate carcinoma cell line, LNCaP, is under strict negative control of

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p53 and its expression can be greatly activated by suppression of wild type p53 activity. Since LNCaP is considered most adequate and conventional among available *in vivo* models of hormone-dependent prostate cancer, these results likely reflect regulation of PSA in naturally occurring tumors. Thus, one of the most useful  
5 diagnostic tumor markers is, in fact, a tissue specific indicator of p53 inactivation in prostate cells. Being dependent on p53 inactivation, elevated production of PSA may therefore be indicative for the ongoing selection of p53-deficient cell variants with the broken control of apoptosis, angiogenesis, and genomic stability, all normally regulated by wild type p53. In fact, the loss of functional p53 by LNCaP cells is  
10 accompanied not only by elevated PSA secretion but also by acquisition of high tumorigenicity and resistance to TNF (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000).

For further detail concerning the above Example, see the inventors' publication: Gurova et al: Expression of prostate specific antigen (PSA) is negatively  
15 regulated by p53 . *Oncogene* 2002, 21: 153-157.

## Example 2

### **Validation of the methods of the invention in sets of p53-/- and p53 wild-type tissues and identification of new cancer markers**

20 The most desirable characteristics of an ideal tumor marker involve tissue/organ specificity of expression and association with definite type of tumor and/or stage of tumor progression. Alternatively, tumor markers may be ubiquitously highly expressed in numerous tumors displaying low expression or lack of expression in normal tissues. Prospective markers can be oncogenes themselves, and thus be  
25 directly involved in malignant transformation (i.e., BCR-ABL in Ph<sup>+</sup>-positive CML and ALL) (Daley et al., *Science* 1990 Feb 16;247(4944):824-30.) On the other hand, the marker genes may be not the active players in carcinogenesis, their overexpression being a consequence of transformation-associated changes in gene regulation. Genes from the first group may be targets for functional inhibition via direct targeting by  
30 drugs, whereas the genes(proteins) from the second group, if localized to the plasma membrane, may be used for targeting of tumor cells via specific antibodies-mediated strategies. Changes in the expression of these genes may also be used as a readout for the establishment of bioassay for the purpose of screening for anti-cancer drugs, e.g. targeted at reactivation of normal tumor suppressor gene function. Marker proteins

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from both groups may serve also as early diagnostic or progressive tumor markers if found in body fluids (i.e., like PSA in the cancer of prostate). Alternatively they may serve as differential diagnosis markers during morphological examination of tumor samples or tissue biopsies.

5           The invention provides a systematic approach for the search of cancer marker genes. This approach is based on the idea that many such genes may be transcriptionally activated in tissues following the loss of the most common tumor suppressor genes like e.g., p53, PTEN, RB, and p16/p19 and that this regulation will be conserved in normal and tumor cells from the same origin. Technically, the gene  
10   discovery may be performed by comparison of gene expression profiles in the fitted tissue pairs derived from normal and genetically modified mice, like i.e. p53 <sup>-/-</sup> mice, p16/p19<sup>-/-</sup> mice, tissues with targeted expression of SV40 large T antigen that simultaneously inactivates both RB and p53 function (TRAMP mice, expressing LT-Ag in prostate). There are some literature indications, as well as examples that support  
15   the feasibility of such an approach. For example, it was demonstrated wild-type p53 can suppress the expression of two neoangiogenesis and progression-related genes known to be highly expressed in tumors, COX2 (Subbaramaiah et al., J Biol Chem 1999 Apr 16;274(16):10911-5) and VEGF (Zhang et al., *Cancer Res* 2000 Jul 1;60(13):3655-61.) Both genes are currently regarded as targets for anti-cancer  
20   therapeutics. However, the connection of COX2 and VEGF to p53 was found long after they were first discovered and their function and tumor association were well established.

          In the present studies presented in Example 1 above, the inventors created an isogenic pair of LNCaP prostate tumor cell lines differing in their p53  
25   status and applied cDNA microarray analysis to look for differentially expressed genes. It was discovered that the baseline expression of several known tumor markers is significantly elevated in LNCaP cells that lack functional p53 protein compared to the same cells that express wt p53. These genes include e.g., COX2, tumor-specific heparin-binding growth factor midkine (possesses angiogenic and anti-apoptotic  
30   properties) (Ikematsu *et al.*, *Br J Cancer* 2000 Sep;83(6):701-6), tumor tissue associated hyaluronan receptor CD44 (Sneath et al., *Mol Pathol.* 1998 Aug;51(4):191-200) and PSA (prostate specific antigen).

COX2 inhibitors are currently in clinical trials against prostate cancer. Midkine was immunohistochemically shown to be expressed specimens 86.3% of

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prostate cancer specimen examined, with metastatic lesions generally showing higher expression than the corresponding primaries; normal prostate tissues were negative or showed only weak staining. Midkine was also detected in 12 of 15 latent cancers (80%) and in 12 of 16 cases of PIN (75%) (Konishi et al., *Oncology* 1999 Oct;57(3):253-7). PSA is the major currently used prostate cancer diagnostic marker. In Example 1 it is shown that its promoter is directly suppressed by wt p53, thus PSA up-regulation in prostate cancer may be indicative for the wt p53 loss. The list of genes which expression was changed following wt p53 suppression in LNCaP cells is attached in the accompanying Excel file (Table 1). The inventors concluded that general proof of concept is achieved and embarked upon a large-scale experiment involving microarray-based comparison of gene-expression profiles in the tissue pairs derived from normal and p53<sup>-/-</sup> mice.

Poly A RNA was extracted from spleen, pancreas, liver, stomach, intestine, colon, lung, brain, bladder, kidney, placenta/uterus and mammary glands of normal and p53-deficient mice and used for fluorescently-labeled probes for microarray hybridizations. All tissue-specific probes were labeled with Cy5 fluorescent marker, while the common control probe (an equal proportion mixture of all the RNAs) was labeled with Cy3. The common control probe was used in order to assess also the tissue-specificity of gene expression. All probes were hybridized to MouseGEM (Incyte). Upon quality control and pair-wise balancing of Cy5 and Cy3 signals, the differential (against common control) gene expression levels were normalized between p53<sup>-/-</sup> tissues and their corresponding normal counterparts. As a result the inventors obtained a table of genes containing their differential expression levels in p53<sup>-/-</sup> tissues compared to the corresponding normal tissues; the genes were sorted according to their expression levels in one particular tissue from maximally up-regulated genes to maximally down-regulated ones (Table 2). Genes showing absolute differential expression levels less than 1.9 were excluded from these tables. Thus, these tables contain the lists of genes with maximal differential tissue-specific expression in p53-deficient mice. It must be noted, that the majority of identified genes has changed their expression in a tissue-specific manner, though some of them like, e.g., choline kinase (known to be up-regulated and activated in numerous cancer types) was up-regulated in p53<sup>-/-</sup> pancreas, stomach, intestine, lung, bladder, uterus, and mammary gland. Another interesting observation is that there was almost no



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overlap between the list of genes that were up- or down-regulated in different p53<sup>-/-</sup> tissues.

Out of the approximately 10,000 genes printed on the microarray, approximately 445 genes that were found to be up-regulated in p53<sup>-/-</sup> tissues were studied in further detail, as they had the largest potential of serving as tumor markers (drug targets and diagnostic markers). These genes appear in the Excel file, Table 3. This table combines the p53-dependent differential expression data with the tissue specificity of gene expression data. The actual differential expression of genes in regard to common control is also presented. As discussed above, the markers are based on genes that are: either

1. up-regulated in a certain p53<sup>-/-</sup> tissue and are normally expressed predominantly in this tissue; or
2. normally expressed at low levels in one or several tissues but are up-regulated in one or numerous p53<sup>-/-</sup> tissues.

As evident from Table 3, genes belonging to both groups were identified. For example, Mest-linked imprinted transcript, anonymous brain protein, and potassium voltage-gated channel (subfamily Q, member2) are specifically expressed in brain and are up-regulated in p53<sup>-/-</sup> brain compared to the normal one. Another example: expression of liver-specific fatty acid transporter, betaine-homocystein methyltransferase and of several unknown genes (ESTs) is significantly increased in p53<sup>-/-</sup> hepatic tissue. On the other hand, genes such as choline kinase that is usually expressed at low levels is significantly enhanced in numerous p53<sup>-/-</sup> tissues (see above). A similar behavior is also observed i.e. for EGF (enhanced in p53<sup>-/-</sup> bladder and mammary gland); carbonic anhydrase 6 (enhanced in p53<sup>-/-</sup> bladder); zinc finger protein 101 (enhanced in p53<sup>-/-</sup> liver). Numerous unknown genes (ESTs) also fall in this the most promising category.

The approximately 445 genes identified as up-regulated in p53<sup>-/-</sup> mice were further prioritized for the purpose of serving as diagnostic markers; the highly preferred diagnostic markers are presented in Table 5 (general cancer markers) and Table 6 (tissue-specific cancer markers). Thus, of the approximately 10,000 genes printed on the array, the inventors were able to select through the methods of the invention a total of 338 genes ideally suited for several diagnostic and prognostic uses in various cancers, as described herein.

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Table 4 sheet 1 provides a list of 32 genes/ polypeptides identified according to the methods of the present example as disclosed herein that are known in the art to be markers for certain cancers, thus validating the effectiveness of the methods of the invention. This table also includes the PubMed indexing numbers of publications that disclose the connection of these genes/ polypeptides to cancer.

In summary, the inventors provide a list of genes characterized in regard to tissue-specificity of their normal expression and induction/reduction in various p53-deficient tissues. A similar expression pattern should be preserved in tumor cells originating from the same tissue. Thus, the identified genes may serve as tumor markers.

### Example 3

#### Validation data for additional tumor suppressor genes

The methods of the invention, as validated in example 2, are not limited only to the use of the tumor suppressor p53, as any other tumor suppressor gene with confirmed involvement in a specific type of cancer may be involved in negative regulation of tissue specific genes by direct (i.e., transcription factors) or indirect (i.e., signaling pathway members) pathways.

The inventors therefore proceeded to test these methods on p53 knockout mice, TRAMP mice and PTEN hemisigous mice (the complete knockout is non-viable). TRAMP transgenic mice express large T-antigen of SV40 under the control of prostate-specific probasin promoter (Jackson labs), and have both tumor suppressor genes p53 and Rb inactivated. PTEN hemisigous mice have only one allele of the tumor suppressor gene PTEN. The experiments were carried out on prostate cells. For each hybridization, RNA was isolated from prostates of 6-8 males of different age in dependence of genotype prior to appearance of initial signs of hyperplasia of prostate according to published data (p53KO, TRAMP and corresponding control C57BL6 mice - 9-10 weeks old, PTEN and corresponding control FVB mice - 6 weeks old). Total RNA was isolated from each prostate separately from 6-8 animals of each genotype. In total two probes for each genotype were prepared and hybridized with a set of three mouse Affymetrix arrays which cover the majority of known mouse transcripts. Genes with reproducible 2 fold overexpression in tumor suppressor gene deficient prostates as compared with wild

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type organs (confirmed specific hybridization) in both two repetitive hybridizations were picked for identification of human homologs.

Remarkably, among 161 genes picked for further analysis, more than 10 were found to be either known or candidate cancer markers although their p53 or Rb dependence had not been previously determined (see Table 4 sheet 2). A significant proportion of other genes that came out of these experiments are known as genes with melanoma or glioma-specific expression that is consistent with frequent acquisition of traces of neuroendocrinal differentiation by prostate cancer cells. Additional genes/ polypeptides previously linked to cancer and identified according to the method described in this Example include: KIAA430, limkainb1 (NP\_596912), that associates with the LIM-kinase 2, which may be critical for metastasis (PMID: 11208874); Glutamate-cystein ligase (modifier subunit), the rate-limiting enzyme in glutathion synthesis, that is overexpressed in numerous tumor types (PMID: 11774239, 11753966); PCNA (proliferating cells nuclear antigen), an auxiliary protein of DNA polymerase delta that is involved in the control of eukaryotic DNA replication, and overexpressed in numerous cancer types (e.g., PMID: 12145573, 12046056, PMID: 11750711, 11606074); Mcmd5, a DNA replication licensing factor under transcriptional control of E2F (PMID: 10327050), (abolishment of Rb function by TRAMP), which is a known marker for cancer (PMID: 2122098, 11839717, 10551502, 9843993); Transducin-like enhancer protein 2 (TLE2), a Nuclear effector molecule and neural/neuroectodermal associated gene overexpressed in synovial sarcoma (PMID: 12414507); Inhibitor of DNA binding 1 (ID1), a negative regulator of helix-loop-helix DNA binding proteins with the following functions: required to maintain the timing of neuronal differentiation in the embryo and invasiveness of the vasculature (hence, neurogenesis and vasculogenesis) (PMID: 10537105), inhibits transcription of trombospodin-1, thus promoting angiogenesis (PMID: 12498716), helps to keep neuroblastoma cells in an undifferentiated state (PMID: 11756408), directly inhibits expression of p16 via repression of Ets and E-protein-mediated transactivation (PMID: 11427735), trichostatin A treatment of ovarian cancer cells causes decrease of Rb phosphorylation and reduction of ID1 expression (thus the observed expression pattern in TRAMP mice is concomitant with Rb inactivation by T-Ag) (PMID: 12479699). This gene has several known associations to cancer: associated with grade and invasiveness of endometrial carcinoma (PMID: 11275368), upregulated in early melanomas (if not, p16 is mutated) (PMID: 11507043),

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expressed in astrocytes and endothelial cells within astrocytomas positively correlating with stage and grade (PMID: 12007145).

These preliminary results clearly support the main concept of the instant invention, and demonstrate that cancer markers can be frequently found among  
5 the genes that are normally under the negative control of tumor suppressors.

Table 4 sheet 2 provides a list of 12 genes/ polypeptides identified according to the methods of the present Example and of Example 2 as disclosed herein that are known in the art to be markers for certain cancers, thus validating the effectiveness of the methods of the invention. This table also includes the PubMed  
10 indexing numbers of publications that disclose the connection of these genes to cancer.

While the invention has been described in terms of specific embodiments, it is understood that variations and modifications will occur to those  
15 skilled in the art. Accordingly, only those limitations appearing in the appended claims should be placed upon the invention. The entire disclosure of all publications and patents cited herein are hereby incorporated by reference.

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RowType	GeneDescription	GeneID	LN56_DIFF	
gene	Human_clone_23586_mRNA_sequence_{Incyte_PD:530629}	530629	5.6	
gene	ESTs_Moderately_similar_to_III_ALU_SUBFAMILY_J_WARNING_ENTRY_!!!!_H.sapiens_{Incyte_PD:855928}	855928	5.5	
gene	Fc_fragment_of_IgG_low_affinity_IIla_receptor_for_(CD16){Incyte_PD:1560730}	1560730	5	
gene	prostaglandin-endoperoxide synthase_2_(prostaglandin_G/H_synthase_and_cyclooxygenase){Incyte_PD:3139163}	3139163	4.9	COX2
gene	Human_GABA-A_receptor_pi_subunit_mRNA_complete_cds_{Incyte_PD:1824443}	1824443	4.8	glutamate receptor (see glioma's paper and my text about prostate)
gene	kalikrein_3_(prostate_specific_antigen){Incyte_PD:1655492}	1655492	4.8	PSA
gene	regulator_of_G-protein_signalling_2_24kD_{Incyte_PD:1218114}	1218114	4.5	novel, sequence is not complete, contains Glutamine
gene	Homo_sapiens_mRNA_for_KIAA0540_protein_partial_cds_{Incyte_PD:2966126}	2966126	4.4	amidotransferases class-II signature and Beach domain (PFAM - did not find functional description)
gene	diaphorase_(NADH/NADPH)_cytochrome_b-5_reductase_{Incyte_PD:2637222}	2637222	4	
gene	Human_tumor_necrosis_factor-inducible_(TSG-6)_mRNA_fragment_adhesion_receptor_CD44_putative_CDS_{Incyte_PD:3142364}	3142364	4	hyaluronan receptor
gene	ESTs_Moderately_similar_to_III_ALU_SUBFAMILY_SC_WARNING_ENTRY_!!!!_H.sapiens_{Incyte_PD:2458029}	2458029	3.6	
gene	ESTs_{Incyte_PD:1305355}	1305355	3.6	
gene	ESTs_{Incyte_PD:2740665}	2740665	3.5	
gene	butyrylcholinesterase_{Incyte_PD:1599272}	1599272	3.5	
gene	ESTs_Weakly_similar_to_X-linked_retinopathy_protein_{H.sapiens}_{Incyte_PD:2311432}	2311432	3.3	
gene	ESTs_{Incyte_PD:2423162}	2423162	3.3	
gene	ESTs_{Incyte_PD:1965673}	1965673	3.3	
gene	ESTs_{Incyte_PD:3519565}	3519565	3.2	
gene	ESTs_{Incyte_PD:1537925}	1537925	3.2	
gene	bactericidal/permeability-increasing_protein_{Incyte_PD:406016}	406016	3.2	
gene	oligophrenin_1_{Incyte_PD:4216520}	4216520	3.1	
gene	ESTs_{Incyte_PD:944140}	944140	3.1	
gene	KIAA0025_gene_product_{Incyte_PD:2054420}	2054420	3.1	

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gene	ESTs_Moderately_similar_to_!!!!_ALU_SUBFAMILY_SP_WARNING_ENTRY_!!!!_I {H.sapiens}_ {Incyte_PD:1574536}	1574536	3.1	
gene	ESTs_ {Incyte_PD:966948}	966948	3	
gene	ESTs_Weakly_similar_to_(define_not_available_4589652)_ {H.sapiens}_ {Incyte_PD: 3749894}	3749894	3	
gene	ESTs_ {Incyte_PD:2045819}	2045819	3	
gene	ESTs_ {Incyte_PD:979945}	979945	3	
gene	ESTs_ {Incyte_PD:2149058}	2149058	3	
gene	prostaglandin_E_receptor_4_(subtype_EP4)_ {Incyte_PD:1631793}	1631793	3	
gene	ESTs_ {Incyte_PD:3252857}	3252857	3	
gene	ESTs_Moderately_similar_to_!!!!_ALU_SUBFAMILY_SX_WARNING_ENTRY_!!!!_I {H.sapiens}_ {Incyte_PD:2447969}	2447969	2.9	
gene	ESTs_ {Incyte_PD:1397926}	1397926	2.9	
gene	frizzled_ {Drosophila}_ homolog_5_ {Incyte_PD:3129290}	3129290	2.9	
gene	ATPase_Na+/K+ transporting_alpha_2_(+)_ polypeptide_ {Incyte_PD:1622542}	1622542	2.8	
gene	Human_desmocollin-2_mRNA_3' UTR_ {Incyte_PD:1403294}	1403294	2.8	
gene	N-acetylgalactosaminidase_alpha- {Incyte_PD:1664863}	1664863	2.8	
gene	protease_inhibitor_12_(neuroserpin)_ {Incyte_PD:2716511}	2716511	2.8	
gene	ESTs_ {Incyte_PD:2556708}	2556708	2.7	
gene	KIAA0575_gene_product_ {Incyte_PD:3094261}	3094261	2.7	
gene	ESTs_ {Incyte_PD:1824332}	1824332	2.7	
gene	Homo_sapiens_mRNA_chromosome_1_specific_transcript_KIAA0495_ {Incyte_PD:1 963554}	1963554	2.7	
gene	ESTs_ {Incyte_PD:2287483}	2287483	2.7	
gene	ESTs_ {Incyte_PD:3144018}	3144018	2.7	
gene	ESTs_ {Incyte_PD:2466668}	2466668	2.6	
gene	ESTs_ {Incyte_PD:2968970}	2968970	2.6	
gene	ESTs_ {Incyte_PD:2748370}	2748370	2.6	
gene	ESTs_Weakly_similar_to_!!!!_ALU_SUBFAMILY_SC_WARNING_ENTRY_!!!!_I {H.sa piens}_ {Incyte_PD:2243954}	2243954	2.6	
gene	transcription_factor_3_(E2A_immunoglobulin_enhancer_binding_factors_E12/E47)_ {I ncyte_PD:640174}	640174	2.6	
gene	Not_mapped_ {Incyte_PD:3463469}	3463469	2.6	
gene	ESTs_ {Incyte_PD:201053}	201053	2.6	
gene	ESTs_ {Incyte_PD:865723}	865723	2.6	
gene	adrenergic_beta-2_receptor_surface_ {Incyte_PD:3200341}	3200341	2.5	

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gene	solute_carrier_family_12_(sodium/chloride_transporters),_member_3_{Incyte_PD:3535415}	3535415	2.5	
gene	ESTs_{Incyte_PD:4061967}	4061967	2.4	
gene	ESTs_Highly_similar_to_!!!_ALU_SUBFAMILY_SP_WARNING_ENTRY_!!!_H.sap			
gene	ESTs_{Incyte_PD:966692}	966692	2.4	
gene	Not_mapped_{Incyte_PD:2542313}	2542313	2.4	
gene	ESTs_{Incyte_PD:1911371}	1911371	2.4	
gene	ESTs_Moderately_similar_to_!!!_ALU_SUBFAMILY_J_WARNING_ENTRY_!!!_H.sapiens_{Incyte_PD:2049587}	2049587	2.4	
gene	ESTs_Moderately_similar_to_protein_serine/threonine_kinase_{H.sapiens}_{Incyte_PD:2789918}	2789918	2.4	
gene	ataxia_telangiectasia_mutated_(includes_complementation_groups_A,C_and_D)_f			
gene	ncyte_PD:394665	394665	2.4	
gene	Not_mapped_{Incyte_PD:2477854}	2477854	2.4	
gene	Not_mapped_{Incyte_PD:2312442}	2312442	2.4	
gene	WD_repeat_domain_2_{Incyte_PD:2210264}	2210264	2.4	
gene	Human_cytochrome_P450-11B_(h11B3)_mRNA_complete_cds_{Incyte_PD:2798468}	2798468	2.4	important for growth of some carcinoid tumors
gene	dopa_decarboxylase_(aromatic_L-amino_acid_decarboxylase){Incyte_PD:2820985}	2820985	2.4	
gene	potassium_channel_subfamily_K_member_1_(TWIK-1){Incyte_PD:1479255}	1479255	2.4	
gene	ESTs_{Incyte_PD:2289901}	2289901	2.3	
gene	ESTs_{Incyte_PD:1602726}	1602726	2.3	
gene	primase_polypeptide_1_(49kD){Incyte_PD:105121}	105121	2.3	
gene	ESTs_{Incyte_PD:2230152}	2230152	2.3	
gene	midkine_(neurite_growth-promoting_factor_2){Incyte_PD:940845}	940845	2.3	cytokine expressed by numerous types of tumors. Our candidate in TCC
gene	ESTs_{Incyte_PD:2149237}	2149237	2.3	
gene	ESTs_{Incyte_PD:1817969}	1817969	2.3	
gene	ESTs_{Incyte_PD:1753445}	1753445	2.3	
gene	ESTs_{Incyte_PD:2882960}	2882960	2.2	
gene	ESTs_{Incyte_PD:213516}	213516	2.2	
gene	ESTs_{Incyte_PD:2359527}	2359527	2.2	
gene	ESTs_Highly_similar_to_(define_not_available_4589636)_H.sapiens_{Incyte_PD:2499488}	2499488	2.2	

Table 1 Page 3

gene	ESTs {IncYTE PD:2662127}		2662127	2.2	
gene	ESTs {IncYTE PD:2544622}		2544622	2.2	
gene	Human clone 23908 mRNA sequence {IncYTE PD:2251851}		2251851	2.2	
gene	phorbolin (similar to apolipoprotein B mRNA editing protein) {IncYTE PD:212573}		212573	2.2	
gene	platelet-activating factor receptor {IncYTE PD:2966535}		2966535	2.2	
gene	EST {IncYTE PD:2448338}		2448338	2.2	
gene	ESTs {IncYTE PD:2136337}		2136337	2.2	
gene	ESTs {IncYTE PD:4003220}		4003220	2.2	
gene	ESTs {IncYTE PD:2667106}		2667106	2.2	
gene	ESTs Weakly similar to !!!!! ALU SUBFAMILY J WARNING_ENTRY !!!!! {H.sapi				
gene	ens {IncYTE PD:465591}		465591	2.2	
gene	ESTs {IncYTE PD:2372541}		2372541	2.2	
gene	E2F transcription factor 6 {IncYTE PD:14588}		14588	2.2	
gene	ESTs {IncYTE PD:2598965}		2598965	2.2	
gene	ESTs Weakly similar to !!!!! ALU SUBFAMILY SB WARNING_ENTRY !!!!! {H.sapi				
gene	ens {IncYTE PD:2075469}		2075469	2.2	
gene	ESTs {IncYTE PD:2296027}		2296027	2.2	
gene	Not mapped {IncYTE PD:2896792}		2896792	2.2	
gene	ESTs Highly similar to putative Rab5-interacting protein {clone L1-57} {H.sapiens} {IncYTE PD:1984130}		1984130	2.2	
gene	ESTs {IncYTE PD:1366043}		1366043	2.1	
gene	ESTs Weakly similar to !!!!! ALU SUBFAMILY J WARNING_ENTRY !!!!! {H.sapi				
gene	ens {IncYTE PD:2133481}		2133481	2.1	
gene	ESTs {IncYTE PD:1888670}		1888670	2.1	
gene	ESTs {IncYTE PD:1349433}		1349433	2.1	
gene	ESTs Weakly similar to putative p150 {H.sapiens} {IncYTE PD:2936403}		2936403	2.1	
gene	ESTs {IncYTE PD:414891}		414891	2.1	
gene	ESTs {IncYTE PD:2060416}		2060416	2.1	
gene	ESTs {IncYTE PD:3104921}		3104921	2.1	
gene	ESTs {IncYTE PD:57997}		57997	2.1	
gene	Not mapped {IncYTE PD:1464613}		1464613	2.1	
gene	ESTs {IncYTE PD:1641775}		1641775	2.1	
gene	Human clone 23933 mRNA sequence {IncYTE PD:2286572}		2286572	2.1	
gene	amiloride binding protein_1 (amine oxidase (copper-containing)) {IncYTE PD:3676190}		3676190	2.1	

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gene	Human guanine nucleotide exchange factor mRNA complete cds {Incyte_PD:1962190}	1962190	2	
gene	ESTs {Incyte_PD:2279230}	2279230	2	
gene	ESTs {Incyte_PD:3719865}	3719865	2	
gene	preferentially expressed antigen of melanoma {Incyte_PD:2007554}	2007554	2	melanoma antigen
gene	ESTs {Incyte_PD:1302785}	1302785	2	
gene	Homo sapiens mRNA from chromosome 5q21-22, clone: FBR89 {Incyte_PD:2501484}	2501484	2	
gene	pancreatic lipase-related protein 1 {Incyte_PD:2084515}	2084515	2	
gene	ESTs {Incyte_PD:2691093}	2691093	2	
gene	ESTs Highly similar to PP2C [H.sapiens] {Incyte_PD:2182353}	2182353	2	
gene	surfactant pulmonary-associated protein B {Incyte_PD:1988674}	1988674	2	
gene	ESTs Moderately similar to [!!!] ALU SUBFAMILY J WARNING_ENTRY [!!!] [H.sapiens] {Incyte_PD:520342}	520342	2	
gene	ESTs Moderately similar to [!!!] ALU SUBFAMILY SQ WARNING_ENTRY [!!!] [H.sapiens] {Incyte_PD:1849453}	1849453	2	
gene	ESTs Weakly similar to (define_not_available_4587207) [H.sapiens] {Incyte_PD:2296344}	2296344	2	
gene	ESTs {Incyte_PD:2317034}	2317034	2	
gene	ESTs Weakly similar to [!!!] ALU SUBFAMILY SB WARNING_ENTRY [!!!] [H.sapiens] {Incyte_PD:1638184}	1638184	2	
gene	ESTs {Incyte_PD:1428856}	1428856	2	
gene	ESTs {Incyte_PD:3508727}	3508727	2	
gene	ESTs Weakly similar to [!!!] ALU SUBFAMILY J WARNING_ENTRY [!!!] [H.sapiens] {Incyte_PD:1431969}	1431969	2	
gene	Not mapped {Incyte_PD:1393855}	1393855	2	
gene	ESTs {Incyte_PD:2045755}	2045755	2	
gene	ESTs {Incyte_PD:1686727}	1686727	2	
gene	ESTs {Incyte_PD:2344817}	2344817	2	
gene	KIAA0335 gene product {Incyte_PD:2308348}	2308348	2	
gene	ESTs {Incyte_PD:1417114}	1417114	2	
gene	ESTs {Incyte_PD:2459069}	2459069	2	
gene	putative gene product {Incyte_PD:1300530}	1300530	2	
gene	breast cancer 2, early onset {Incyte_PD:2468523}	2468523	2	
gene	nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein {Incyte_PD:81490}	81490	2	

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gene	kinesin_family_member_5C_{Incyte_PD:1596268}	1596268	-2
gene	ESTs_Highly_similar_to_CDV-1R_protein_[M.musculus]_{Incyte_PD:1494531}	1494531	-2
gene	ESTs_{Incyte_PD:2618859}	2618859	-2
gene	ESTs_{Incyte_PD:2286816}	2286816	-2
gene	activating_transcription_factor_4_{tax-responsive_enhancer_element_B67}_{Incyte_PD:2916261}	2916261	-2
gene	ESTs_{Incyte_PD:1472206}	1472206	-2
gene	desmocollin_2_{Incyte_PD:496003}	496003	-2
gene	Not_mapped_{Incyte_PD:341263}	341263	-2
gene	ESTs_{Incyte_PD:1440279}	1440279	-2
gene	differentiated_Embryo_Chondrocyte_expressed_gene_1_{Incyte_PD:1732479}	1732479	-2
gene	lectin_galactoside-binding_soluble_3_(galectin_3)_{Incyte_PD:2921194}	2921194	-2
gene	calbindin_1_(28kD)_{Incyte_PD:629769}	629769	-2
gene	serine_protease_inhibitor_Kazal_type_1_{Incyte_PD:2373608}	2373608	-2
gene	golgi_SNAP_receptor_complex_member_2_{Incyte_PD:3279439}	3279439	-2
gene	Rho-associated_coiled-coil_containing_protein_kinase_1_{Incyte_PD:1351711}	1351711	-2
gene	plectin_1_intermediate_filament_binding_protein_500kD_{Incyte_PD:1907232}	1907232	-2
gene	ESTs_Weakly_similar_to_DAP-1_beta_[H.sapiens]_{Incyte_PD:2902846}	2902846	-2
gene	actinin_alpha_4_{Incyte_PD:1597330}	1597330	-2
	ubiquitin-activating_enzyme_E1_(A1S9T_and_BN75_temperature_sensitivity_complementing)_{Incyte_PD:1674422}	1674422	-2
gene	apoptosis_inhibitor_3_{Incyte_PD:2912879}	2912879	-2
gene	Human_mRNA_for_unknown_product_partial_cds_{Incyte_PD:1402715}	1402715	-2
gene	ESTs_Highly_similar_to_DIAMINE_ACETYLTRANSFERASE_[H.sapiens]_{Incyte_PD:63038}	63038	-2
gene	ESTs_{Incyte_PD:1912284}	1912284	-2
gene	Human_autoantigen_mRNA_complete_cds_{Incyte_PD:3374419}	3374419	-2
gene	ESTs_{Incyte_PD:565269}	565269	-2
gene	hect(homologous_to_the_E6-AP_(UBE3A)_carboxyl_terminus)_domain_and_RCC1_(CHC1)-like_domain_(RLD)_1_{Incyte_PD:4292515}	4292515	-2
gene	phosphorylase_glycogen_muscle_(McArdle_syndrome_glycogen_storage_disease_type_V)_{Incyte_PD:2635943}	2635943	-2.1
gene	KIAA0336_gene_product_{Incyte_PD:3520448}	3520448	-2.1

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gene	Homo sapiens SOX22 protein (SOX22) mRNA, complete cds {Incyte_PD:2824870}	2824870	-2.1
gene	Homo sapiens beta_III_spectrin (SPTBN2) mRNA, partial cds {Incyte_PD:3432208}	3432208	-2.1
gene	ESTs, Weakly similar to (define not available 4929591) [H.sapiens] {Incyte_PD:3596244}	3596244	-2.1
gene	ubiquitin specific protease 5 (isopeptidase T) {Incyte_PD:2493777}	2493777	-2.1
gene	Homo sapiens mRNA for KIAA0841 protein, partial cds {Incyte_PD:3971091}	3971091	-2.1
gene	laminin, alpha_3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin) {Incyte_PD:1818527}	1818527	-2.1
gene	Human mRNA for KIAA0185 gene, partial cds {Incyte_PD:2503208}	2503208	-2.1
gene	desmoplakin (DPI, DPL) {Incyte_PD:179929}	179929	-2.1
gene	cyclin-dependent kinase inhibitor 1A (p21, Cip1) {Incyte_PD:1804548}	1804548	-2.1 p21
gene	alpha_thalassemia/mental retardation syndrome X-linked {Incyte_PD:4106629}	4106629	-2.2
gene	phosphatidylinositol-4-phosphate 5-kinase, type II, beta {Incyte_PD:1315666}	1315666	-2.2
gene	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha) {Incyte_PD:1841462}	1841462	-2.2
gene	keratin_7 {Incyte_PD:1649959}	1649959	-2.2
gene	Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds {Incyte_PD:1302221}	1302221	-2.2
gene	ESTs {Incyte_PD:8552}	8552	-2.2
gene	vav_2 oncogene {Incyte_PD:3744592}	3744592	-2.3
gene	epithelial membrane protein 1 {Incyte_PD:1624024}	1624024	-2.3
gene	ESTs {Incyte_PD:2129939}	2129939	-2.3
gene	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) {Incyte_PD:179598}	179598	-2.3
gene	insulin-like growth factor_1 receptor {Incyte_PD:2597262}	2597262	-2.3
gene	protein kinase C substrate 80K-H {Incyte_PD:1723971}	1723971	-2.3
gene	guanylate binding protein 2, interferon-inducible {Incyte_PD:1610993}	1610993	-2.3
gene	interferon, gamma-inducible protein 16 {Incyte_PD:2508261}	2508261	-2.3
gene	N-myc downstream regulated {Incyte_PD:2055569}	2055569	-2.3
gene	ESTs {Incyte_PD:3971258}	3971258	-2.4
gene	Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS {Incyte_PD:2957175}	2957175	-2.4
gene	protein tyrosine phosphatase, receptor type, J {Incyte_PD:3818113}	3818113	-2.4
gene	Human cleavage signal 1 protein, mRNA, complete cds {Incyte_PD:2054053}	2054053	-2.4

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gene	ESTs {Incyte_PD:187276}	187276	-2.4	
gene	hypothetical_protein_of_unknown_function_{Incyte_PD:1402462}	1402462	-2.5	
gene	Human_mRNA_for_KIAA0066_gene_partial_cds_{Incyte_PD:3042637}	3042637	-2.5	
gene	BMX_non-receptor_tyrosine_kinase_{Incyte_PD:1655995}	1655995	-2.5	important for NE differentiation
gene	nel (chicken)-like 2_{Incyte_PD:2285502}	2285502	-2.5	
gene	homolog_of_Drosophila_past_{Incyte_PD:1336738}	1336738	-2.5	
gene	ESTs {Incyte_PD:1382947}	1382947	-2.5	
gene	ESTs {Incyte_PD:1967531}	1967531	-2.5	
gene	ESTs {Incyte_PD:2369022}	2369022	-2.5	
gene	cannabinoid_receptor_1_(brain){Incyte_PD:112853}	112853	-2.6	antagonizes NGF stimulation of trk. Trk's are targets in prostate cancer
gene	keratin_hair_basic_1_{Incyte_PD:1919158}	1919158	-2.6	traetemt; tumors produce NGF
gene	S100_calcium-binding_protein_A4_(calcium_protein_calvasculin_metastasin_murine_placental_homolog){Incyte_PD:1222317}	1222317	-2.6	
gene	fibroblast_activation_protein_alpha_{Incyte_PD:2483605}	2483605	-2.6	
gene	Homo_sapiens_KIAA0421_mRNA_partial_cds_{Incyte_PD:4253663}	4253663	-2.6	
gene	Not_mapped_{Incyte_PD:2204871}	2204871	-2.7	
gene	lamin_B2_{Incyte_PD:2414632}	2414632	-2.7	
gene	KIAA0138_gene_product_{Incyte_PD:1731569}	1731569	-2.7	
gene	H.sapiens_mRNA_for_protein-tyrosine-phosphatase_D1_{Incyte_PD:2605804}	2605804	-2.7	
gene	axonal_transport_of_synaptic_vesicles_{Incyte_PD:3856893}	3856893	-2.7	
gene	Homo_sapiens_mRNA_cDNA_DKFZp586F0219_(from_clone_DKFZp586F0219){Incyte_PD:220566}	220566	-2.8	
gene	nuclear_factor_I/C_CCAAT-binding_transcription_factor_{Incyte_PD:1670221}	1670221	-2.8	
gene	ESTs {Incyte_PD:1540157}	1540157	-2.8	
gene	5T4_oncofetal_trophoblast_glycoprotein_{Incyte_PD:1283532}	1283532	-2.8	
gene	glucose-6-phosphatase_catalytic_(glycogen_storage_disease_type_I_von_Gierke_disease){Incyte_PD:4287327}	4287327	-2.8	
gene	interleukin_6_signal_transducer_(gp130_oncostatin_M_receptor){Incyte_PD:21723}	2172334	-2.8	growth suppressor
gene	hydroxyprostaglandin_dehydrogenase_15-(NAD){Incyte_PD:1578941}	1578941	-2.8	
gene	v-myb_avian_myeloblastosis_viral_oncogene_homolog-like_2_{Incyte_PD:494905}	494905	-2.9	

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gene	Homo sapiens Nedd4-like ubiquitin-protein ligase WWP2 mRNA, complete cds {Incyte PD:869818}	869818	-2.9
gene	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 {Incyte PD:1736926}	1736926	-3
gene	Human mRNA for KIAA0220 gene, partial cds {Incyte PD:2657738}	2657738	-3
gene	splicing factor, arginine/serine-rich 6 {Incyte PD:1728574}	1728574	-3
gene	interleukin enhancer binding factor 3, 90kD {Incyte PD:1674263}	1674263	-3.1
gene	ESTs {Incyte PD:1635864}	1635864	-3.2
gene	regulator of G-protein signalling 4 {Incyte PD:617517}	617517	-3.3
gene	eukaryotic translation initiation factor 4 gamma_1 {Incyte PD:1965695}	1965695	-3.4
gene	REMOVED FROM DATABASE {Incyte PD:85246}	85246	-3.4
gene	zinc finger protein 162 {Incyte PD:2655068}	2655068	-3.5
gene	Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds {Incyte PD:4251662}	4251662	-3.7
gene	Homo sapiens ataxin-2-like protein A2LP (A2LG) mRNA, complete cds {Incyte PD:1712724}	1712724	-3.7
gene	quiescin Q6 {Incyte PD:1854220}	1854220	-3.8
gene	Human transporter protein (g17) mRNA, complete cds {Incyte PD:86661}	86661	-3.9
gene	nuclear mitotic apparatus protein 1 {Incyte PD:2700234}	2700234	-3.9
gene	yotiao {Incyte PD:3868809}	3868809	-4.1
gene	myosin heavy polypeptide 11, smooth muscle {Incyte PD:1866751}	1866751	-4.1
gene	cut (Drosophila)-like 1 (CCAA1 displacement protein) {Incyte PD:2372648}	2372648	-4.1
gene	filamin A, alpha (actin-binding protein-280) {Incyte PD:1708528}	1708528	-4.2
gene	nucleoporin 98kD {Incyte PD:1611993}	1611993	-4.2
gene	ESTs_Highly_similar_to_(define_not_available_3986200) [H.sapiens] {Incyte PD:1554358}	1554358	-4.4
gene	Human mRNA for KIAA0194 gene, partial cds {Incyte PD:1429306}	1429306	-4.5
gene	microtubule-associated protein 4 {Incyte PD:2992994}	2992994	-4.6
gene	U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p {Incyte PD:3616229}	3616229	-4.7
gene	ser-Thr protein kinase related to the myotonic dystrophy protein kinase {Incyte PD:1602261}	1602261	-4.8
gene	hect domain and RLD 2 {Incyte PD:2739109}	2739109	-4.9
gene	KIAA0018 gene product {Incyte PD:2962167}	2962167	-4.9

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gene	laminin_gamma_1 (formerly_LAMB2) {Incyte_PD:1599344}	1599344	-4.9	
gene	Not_mapped {Incyte_PD:3427594}	3427594	-5.5	
gene	protein_phosphatase_1_regulatory_subunit_10 {Incyte_PD:2314555}	2314555	-5.7	
gene	general_transcription_factor_III_C_polypeptide_1_(alpha_subunit_220kD) {Incyte_PD:486304}	486304	-6.7	
gene	ESTs_Highly_similar_to_Ran/TC4-binding_nucleopore_protein_[H.sapiens] {Incyte_PD:3030988}	3030988	-7	
gene	Homo_sapiens_mRNA_for_KIAA0911_protein_complete_cds {Incyte_PD:2578710}	2578710	-7.4	
gene	vaij-tRNA_synthetase_1 {Incyte_PD:1829709}	1829709	-28	

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Description	spl		panc		liv		stom		int		col		br		lung		blad		kidn		p/ut		mam	
	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor	PL-18	BDEnor
AA107035 guanylate cyclase activator 2b (retina)	-1.2	-1.3	-1.0	-1.1	-1.1	-1.1	-1.1	-1.1	3.1	3.2	1.17304+-	1.2	-1.5	-1.9	-1.2	1.2	-1.2	-1.0	-1.1	-1.1	-1.1	-1.3	6.5	5.84792
AA671177 RIKEN cDNA 6930412E23 gene	-1.3	-1.0	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1
W17865 uterine-specific prolactin-rich acidic protein	-1.4	-1.7	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4
AA242201 serine protease inhibitor, Kazal type 3	1.5	1.1	-1.4	-1.1	-1.4	-1.1	-1.4	-1.1	2.5	-1.0	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8
AA242102 villin	1.1	-1.4	-1.4	-1.3	-1.4	-1.3	-1.4	-1.3	1.3	1.2	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6
AI046662 lactate dehydrogenase 3, cytoplasmic isoform	1.2	-1.6	-1.3	-1.5	-1.3	-1.5	-1.3	-1.5	1.3	1.27823-	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2
AA220024 trophoblast specific protein	1.5	-2.0	-1.2	-1.5	-1.2	-1.5	-1.2	-1.5	1.1	-1.0	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2
AI549624 RIKEN cDNA 0610041E05 gene	1.8	1.8	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	3.6	1.9	-1.01549+-	1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1
AI326499 epidermal growth factor	1.3	-1.4	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	1.7	-1.1	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4
AI876997 carboxyl ester lipase	1.5	1.3	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-3.9	-1.9	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3
AA460630 choline kinase	1.7	1.9	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	3.1	2.0	1.31548+-	1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3
W14224 N-myc downstream regulated 1	1.1	1.0	1.0	1.1	1.0	1.1	1.0	1.1	1.9	-1.0	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2
AA520824 fatty acid binding protein 2, intestinal	-1.5	-1.5	-1.7	-1.7	-1.7	-1.7	-1.7	-1.7	-1.1	2.6	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3	-2.3
AI527496 Mus musculus mRNA, complete cds, similar to L-aminic acid oxidase	1.6	-1.2	-1.5	-1.2	-1.5	-1.2	-1.5	-1.2	-1.1	-1.19867-	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6
AI447967 ESTs	1.1	1.7	1.0557+	2.5	1.0557+	2.5	1.0557+	2.5	1.6563+	-1.0805+-	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8
AA686976 ESTs	1.1	1.8	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	1.7	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-	1.7361+-
AA080175 claudin 8	-1.0	1.1	1.3	1.1	1.3	1.1	1.3	1.1	1.1	-1.00278-	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2
AI481982 EST	1.5	1.7	1.0	2.0	1.0	2.0	1.0	2.0	1.4283*	-1.60668+-	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8
AI563220 ESTs	1.47814*	-1.0	1.3	1.3	1.3	1.3	1.3	1.3	1.68813*	-1.30242-	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1
AA792499 ankyrin-like repeat protein	1.8	-1.8	-1.5	-1.1	-1.5	-1.1	-1.5	-1.1	1.2	1.05661-	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4
AI549654 programmed cell death_10	1.24627+	2.02725-	-1.0038+	2.1	-1.0038+	2.1	-1.0038+	2.1	1.5	1.10261+-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-	2.00234-
AA210488 ESTs	1.7	1.8	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	1.5	1.2483+-	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2
AI614454 reduced in osteosclerosis transporter	1.7	-1.1	-1.8	-1.8	-1.8	-1.8	-1.8	-1.8	1.7	1.11125-	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3
AA288467 glycosylation dependent cell adhesion molecule_1	-1.0	-1.8	1.2	1.2	1.2	1.2	1.2	1.2	-1.1	1.2	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1
AA290390 cell death-inducing DNA fragmentation factor_alpha subunit-like effector_B	1.2	-1.5	1.4	1.2	1.4	1.2	1.4	1.2	1.3	1.1	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5
AA445667 RIKEN cDNA 4632401C06 gene	1.3	-1.2	-2.0	2.1	-2.0	2.1	-2.0	2.1	-1.0	1.1	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3

TABLE 2

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AA623060_RIKEN_cDNA_2410124L17_gene	1.5	1.5	1.1	2.4	1.36143*	-1.3	1.3	1.7425*	1.7	1.4	2.0	1.9
AA617112_ESTs	1.4	1.4	-1.2	3.3	1.7	-1.01971~	1.3	1.8	1.7	1.3	1.8	1.9
AA064586_testis_specific_gene_A2	1.1	-1.5	1.2	1.8	1.3	1.9371~	-1.8	-1.0	1.3	1.1	1.4	1.8
AA073925_ESTs	1.3	1.8	-1.4	2.5	2.0	-1.27077~	1.1	1.9	1.9	1.2	1.0	1.9
AI180945_ESTs_Moderately similar to S-ACYL_FATTY_ACID_SYNTHASE_THIOESTERASE, MEDIUM CHAIN [R.norvegicus]	1.4	-1.5	1.5	1.5	1.1	-1.11723~	-1.8	-1.0	1.3	1.1	1.2	1.2
AI892299_RIKEN_cDNA_5830499B15_gene	1.0	-1.3	1.1	1.8	1.3	-2.1	-1.8	-1.0	1.5	1.2	1.2	1.2
AI466648_RIKEN_cDNA_5730427C23_gene	-1.1	-1.5	-1.2	1.2	-1.0	1.20303~	-1.1	-1.2	1.2	1.2	1.2	1.0
AI154946_arginase_type_II	-1.1	1.0	-1.2	-1.1	-1.2	2.84324~	-1.6	1.1	1.0	1.2	1.1	1.9
WI2985_annexin_A10	1.5	-1.7	-1.1	-2.3	-8.5	-1.03567~	-1.3	-1.1	1.1	-1.0	1.0	-1.9
AIW209707_hemoglobin_Z_beta-like_embryonic_chain	-1.5	-1.5	1.1	-1.8	-1.4	-1.80487~	1.7	-1.2	-1.4	1.1	-2.7	-1.9
AI593096_ESTs_Weakly similar to NTC1_MOUSE_NEUROGENIC_LOCUS_NOTCH_HOMOLOG_PROTEIN_1_PRECURSOR [M.musculus]	-1.3	-1.3	-1.0	1.1	1.2	1.78593~	-1.2	-1.2	-1.5	-1.3	-1.7	-1.9
AA725961_ESTs	-	-	-	1.33228	-	-	-	-	-	-	-	-
AA607044_RIKEN_cDNA_2700099C19_gene	1.25704+	1.37307+	1.03755+	+	-1.0	1.4912+~	-1.2	-1.178+	-1.3	-1.2	-1.1	-1.9
AA611085_glypican_1	-1.4	-1.3	-1.5	-2.2	-1.0	-1.4	-1.1	-1.4	-1.4	-1.3	-1.3	-1.9
AA675111_RIKEN_cDNA_1810007A24_gene	1.2665+	1.05915+	1.19353+	+	1.10085	2.07471~	-1.26953+	1.20291+	1.04301+	-1.3	-1.1	-1.9
AA066763_hemoglobin_beta_adult_major_chain	1.4	1.3	-1.0	-2.1	-14.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AA106071_hemoglobin_beta_adult_major_chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.8	-1.1	-1.3	1.5	-1.8	-2.0
AA840565_RIKEN_cDNA_1300019D08_gene	1.3	-1.4	1.2	-3.0	-1.1	-4.3	3.2	1.1	-1.3	1.8	-1.7	-2.0
AA718468_ESTs	-1.2	-1.2	-1.1	-1.1	-1.0	1.20536~	-1.5	-1.4	-1.1	-1.3	-1.2	-2.1
AI593099_RIKEN_cDNA_2210410L06_gene	-	-	1.40655+	1.07363+	-1.2	1.1	1.07681+	-1.09891+	-1.3	+	-1.3	-2.1
AI158547_ESTs	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5	-2.1
WI41372_uncoupling_protein_mitochondrial	-1.0	1.24928+	1.05647+	+	1.32972	-1.49506+~	-1.5	1.33286+	-1.1477+	-1.3	1.2	-2.2
AA182334_immunoglobulin_heavy_chain_1_serum_IgG2a	1.2	-1.1	-1.0	-1.1	1.0	1.05988+~	1.1	-1.8	1.1	-1.1	-1.1	-2.2
WI3918_serine_(or_cysteine)_proteinase_inhibitor_clade_F_(alpha-2_antiplasmin_pigment_epithelium_derived_factor)_member_2	1.0	-	-	-	-	-1.84425~	-1.14317+	1.1	-1.1	1.2	1.1	-2.2
	-1.7	-1.1	1.5	-1.1	-1.1	-1.36639~	1.2	-3.1	1.1	1.4	-1.8	-2.2

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TABLE 2



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AA967024 arginine vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-2.7	-2.0	-1.4	-1.3	1.4	-1.2	-2.3
AA065835 corticosteroid binding globulin	1.0	1.2	1.3	-1.1	1.2	1.4	-2.4	-2.3	1.1	-1.0	-1.3	-2.4
AA138265 RIKEN_CDNA_2010309G21_gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	1.1	-1.3	-1.0	-1.0	-2.4
AA152940 immunoglobulin kappa chain variable 28 (V28)	1.3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	1.8	-1.1	-2.5
AA822106_ESTs_Weakly_Similar_to_CO6A_HUMAN_COMPLEMENT_COMPONENT_C8_ALPHA_CHAIN_PRECURSOR [Hsapiens]	2.7	-1.7	2.2	-1.0	1.1	2.80788~	-1.8	-20.2	-1.5	-1.3	-1.4	-2.7
AA495194 immunoglobulin kappa chain variable 20 (V20 family)	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.6	-1.0	1.4	-1.0	-2.7
AI386058 serum albumin variant	2.9	-1.7	2.0	1.1	-1.1	1.68346~	-1.3	-23.1	-1.4	-1.5	-1.3	-2.9
AI158823 immunoglobulin heavy chain 3 (serum IgG2b)	-1.0	-1.6	1.0	1.5	1.5	-2.52501~	1.2	1.2	1.4	-1.0	1.2	-3.4

TABLE 2

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BREAST

placenta/uterus												
Description	spl	panc	liv	stom	int	col	br	lung	blad	kidn	plut	mam
AA181982_EST	1.5	1.7	1.0	2.9	1.4283*	-1.8066+~	1.8	2.331821	2.084741	1.8	2.5	2.0
AA19524_RIKEN_cDNA_0610041E09_gene	1.8	1.9	-1.3	3.6	1.9	-1.01549+~	1.1	2.2	2.1	1.6	2.5	2.3
AA270885_parvalbumin	-1.1	-1.4	-1.4	1.4	1.3	2.0	-1.5	1.2	1.1	1.2	2.9	-1.2
AA469630_choline_kinase	1.7	1.9	-1.4	3.1	2.0	1.31548+~	1.3	2.3	2.0	1.6	2.2	2.1
AA447967_ESTs	1.1	1.7	1.0557+	2.5	1.68583+	-1.08065+~	2.8	1.6	1.7	1.8	2.1	2.1
AA754922_stearoyl-Coenzyme A desaturase_1	-1.1	-1.1	-1.4	1.8	1.4	1.38758~	-1.1	-1.2	-1.0	-1.2	2.1	-1.8
AA614443_3'-phosphoadenosine 5'-phosphosulfate synthase_2	1.2	-1.2	1.5	1.2	-3.7	-1.4	-1.3	1.4	1.5	1.3	2.1	1.7
AA553232_ribosomal_protein_S6	1.2	1.5	1.0	2.2	1.2	-1.20582+~	1.8	1.6	1.8	1.4	2.1	1.7
AA676997_carboxyl_ester_lipase	1.5	1.8	-1.4	-2.3	-8.9	-1.9	-1.3	-1.4	-1.1	1.1	2.0	2.2
AA561920_RalBP1_associated_Eps_domain_containing_protein	1.4	1.7	-1.1	2.6	1.5	-1.1	1.2	1.8	1.8	1.7	2.0	1.7
AA544433_dihydroorotate_dehydrogenase	1.2	1.5	1.0	3.2	1.7	1.2437+~	1.4	1.6	1.7	1.4	2.0	1.7
AA037649_transition_protein_1	-1.1	1.2	-1.2	2.1	1.4	-1.3	-1.4	1.5	1.2	1.2	2.0	1.8
AA550886_RIKEN_cDNA_1810010M01_gene	1.1	1.4	-1.2	1.4	1.6	-1.0	-1.1	1.6	1.2	1.2	2.0	1.8
AA473562_ESTs_Moderately_similar_to_allas_DLC1_[H.sapiens]	1.3	1.5	1.2	2.0	1.8	-1.306+~	1.59204+	1.88584+	1.5	1.4	2.0	2.1351+
AA623060_RIKEN_cDNA_2410124L17_gene	1.5	1.5	1.1	2.4	1.36143*	-1.3	1.8	1.77425+	1.7	1.4	2.0	1.9
AA899173_defensin_related_cryptidin_6	-1.2	1.1	-1.2	1.6	1.7	2.5	-1.3	1.5	1.1	1.0	1.9	1.5
AA588976_ESTs	1.1	1.8	-1.5	2.8	1.7	1.17361+~	2.3	1.68688+	1.7	1.4	1.9	2.1
AA517906_T-box_15	1.26469+	1.12314+	-1.10579+	2.07123+	1.43344+	-1.26463+~	1.98585+	1.4842+	1.35698+	1.49743+	1.9	1.2
AA159231_Public_domain_EST	1.3	1.8	1.0	2.2	1.7	-1.58578+~	1.3	1.8	2.0	1.5	1.9	1.8
AA517691_ESTs	1.3	1.6	-1.2	2.3	1.32145*	-1.2	1.8	1.8	1.7	1.5	1.9	1.5
AA073925_ESTs	1.3	1.8	-1.4	2.5	2.0	-1.27077~	1.1	1.9	1.9	1.2	1.9	1.9
AA473526_carnitine_acetyltransferase	-1.0	1.6	-1.3	1.3	1.5	-1.2	1.4	1.1	1.1	1.2	1.9	-1.1
AA789873_ATPase_H+-transporting_lyosomal_(vacuolar_proton_pump)_42kd	-1.5	1.4	1.3	1.0	1.4	1.9	-1.1	-1.9	-1.5	-1.0	-1.9	-1.2
W08947_non-catalytic_region_of_tyrosine_kinase_adaptor_protein_2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.2
W36474_metallothionein_2	-1.2	-2.2	2.1	1.2	1.9	1.8	1.1	-1.6	-1.1	1.6	-1.9	1.0
AA867621_S-phase_kinase-associated_protein_2_(p45)	-1.8	-1.2	2.0	1.5	1.2	2.74757+	-1.73102+	-2.2	-1.8	-1.4	-1.9	-1.3
AA636765_metallothionein_1	1.0	1.1	2.5	1.2	2.4	1.6	1.2	-1.6	-1.3	1.6	-1.9	-1.2
AA608086_run_related_transcription_factor_3	-2.0	1.1	1.2	1.4	1.4	1.88224+	-1.75763+	-2.0	-1.6	-1.3	-1.9	-1.0
AA821932_small_inducible_cytokine_A6	1.0	-1.0	1.8	-1.6	1.3	1.2	-1.3	-3.4	-1.2	1.3	-1.9	-1.7
AA684320_activ_receptor_interacting_protein_1	-1.9	1.4	1.3	1.3	1.5	2.60454+	1.0	-2.7	-1.4	-1.1	-1.9	-1.3
AA325603_apolipoprotein_E	1.2	1.3	1.5	-1.7	1.5	-1.0	1.5	-1.9	-1.3	-1.5	-2.0	-1.2
AA822116_transferrin	1.2	-1.1	1.5	-1.5	-1.4	1.56627~	-1.3	-7.7	-1.0	1.1	-2.0	-1.6

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TABLE 2

W99034_ESTs	-1.2	1.3	2.2	1.5	1.5	1.6418~	1.0	-2.0	-1.4	-1.3	-2.0	1.0
A0066016_RIKEN_cDNA_1190002H23_gene	-1.6	1.2	1.2	1.5	1.5	3.38218~	-2.0	-2.4	-1.4	-1.5	-2.0	-1.3
AA763276_small_muscle_protein_X-linked	-1.7	-1.4	1.1	1.6	1.2	1.9	-4.6	-2.5	-1.6	-1.2	-2.0	-1.5
AA607572_RIKEN_cDNA_1810017F10_gene	-1.3	1.1	1.4	1.1	-1.0	1.50739~	1.0	-1.8	-1.9	-1.3	-2.0	-1.6
AA437863_RIKEN_cDNA_1200013I08_gene	-1.6	1.0	1.4	1.4	1.3	2.48975~	-1.4	-2.0	-1.7	-1.1	-2.0	-1.3
AA497627_intersectin_(SH3_domain_protein_1A)	-1.6	1.0	1.1	2.0	1.5	2.70712~	-1.0	-1.8	-1.5	-1.2	-2.1	-1.2
A1047903_topoisomerase_(DNA)_III_beta	-1.7	-1.0	1.4	1.1	1.1	2.1785~	-1.4	-2.5	-1.7	-1.5	-2.1	-1.5
AA711868_slalodhesin	-1.4	1.2	1.4	1.4	1.4	2.7327~	-1.2	-1.8	-1.4	-1.2	-2.1	-1.4
AA013726_callectrin_J	-1.0	-1.0	-1.2	1.8	1.8	-1.4	-1.2	1.6	1.2	1.1	-2.1	1.5
A1428661_ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.6	-2.6	-2.1	-1.7	-2.2	-1.5
AA860530_Public_domain_EST	-1.5	-1.0	1.5	1.2	1.2	1.56932~	1.5	-2.2	-1.1	-1.2	-2.2	-1.1
A1324392_alpha_tetropoetin	-1.1	-1.8	-1.1	-1.3	-1.4	-1.3	-1.3	-1.5	-1.0	-1.3	-2.2	-1.8
W65070_ESTs	-1.2	1.4	2.1	1.7	1.6	1.8	1.1	-2.6	-1.4	-1.4	-2.3	-1.1
AA024217_Public_domain_EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AA174336_synaptonemal_complex_protein_3	-2.8	1.2	2.6	1.4	1.5	2.74133~	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA624843_hemoglobin_Y_beta-like_embryonic_chain	-1.4	-1.6	1.1	-1.2	-1.1	1.3	-1.7	-1.6	-1.3	-1.0	-2.3	-1.5
AA71229_ESTs_Weakly_similar_to_zinc_finger_protein_95_[M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.716~	-2.0	-3.3	-2.2	-1.4	-2.4	-1.4
AA272836_aquaporin_8	-1.1	1.2	-1.1	1.4	1.4	-2.8	1.2	1.0	1.0	1.2	-2.4	1.3
AA546645_cell_division_cycle_2_homolog_(S._pombe)-like_2	-2.1	-1.1	1.3	1.4	1.1	2.3~	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA874101_tumor-associated_calcium_signal_transducer_2	-2.6	-1.1	1.5	1.3	1.2	8.539~	-1.7	-2.1	-1.5	-1.5	-2.4	-1.2
AA797886_ESTs_Weakly_similar_to_ORF2_[M.musculus]	-1.8	1.4	1.2	-1.0	1.4	1.8	-1.4	-1.3	-1.7	-1.5	-2.4	-1.2
AA822098_apolipoprotein_A-I	-1.9	-1.5	1.1	-2.4	2.4	2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.6
AA414078_DNA_segment_Chromosome_7_ERATO_Dot_486_expressed	-1.7	1.2	1.4	1.2	1.2	2.63618~	1.0	-2.0	-1.4	-1.1	-2.5	-1.2
AA176045_forkhead_box_C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.6	-2.5	-1.1
AA034678_rhotekin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4
AAW209707_hemoglobin_Z_beta-like_embryonic_chain	-1.5	-1.5	1.1	-1.8	-1.4	-1.80487~	1.7	-1.2	-1.4	1.1	-2.7	-1.9
AA041727_tumor-suppressing_subchromosomal_transferable_fragment_3	-2.1	1.1	1.8	-1.2	1.1	2.05235~	-1.8	-3.0	-2.1	-1.8	-2.9	-1.0
AA795220_ADPribosylarginine_hydrolase	1.0	-1.1	1.2	1.1	-1.1	-1.29404~	1.1	1.1	1.1	1.0	-3.3	-1.0
AA189266_ESTs	-3.2	1.4	1.5	1.5	1.3	1.7	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
AA56995_hemochitin_X_alpha-like_embryonic_chain_in_Hba_complex	1.1	-1.6	-1.3	-1.2	-2.2	1.11232~	-2.1	-2.0	1.0	-1.2	-4.0	-1.6

TABLE 2

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Kidney	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
	PL- 4B_BDEnor	PL- 2B_BDEnor	PL- 8B_BDEnor	PL- 8B_BDEnor	PL- 3B_BDEnor	PL-6B_BDEnor	PL- 1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
AA762401_E91s	-1.67339+	-1.41617+	-1.23697+	1.12201+	-1.35665+	-1.61968+-	1.32548+	-1.24845+	1.3	3.8	-1.1	1.4
AI431911_Mus_musculus_clone_MGC-6727_mRNA_complete cds	-1.1	-2.0	-1.8	1.0	-1.8	-2.3	-1.5	-2.4	-1.4	3.8	-1.4	-1.4
AA760002_beta-glucuronidase_structure	-1.2	-1.1	1.2	-1.1	-1.1	1.4	-1.4	1.1	1.1	2.4	-1.1695*	-1.1
AA106125_cytochrome_P450_2a4	1.3	-1.3	3.0	1.3	1.4	1.0	-2.4	1.3	1.1	2.3	1.1	1.1
AI155437_Mus_musculus_20alpha-HSD_mRNA_for_20alpha-hydroxysteroid dehydrogenase, complete cds	1.3	-1.5	-1.2	1.1	1.3	1.15702+-	-1.2	1.1	-1.0	2.2	-1.2	1.1
AI614454_reduced_in_osteosclerosis_transposon	1.7	-1.1	-1.8	1.9	1.7	1.11125-	1.3	1.2	1.2	2.2	1.5	1.9
AA821997_myoglobin	-1.0	-2.5	1.0	1.1	1.0	-1.2	-1.8	-1.7	-4.3	2.2	-1.1	-1.7
W16059 glutathione S-transferase omega_1	1.2	-1.1	1.7	-1.4	-1.1	-1.2	1.2	1.2	1.4	2.2	-1.0	1.0
AA674177_cytochrome_P450_2a4	1.2	-1.6	2.8	1.1	1.3	1.72883+-	-2.1	1.2	-1.0	2.1	-1.1	-1.2
AA087441_RIKEN_cDNA_061001L04_gene	1.2	1.1	1.3	1.3	-1.1	1.1497-	-1.0	1.2	1.6	2.1	1.2	-1.1
AA146478_Mus_musculus_mRNA_(3C10)_for_IgA_V-D-J-heavy_chain	-1.3	1.0	-1.6	2.7	-2.0	-2.4	-1.1	-1.4	1.5	2.0	1.1	1.6
AA096815_Public_domain_EST	1.2	-1.3	1.2	1.5	1.2	2.2387+-	-1.9	-1.2	1.3	2.0	1.0	1.4
AA145454_insulin-like growth factor binding protein_4	1.0	-1.5	1.3	-1.2	-1.1	1.0	-1.1	1.0	1.4	2.0	-1.0	-1.2
AI549666_ESTs	1.35481+	1.85119+	1.04863+	2.2	1.85187+	1.52793+-	1.07014+	1.61878+	1.7	2.0	1.9205047+	
AA108417_insulin-like growth factor binding protein_4	-1.0	-1.5	1.2	-1.2	-1.1	-1.3	1.0	-1.2	1.2	2.0	-1.1	-1.3
AA450534_gluamine_synthetase_pseudogene_1	1.1	-1.1	1.2	1.4	1.2	-1.3	1.4	1.4	1.3	1.9	1.4	1.1
AI552658_ESTs	-1.3	1.1	-1.2	1.2	-1.1	1.06884+-	1.2	-1.1	-1.0	1.9	-1.3	-1.0
AI390138_RIKEN_cDNA_3930401B19_gene	-1.4	-10.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1
AA681098_ESTs	-1.13993+	-1.31577+	1.39877+	1.02396+	-1.06627+	1.49883+-	-1.69915+	1.35989+	1.13503+	-1.9	1.3409+	-1.19374+
AI385457_retinol binding protein_2_cellular	-2.0	-2.1	-1.6	-1.9	1.5	-1.9	-1.3	-1.9	-1.6	-1.9	-1.5	-1.7
AI894032_troil_factor_2_(spasmodic protein_1)	-1.1	1.8	-1.2	-2.0	-82.1	-1.89777-	-1.4	1.0	-1.4	-1.9	-1.0	1.4
AI597097_Public_domain_EST	1.3	1.9	-1.1	-1.0	-1.6	1.2	1.2	-1.0	1.2	-1.9	1.0	-1.3

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AI036489 cyclin G	-1.2	1.0	1.3	-1.8	-1.8	-2.26973~	1.2	-1.4	-1.4	-2.0	-1.0	-1.1
AI385510 cadherin 13	-1.2	-1.6	-1.0	1.2	-1.5	-1.0	-1.1	1.1	-1.6	-2.1	-1.2	-1.0
AI536309 RIKEN cDNA 2210410L06 gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5	-2.1
AA822098 apolipoprotein A-I	-1.9	-1.5	1.1	-2.4	-2.4	-2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.6
AA684191 CDC-like kinase	1.5	-2.1	-1.3	-1.1	-2.0	-1.4	-1.3	1.8	1.4	-2.1	1.4	1.2
AA822105 major urinary protein 1	-1.1	-2.4	-28.7849*	-7.8	-1.1	1.43224~	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2
AA434680 ESTs	-1.1	-1.1	-1.0	-1.0	-1.7	1.2	-1.0	-1.0	-1.1	-2.2	-1.0	-1.2
AA108495 deoxyribonuclease I	1.1	-1.8	-1.1	1.2	1.4	-2.1	-2.3	-1.2	-1.7	-2.4	1.3	-1.6
AA184421 ESTs	-1.1	1.0	-1.0	1.0	-1.4	1.1	1.4	1.2	-1.3	-2.4	-1.1	-1.1
AA060880 RIKEN cDNA 1700023M09 gene	-1.1	-1.8	-1.1	1.4	-1.5	1.0	-1.3	1.1	-1.7	-2.7	-1.1	1.1

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TABLE 2

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bladder	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL_4B_BDEnor	PL_2B_BDEnor	PL_6B_BDEnor	PL_8B_BDEnor	PL_3B_BDEnor	PL_5B_BDEnor	PL_1B_BDEnor	PL_7B_BDEnor	PL_9B_BDEnor or	PL_10B_BDEnor	PL_11B_BDEnor or	PL_12B_BDEnor or
W34620 kallikrein_26	1.2	1.1	-1.1	-1.4	-1.9	-1.2	-1.5	2.8	10.1	1.1	-1.1	-1.4
AA498574 kallikrein_6	1.8	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	2.8	7.2	1.1	1.0	1.3
AA760185 carbonic anhydrase_8	-1.2	-1.7	-1.0	-1.2	-1.2	1.5	-2.0	1.8	6.4	-1.6	-1.2	-1.4
W35921 dentilung_coll_and_parietal_protein	-1.1	-1.2	-1.1	1.1	1.1	1.1	-1.4	1.7	5.2	-1.4	1.1	1.1
A1326499 epidermal growth factor	1.3	-1.4	-1.2	1.7	-1.1	-1.4	-1.4	1.5	3.9	1.3	1.7	2.3
AA468852 cysteine rich protein_81	1.1	1.1	-1.1	-1.1	1.1	-1.03021~	-1.0	2.1	3.0	-1.0	1.1	1.2
AA612413 chitinase_acidic	-1.1	-1.3	1.8	-1.2	1.2	3.09734~	-2.3	1.2	2.6	-1.2	-1.2	-1.0
W11432 Leman colled-coil protein	-1.1	-1.3	1.2	-1.1	-1.1	-1.06812~	-1.1	1.3	2.3	-1.1	1.2	1.2
AA619838 ESTs	1.08217+	-1.76658+	1.14152+	-1.0	-1.10855+	-1.28423~	1.00186+	-1.11217+	2.2	1.3	-1.11428+	-1.3
AA765749 submaxillary gland androgen regulated protein 1	-1.1	-1.6	1.0	-1.3	-1.2	1.5	-2.0	1.3	2.2	-1.2	-1.2	-1.8
A1652219 ESTs	1.2087+	1.576+	-1.18563+	2.3	1.8	-1.26743~	2.14507+	1.53405+	2.1	1.8	1.85635+	1.8213+
A1549624 RIKEN cDNA 0610041E09 gene	1.8	1.9	-1.3	3.8	1.9	-1.01549~	1.1	2.2	2.1	1.9	2.5	2.3
AA623175 ESTs	1.5	1.5	-1.0	2.4	1.6	-1.30902~	1.4	2.3	2.1	1.7	2.2885+	1.6
AA469630 choline kinase	1.7	1.9	-1.4	3.1	2.0	1.31548~	1.3	2.3	2.0	1.8	2.2	2.1
A1653220 ESTs	1.47814+	-1.0	1.3	1.9	1.16813+	-1.30242~	-1.1	2.14498+	2.0	1.8	2.57946+	2.0
AA469724 WW domain binding protein 5	1.3	1.4	-1.1	2.0	1.5	1.0	1.1	1.7	2.0	1.3	1.8	1.8
AA159231 Public domain EST	1.3	1.4	1.0	2.2	1.7	-1.58578~	1.3	1.6	2.0	1.5	1.9	1.8
AA155097 ESTs	1.4	1.1	1.1	2.0	1.2	-1.2	1.4	1.95682+	2.0	1.2	1.7	1.6
AA445667 RIKEN cDNA 4632401C08 gene	1.3	-1.2	-2.0	2.1	-1.0	1.1	1.3	-1.2	1.9	1.4	1.8	1.9
AA561920 RabP1 associated Eps domain containing protein	1.4	1.7	-1.1	2.8	1.5	-1.1	1.2	1.8	1.9	1.7	2.0	1.7
W82228 annexin_A3	1.5	-1.4	1.0	-1.7	-1.7	-1.86744~	1.1	1.4	1.9	1.0	1.3	1.1
AA073925 ESTs	1.3	1.6	-1.4	2.5	2.0	-1.27077~	1.1	1.9	1.9	1.2	1.8	1.9
AA607572 RIKEN cDNA 1810017F10 gene	-1.3	1.1	1.4	1.1	-1.0	1.50739~	1.0	-1.8	-1.9	-1.3	-2.0	-1.6
AA199011 histocompatibility 2_class II antigen_A_alpha	-1.1	-1.3	1.1	1.0	1.3	-4.5	1.2	1.1	-1.9	1.3	-1.0	-1.2
AA880220 jagged_1	-1.3	-1.1	-1.2	-1.4	1.1	-1.6	1.3	-1.2	-1.9	-1.0	-1.5	-1.3
AA024217 Public domain EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AA681602 endolase_3_beta_muscle	1.1	-1.7	-1.0	-1.4	1.3	-1.5	-2.5	-1.3	-1.9	1.1	1.2	-1.4
AA759679 Ia-associated invariant chain	-1.0	-1.8	-1.6	-1.9	1.5	-3.7	-2.8	-1.0	-1.9	-1.0	-1.3	-1.4
AA414790 leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-2.0	-1.7	-1.6	-1.8
AA982254 RIKEN cDNA 2210010C04 gene	2.3	1.6	-1.3	-2.0	-9.5	-1.3	1.9	-1.5	-2.0	-1.4	-1.1	-1.1
A1909242 RIKEN cDNA 2310005E10 gene	1.1	-1.1	-1.2	-1.3	-1.3	-1.56397~	-1.1	-1.0	-2.0	-1.1	-1.0	1.1
AA839138 CD8 antigen_alpha chain	-1.3	-1.08773+	-1.3	-1.8	1.2	-2.63867~	-4.0	1.0	-2.0	1.1	1.0	-1.1

TABLE 2

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BLADDER

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AA474336 synaptonemal complex protein 3	-2.6	1.2	2.8	1.4	1.5	2.74133~	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA671135 myosin heavy chain, cardiac muscle, adult	-1.1	-1.7	1.3	1.2	1.1	2.1	-1.9	-1.3	-2.1	1.4	-1.2	-1.3
AA770924 troponin T3, skeletal, fast	1.4	-1.5	1.1	1.2	1.0	-1.7	-1.8	-1.1	-2.1	1.0	1.2	-1.2
AA034678 rholekin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.8	-1.4
AA428661 ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.6	-2.6	-2.1	-1.7	-2.2	-1.5
AA014727 tumor-suppressing subchromosomal transferable fragment 3	-2.1	1.1	1.8	-1.2	1.1	2.05235~	-1.8	-3.0	-2.1	-1.8	-2.9	-1.0
AA667301 troponin I, cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.41297~	-2.0	-2.0	-2.2	*	-1.0	1.3
AA675111 RIKEN cDNA 1810007A24 gene	1.4	1.3	-1.0	-2.1	-14.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AA771229 ESTs, Weakly similar to zinc finger protein 95 [M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.7415~	-2.0	-3.3	-2.2	-1.4	-2.4	-1.4
AA881388 ESTs	-1.1	1.0	-1.1	-1.2	1.1	-1.2	1.2	-1.28277~	-2.3	-1.0	-1.0	-1.0
W10293 androgen regulated vas deferens protein	1.2	1.4	-1.1	1.4	1.2	-1.3	-1.3	1.5	-2.3	1.2	-1.0	1.6
AA176045 forkhead box C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.6	-2.5	-1.1
AA546645 cell division cycle 2 homolog (S. pombe)-like 2	-2.1	-1.1	1.3	1.4	1.1	2.3	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA221794 regulator of G-protein signaling 2	1.0	-1.7	-1.4	-1.3	1.2	-1.29501~	1.0	-1.0	-2.3	-1.1	-1.3	-1.3
AA451882 RIKEN cDNA 0910001A18 gene	1.8	1.3	-1.1	-2.5	-14.7	-2.6	1.2	-1.2	-2.3	-1.1	-1.3	-1.3
AA82132 cytochrome c oxidase, subunit VI, a, polypeptide 2	1.1	-1.3	1.1	-1.0	1.1	-1.57226~	-1.2	-1.7	-2.4	1.0	-1.0	-1.4
AA065510 defensin beta 1	1.4	-1.4	1.1	-1.0	1.2	1.33028~	-1.8	-1.2	-2.5	-1.1	-1.1	-1.3
AA386046 trypsin 4	1.7	1.8	1.1	-1.8	-15.9	-2.6	1.8	-1.5	-2.5	-1.1	-1.3	-1.2
W15001 CD52 antigen	1.1	-1.7	1.2	1.1	1.1	-2.3	-1.2	-1.2	-2.5	1.1	-1.1	-1.0
AA238062 CD52 antigen	1.1	-1.6	-1.3	1.0	-1.1	-1.9	-1.6	-1.3	-2.6	-1.1	-1.2	-1.1
AA237793 rat regenerating islet-derived, mouse homolog 1	2.5	1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA717025 Mus_musculus.10 day old male pancreas cDNA_RIKEN_fulllength_end	1.9	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1	-1.4
ched library, clone:1810009A17, full insert sequence	1.1	-1.6	1.4	-1.1	1.0	1.65959~	-2.0	-1.2	-3.0	-1.3	-1.3	-1.3
AA771566 troponin C, fast skeletal	-3.2	1.4	1.5	1.5	1.3	1.7	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
AA189266 ESTs	-1.1	-1.0	1.5	1.4	1.5	1.58052~	-1.2	-1.1	-3.4	-1.3	1.2	1.2
AA097074 aquaporin 2	1.2	-1.4	-1.1	1.3	1.1	-1.65763~	1.0	-1.3	-3.7	-1.1	1.2	-1.4
AA712003 resistin like alpha	2.3	1.4	-1.2	-2.7	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA675064 elastase 2	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AA790398 ribonuclease 1, pancreatic	-1.0	-2.5	1.0	1.1	1.0	-1.2	-1.8	-1.7	-4.3	-2.2	-1.1	-1.7
AA821997 myoglobin	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.3	-1.2	-4.4	-1.1	-1.1	-1.2
AA821864 amylase 2, pancreatic	1.5	1.3	-1.4	1.1	2.5	-1.0	-1.8	1.2	-9.2	-1.0	1.0	2.5
AA242201 serine protease inhibitor, Kazal type 3												

TABLE 2

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BLADDER

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lung	spl	panc	liver	stom	int	col	brain	lung	blad	kidn	pl/ut	mam
Description	PL- 4B_BDEn	PL- 2B_BDEn	PL- 9B_BDEn	PL- 9B_BDEn	PL- 9B_BDEn	PL- 9B_BDEn	PL- 1B_BDEn	PL- 7B_BDEn	PL- 9B_BDEn	PL- 10B_BDEn	PL- 11B_BDEn	PL- 12B_BDEn
AA445751 heat shock protein cognate 70, testis	1.1	1.1	1.0	-1.2	-1.1	-1.3	-1.8	3.8	-1.0	1.1	-1.2	1.1
AA146996 heat shock protein 70 kDa 1	1.1	-1.1	-1.0	1.2	-1.8	-2.0	-1.7	3.7	1.1	1.1	-1.0	-1.1
AA087863 RIKEN cDNA 2310017218 gene	1.2	1.2	1.0	-1.1	1.2	-1.58765~	1.5	2.9	1.0	1.1	-1.4	-1.8
W34620 kallikrein 28	1.2	1.1	-1.1	-1.4	-1.9	-1.2	-1.5	2.8	1.0	1.1	-1.1	-1.4
AA498874 kallikrein 6	1.8	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	2.8	7.2	1.1	1.0	1.3
AA002910 FBJ osteosarcoma oncogene	-1.0	-1.3	-1.4	-1.3	-1.1	-2.28344~	1.3	2.7	1.6	1.0	-1.1	-1.0
AA433639 heat shock protein cognate 70, testis	1.7	1.1	-1.1	1.3	1.2	-1.6	-1.5	2.4	1.2	1.2	1.4	1.5
AA623175 ESTs	1.5	1.5	-1.0	2.4	1.6	-1.30902~	1.4	2.3	2.1	1.7	2.2885~	1.8
AA469630 choline kinase	1.7	1.9	-1.4	3.1	2.0	1.31548~	1.3	2.3	2.0	1.6	2.2	2.1
AA657278 DnaJ (Hsp40) homolog, subfamily B, member 1	1.3	1.12886+	1.1	1.5	1.0	-1.4908~	1.1	2.2	1.4	1.2	1.3	1.4
AI549824 RIKEN cDNA 0610041E09 gene	1.8	1.9	-1.3	2.6	1.9	-1.01549~	1.1	2.2	2.1	1.8	2.5	2.3
AA466852 cysteine rich protein 61	1.1	1.1	-1.1	-1.1	1.1	-1.03021~	-1.0	2.1	3.0	-1.0	1.1	1.2
AA412879 RIKEN cDNA C330006J08 gene	1.6	1.8	-1.0	2.4	1.2	-1.3	1.3	2.0	1.8	1.5	1.7	1.7
AA073925 ESTs	1.3	1.6	-1.4	2.5	2.0	-1.27077~	1.1	1.9	1.9	1.2	1.9	1.9
AA726092 RIKEN cDNA 4933419D20 gene	1.1	1.1	1.4	1.0	1.5	1.86913~	-1.28553+	1.9	1.3	1.5	1.1	-1.1
AI551943 ESTs, Weakly similar to JC2378, acetyl-CoA C-acetyltransferase [H.sapiens]	1.2	1.1	-1.4	2.4	1.3	1.05496~	1.4	1.9	1.7	1.7	1.7	1.3
AI549843 RIKEN cDNA 1300017N15 gene	1.3	1.7	-1.1	2.4	1.4	1.0687~	1.4	1.9	1.6	1.4	1.6	1.6
AA209882 nuclear receptor subfamily 4, group A, member 1	-1.0	-1.0	-1.0	-1.8	-1.3	-1.06815~	-1.8	1.9	1.3	-1.0	1.1	-1.1
AA062457 RIKEN cDNA 0610006F02 gene	1.2	-1.1	1.3	1.1	1.1	-1.4	-2.3	-1.9	1.1	-1.3	-1.1	1.3
AI552705 ESTs, Weakly similar to NPT1, MOUSE RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN, 1 [M.musculus]	1.1	-1.2	-1.1	1.5	1.0	1.88641~	1.1	-1.9	-1.3	1.5	-1.1	-1.3
AI325603 apolipoprotein E	1.2	1.3	1.6	-1.7	1.5	-1.0	1.5	-1.9	-1.3	-1.5	-2.0	-1.2
AA789873 ATPase, H+ transporting, lysosomal (vacuolar proton pump), 42kD	-1.5	1.4	1.3	1.0	1.4	1.9	-1.1	-1.8	-1.5	-1.0	-1.9	-1.2
AI326605 cyclin-dependent kinase inhibitor 1A (P21)	-1.1	-1.1	1.2	1.3	1.3	-1.04083~	-1.6	-1.9	-1.5	-1.3	-1.0	1.2
AI595258 elongation of very long chain fatty acids (FEN1/Elo2_SUR4/Elo3_ yeast)-like 2	-1.4	1.2	1.3	1.1	1.3	1.5	-1.7	-1.9	-1.7	-1.0	-1.7	-1.3
AA051884 apolipoprotein A-II	1.1	1.3	-1.0	1.1	-1.0	-1.2	-1.6	-1.9	1.1	-1.0	-1.0	1.3
AA790386 ribonuclease 1, pancreatic	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AI465691 ESTs	-1.6	1.1	1.2	1.2	1.3	1.84840~	-2.17089+	-1.9	-1.6	-1.2	-1.5	-1.5
AI385457 retinol binding protein 2, cellular	-2.0	-2.1	-1.5	-1.9	1.5	1.9	-1.3	-1.9	-1.6	-1.9	-1.5	-1.7
AA075084 elastase 2	2.3	1.4	-1.2	-2.7	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA824095 RIKEN cDNA 2810203H19 gene	-1.0	-1.2	1.3	-1.9	-1.3	1.2	-1.7	-1.9	-1.1	1.0	-1.4	-1.4
AA107035 guanylate cyclase activator 2b (retina)	-1.2	-1.3	1.1	-1.1	3.1	3.2	-1.5	-1.9	-1.2	1.2	-1.3	5.5

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TABLE 2



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AA572540_RIKEN cDNA 1700124F02_gene	-1.10123+	-1.00385+	2.1	-1.2	1.2	1.18494+-	1.26699+	-1.9	-1.3	-1.0	-1.2	-1.2
W16266_cytochrome c oxidase, subunit VIIa_1	-1.0	-1.8	-1.0	-1.1	1.2	-1.2	-1.1	-1.9	-1.5	-1.1	1.0	-1.8
AA106072_Public domain EST	1.0	-1.7	1.7	-1.1	1.0	2.9688-	-2.2	-1.9	1.0	1.3	-1.3	1.1
AA572523_ tryptophan 2,3-dioxygenase	-1.0	-1.01188+	1.4	1.1	1.1	1.1083~	-1.25829+	-2.0	-1.1	1.1	-1.1	-1.1
AA085775_gap junction membrane channel protein beta_1	1.2	1.1	1.4	-1.5	-1.8	1.1	-1.6	-2.0	-1.2	1.3	-1.3	1.2
AA082408_ESTs, Moderately similar to proteasome inhibitor hP31_subunit [H.sapiens]	-1.3	1.2	1.6	1.1	1.3	2.7	-1.7	-2.0	-1.3	-1.2	-1.5	-1.1
AA617321_ESTs, Moderately similar to OXRTGU_L1-gulonolactone oxidase [R.norvegicus]	1.01627+	-1.07473+	1.1	-1.0	-1.1	1.11102+-	1.09078+	-2.0	-1.0	-1.0	1.3	1.0
AA546945_tyrosine_3-monooxygenase/tryptophan_5-monooxygenase activation protein, zeta polypeptide	-1.3	1.3	1.4	-1.1	1.2	1.9	-1.2	-2.0	-1.5	-1.2	-1.8	-1.1
A1325764_midkine	-1.2	-1.5	-1.5	-1.5	-1.2	-1.2	-1.1	-2.0	-1.2	-1.2	-1.3	-1.4
W08617_zinc finger protein_67	-1.5	-1.1	1.2	-1.2	1.1	1.2	-1.4	-2.0	-1.7	-1.3	-1.8	-1.4
AA437863_RIKEN cDNA 1200013J08_gene	-1.6	1.0	1.4	1.4	1.3	2.48975-	-1.4	-2.0	-1.7	-1.1	-2.0	-1.3
AA414078_DNA segment, Chr 7, ERATO Doi 486, expressed	-1.7	1.2	1.4	1.2	1.2	2.83518-	1.0	-2.0	-1.4	-1.1	-2.5	-1.2
W99034_ESTs	-1.2	1.3	2.2	1.5	1.6	1.63416-	1.0	-2.0	-1.4	-1.3	-2.0	1.0
AA667301_troponin I, cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.41287~	-2.0	-2.0	-2.2	3.55726**	-1.0	1.3
A1608086_runt related transcription factor_3	-2.0	1.1	1.2	1.4	1.4	1.85234+-	-1.75763+	-2.0	-1.6	-1.3	-1.9	-1.0
W56995_hemoglobin X, alpha-like embryonic chain in Hba complex	1.1	-1.6	-1.3	-1.2	-2.2	1.11232~	-2.1	-2.0	1.0	-1.2	-4.0	-1.6
AA771393_cytochrome P450, 2d10	1.2	-1.4	1.3	-1.0	1.4	1.0	1.2	-2.0	1.2	1.1	-1.1	-1.0
A1893936_hepatic nuclear factor_4	1.0	1.1	1.4	-1.1	1.1	-1.3	-1.7	-2.0	1.3	1.2	-1.1	1.2
A1536309_RIKEN cDNA 2210410L06_gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5	-2.1
AA475351_cytochrome P450, steroid inducible 3a13	1.1	-1.1	1.4	-1.1	1.3	1.59521-	1.3	-2.0	1.1	1.0	1.3	1.1
W62007_neuron specific gene family member_2	-1.5	-1.5	-1.9	-2.3	-1.3	-1.0	1.4	-2.0	-1.6	-1.4	-1.3	-1.5
AA086994_solute carrier family_27 (fatty acid transporter), member_2	-1.3	-1.5	1.4	1.4	-1.0	1.9973~	-1.3	-2.0	-1.1	1.2	1.1	1.1
AA231039_necln	-1.8	1.3	1.1	2.3	1.7	3.5	1.0	-2.0	-1.3	-1.2	-1.7	1.0
AA016759_min1 chromosome maintenance deficient 6 (S. cerevisiae)	-1.4	1.1	1.1	1.1	1.3	1.6	-2.9	-2.0	-1.4	-1.3	-1.6	-1.1
A1508995_poliiovirus receptor-related_1	-1.6	1.3	1.3	-1.0	1.3	1.78243+-	-1.2	-2.0	-1.5	-1.4	-1.7	-1.3
AA107101_prostate stem cell antigen	-1.1	-1.4	-1.3	-2.1	-6.1	1.51614~	-1.8	-2.1	-1.0	-1.1	-1.4	-1.4
AA874101_tumor-associated calcium signal transducer_2	-2.6	-1.1	1.5	1.3	1.2	6.531-	-1.7	-2.1	-1.5	-1.5	-2.4	-1.2
W13619_small EDRK-rich factor_1	1.1	1.1	1.0	-1.0	-1.0	-1.89596~	1.1	-2.1	-1.1	-1.1	-1.1	-1.3
AA874987_RIKEN cDNA 1110036G14_gene	-1.1	1.3	-1.1	-2.1	1.2	1.5	-1.3	-2.1	-1.4	-1.4	-1.8	-1.2
AA92480_ESTs, Weakly similar to retinal short-chain dehydrogenase/reductase retSDR1 [M.musculus]	1.7	1.6	2.1	1.1	-1.2	2.00363	-1.5	-2.1	1.2	-1.2	1.0	-1.7
AA067002_methionine adenosyltransferase L, alpha	1.4	1.3	1.2	1.3	1.3	1.2989~	-1.6	-2.1	1.3	1.1	1.2	1.6
W78548_alpha internexin neuronal intermediate filament protein	1.3	-1.2	-1.2	1.4	1.0	1.9213	1.2	-2.1	-1.2	-1.4	-1.4	-1.6
AA880322_celponitin_1	-1.2	-1.4	-1.1	-1.1	1.1	-2.6	-1.7	-2.1	-1.5	-1.2	-1.4	-1.0

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TABLE 2

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AI323053 forkhead box D3	-1.5	1.0	1.4	1.0	1.2	3.0	-1.4	-2.1	-1.5	-1.3	-1.7	-1.3
AA223986 inhibitor of DNA binding 4	-2.0	1.3	1.2	1.5	1.4	2.608841~	1.1	-2.1	-1.1	-1.5	-1.6	-1.2
AA966993 muS homolog 5 (E. coli)	-1.5	1.3	1.7	1.3	1.3	2.26141~	-1.0	-2.1	-1.4	-1.3	-1.8	-1.0
AA096594 RIKEN cDNA 2900089E13 gene	-1.5	1.1	1.3	1.4	1.1	1.8	-1.2	-2.1	-1.3	-1.2	-1.8	-1.3
AI366082 carbonic anhydrase 3	1.1	-1.3	2.1	-1.5	1.1	-2.4	-1.7	-2.1	-1.3	-1.2	-1.6	-1.5
AA880530 Public domain_EST	-1.5	-1.0	1.5	1.2	1.2	1.64332~	1.5	-2.2	-1.1	-1.2	-2.2	-1.1
AA049060 inter-alpha-trypsin inhibitor, heavy chain 4	1.5	1.3	1.2	-1.2	-1.0	1.06302~	-2.1	-2.2	1.7	1.1	1.4	1.3
AA571365 Mus_musculus_MRP56_mRNA_for_mitochondrial_ribosomal_protein_S6_part1 cds	-1.2	-1.1	1.3	1.3	1.3	2.8	-1.9	-2.2	-1.2	-1.0	-1.4	-1.3
AI510586 Mus_musculus_high-affinity_Na+/dicarboxylate_cotransporter_NaDC3_mRNA_complete_cds	-1.3	-1.4	-1.1	-1.3	-1.1	2.21173~	-1.2	-2.2	-1.3	1.2	-1.4	1.2
W09847 non-catalytic region of tyrosine kinase adaptor protein 2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.2
AA755970 natriuretic peptide precursor type A	1.1	-1.8	1.2	1.3	-1.1	2.47857~	-1.3	-2.2	-1.8	1.2	-1.4	-1.7
AA237986 cytochrome P450_3a25	1.5	-1.2	1.3	-1.1	1.0	2.35788~	-1.1	-2.2	1.2	1.1	1.0	1.3
AA674821 folate receptor_1 (adult)	-1.1	-1.3	1.2	1.3	1.1	1.5	-1.2	-2.2	-1.4	1.2	-1.2	1.3
AA755277 inter-alpha-trypsin inhibitor, heavy chain 1	1.2	-1.2	1.1	-1.0	1.3	1.71355~	-1.96147+	-2.2	1.2	-1.3	-1.0	-1.1
AA667621 S-phase_kinase-associated_protein_2 (p45)	-1.8	-1.2	2.0	1.5	1.2	2.74757~	-1.73102+	-2.2	-1.8	-1.4	-1.9	-1.3
AA066739 RIKEN cDNA 2600001B17 gene	-1.6	1.3	1.5	1.0	1.3	1.2	-1.4	-2.2	-1.5	-1.3	-1.8	-1.2
W36030 Friedrich ataxia	-1.5	1.1	1.4	1.1	1.2	1.66415~	-1.6	-2.3	-1.5	-1.4	-1.7	-1.3
AA066835 corticosteroid binding globulin	1.0	1.2	1.8	-1.1	1.2	1.4	-2.4	-2.3	1.1	-1.0	-1.3	-2.4
AA674450 RIKEN cDNA 1300007O05 gene	1.3	-1.8	1.7	1.2	1.3	1.94848~	-1.2	-2.4	1.1	-1.1	-1.0	-1.1
AA881492 ESTs	-2.0	1.3	1.1	-1.2	1.1	1.1	1.0	-2.4	-1.5	-1.5	-1.7	-1.1
AA242360 cytochrome P450_1a2, aromatic compound inducible	1.3	-1.5	1.4	-1.1	-2.8	-1.33495~	-1.37353+	-2.4	1.8	1.1	1.2	1.2
AA238308 complement component 4 binding protein	1.5	-1.1	1.2	-1.4	1.2	-1.42054~	-1.1	-2.4	1.4	-1.3	1.1	1.0
AI481911 Mus_musculus_clone_MGC-6727_mRNA_complete_cds	-1.1	-2.0	-1.8	1.0	-1.8	-2.3	-1.5	-2.4	-1.4	3.8	-1.4	-1.4
W82417 apolipoprotein CIV	1.5	-1.4	1.4	-1.0	-1.0	-1.16601~	-1.64355+	-2.4	-1.1	-1.2	-1.1	-1.4
AA242413 asialoglycoprotein receptor 1	1.4	-1.1	1.3	-1.1	1.0	-1.17665+~	-1.2	-2.4	1.1	1.1	1.1	1.1
AA066016 RIKEN cDNA 1190002H23 gene	-1.6	1.2	1.2	1.5	1.5	3.33219~	-2.0	-2.4	-1.4	-1.6	-2.0	-1.3
AA034678 rhoteikin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4
AA763276 small muscle protein_X-linked	-1.7	-1.4	1.1	1.6	1.2	1.9	-4.6	-2.5	-1.6	-1.2	-2.0	-1.5
AI047903 topoisomerase (DNA)_III beta	-1.7	-1.0	1.4	1.1	1.1	2.1785~	-1.4	-2.5	-1.7	-1.5	-2.1	-1.5
W65070 ESTs	-1.2	1.4	2.1	1.7	1.6	1.8	1.1	-2.6	-1.4	-1.4	-2.3	-1.1
AI428661 ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.6	-2.6	-2.1	-1.7	-2.2	-1.5
AA881013 cytochrome P450_2c37	1.0	-1.1	2.8	1.1	1.8	1.5	-1.2	-2.6	1.0	1.1	-1.1	1.5
AI322367 insulin-like growth factor 2	-1.2	-1.8	-1.4	-1.9	-1.5	1.4	-1.5	-2.6	-1.2	-1.6	-1.2	-1.8
AI324412 UDP-glucuronosyltransferase 2 family_member_5	1.3	-1.3	1.5	1.0	-1.1	1.91048~	-1.1	-2.7	1.0	-1.5	-1.1	1.1

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TABLE 2

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AA967219 retinol binding protein_4, plasma	1.1	-1.5	1.3	1.1	1.1	1.3	-1.8	-2.7	1.0	-1.2	-1.6	-1.5
W08430 serine protease inhibitor 1-4	1.3	1.3	-1.2	1.1	-1.2	-1.8	1.1	-2.7	1.0	1.1	1.2	1.2
AA684320 activin receptor interacting protein 1	-1.9	1.4	1.3	1.3	1.5	2.80454~	1.0	-2.7	-1.4	-1.1	-1.9	-1.3
AA980366 vitronectin	1.1	1.5	1.3	1.1	-1.1	2.20376~	1.2	-2.9	-1.1	-1.3	-1.4	-1.3
AA24687 orosomucoid 2	1.3	-1.4	1.5	-1.8	-1.4	-1.70975~	-1.6	-3.0	-1.2	-1.2	1.4	-1.6
AA014727 tumor-suppressing subchromosomal transferable fragment 3	-2.1	1.1	1.8	-1.2	1.1	2.05235~	-1.8	-3.0	-2.1	-1.8	-2.9	-1.0
AA546645 cell division cycle 2 homolog (S. pombe)-like 2	-2.1	-1.1	1.3	1.4	1.1	2.3	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA176045 forkhead box C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.6	-2.5	-1.1
W33918 serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	1.7	-1.1	1.5	-1.1	-1.1	-1.36639~	1.2	-3.1	1.1	1.4	-1.6	-2.2
AI326560 complement component factor i	1.3	-1.2	1.7	-1.5	-1.6	1.76989~	1.2	-3.1	1.1	-1.0	-1.5	-1.1
AA771228 ESTs, Weakly similar to zinc finger protein 95 [M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.7115~	-2.0	-3.3	-2.2	-1.4	-2.4	-1.4
AA821932 small inducible cytokine A6	1.0	-1.0	1.6	-1.6	1.3	1.2	-1.3	-3.4	-1.2	1.3	-1.9	-1.7
AA212714 murinoglobulin 2	1.4	-1.5	1.4	-1.4	-1.1	1.0114~	-1.3	-3.4	-1.0	1.2	1.5	1.4
AA106793 plasminogen	1.1	-1.6	1.3	1.0	1.1	2.40205~	-2.2	-3.6	1.0	1.0	-1.4	-1.1
AA474336 synaptosomal complex protein 3	-2.8	1.2	2.8	1.4	1.5	2.14133~	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AI893895 cytochrome P450, 2d9	1.2	-1.7	1.3	-1.4	-1.4	1.7	-1.9	-3.7	1.1	-1.0	1.1	1.1
AA822002 cytochrome P450, 2c40	1.3	-1.2	1.9	1.3	1.4	1.4	1.1	-3.9	-1.1	-1.2	-1.3	-1.2
AA739490 serine protease inhibitor-2 related sequence 1	1.5	-1.2	1.5	1.4	1.3	1.2	1.2	-3.9	1.1	-1.1	1.1	1.1
W14912 kallikrein binding protein	1.5	-1.7	1.5	-1.4	-1.2	-1.3	1.2	-4.0	-1.0	1.0	-1.1	-1.2
AI117779 orosomucoid 1	1.1	-1.8	1.3	-1.5	-1.3	-1.64866~	-1.8	-4.2	-1.4	-1.2	1.2	-1.5
AA388066 regucalcin	1.2	-1.3	1.5	-1.1	1.2	1.00609~	-1.2	-4.2	1.0	1.0	1.1	-1.2
AA024217 Public domain EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AA261401 serum amyloid P-component	1.4	-1.3	-1.2	-1.4	-1.0	-1.65106~	1.0	-4.3	1.0	1.1	1.0	1.3
AA016788 ESTs, Moderately similar to Ebp1 protein [M.musculus]	1.2	-1.0	1.2	-1.0	1.3	1.47097~	-1.4	-4.5	-1.1	-1.6	-1.1	-1.3
W34349 coagulation factor XII (Hageman factor)	1.1	1.1	1.2	1.1	1.1	1.07468~	1.1	-4.6	-1.3	-1.1	-1.2	1.2
AA272831 betaine-homocysteine methyltransferase	1.3	-1.3	2.0	-1.0	1.1	-1.62438~	1.1	-4.7	1.3	-1.3	1.2	-1.1
AA822028 group specific component	1.5	-1.4	1.0	1.0	1.3	1.5	-1.4	-5.1	1.2	1.2	-1.1	1.1
AI386236 DNA segment, Chr 1, University of California at Los Angeles_3	-1.0	-1.5	1.66267~	1.3	-1.5	1.3	-1.1	-5.1	-1.4	-1.2	-1.2	-1.5
AI466451 fatty acid binding protein 1, liver	-1.5	-1.5	1.4	-1.2	-1.2	3.27698~	-1.3	-5.1	-1.3	-1.2	-1.3	-1.2
AA771396 4-hydroxyphenylpyruvic acid dioxygenase	1.1	-1.4	1.2	1.1	1.4	1.1	-2.1	-5.2	1.3	-1.2	1.1	1.5
AA189266 ESTs	-3.2	1.4	1.5	1.5	1.3	1.3	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
AA670733 murinoglobulin 2	1.7	-1.1	1.2	1.4	1.3	1.63761~	-1.4	-5.8	-1.2	1.0	1.1	-1.2
AA980395 apolipoprotein H	1.3	-1.3	1.4	1.4	1.2	1.77985~	-1.0	-7.1	1.3	1.2	1.1	1.1
AA822116 transthyretin	1.2	-1.1	1.5	-1.5	-1.4	1.55827~	-1.3	-7.7	-1.0	1.1	-2.0	-1.6

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AA066867	RIKEN cDNA 3010002H13 gene	1.3	-1.1	1.0	-1.1	-2.0	1.48546~	1.4	-7.9	-1.1	-1.1	-1.7	-1.2
W54403	ATPase, Cu++ transporting, beta polypeptide	1.2	-2.1	1.1	-1.0	1.2	1.3	-2.9	-7.9	1.1	-1.1	-1.1	1.2
AA675399	murinoglobulin 1	1.5	-1.5	1.1	-1.0	1.0	2.76483~	-1.8	-7.9	-1.1	-1.1	1.3	1.0
AA847335	cytochrome P450, steroid inducible 3a11	1.5	-1.4	1.1	1.1	2.2	8.36011~	-1.3	-8.0	-1.0	-1.1	1.2	1.1
AA822098	apolipoprotein A-I	-1.9	-1.5	1.1	-2.4	2.4	2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.6
AA066997	alpha-2-macroglobulin	1.3	-1.4	1.0	1.1	1.2	1.52434~	1.1	-10.5	-1.1	-1.7	1.3	-1.2
AA822009	hemopexin	1.1	-1.2	-1.1	1.2	1.1	2.36586~	-1.6	-11.1	1.2	-1.6	-1.3	1.2
W13979	serine protease inhibitor 1-5	1.1	-1.7	1.2	-1.3	-1.3	-1.1	-1.5	-14.7	-1.2	-1.1	-1.4	-1.5
W37032	serine protease inhibitor 1-3	1.1	-1.6	1.4	-1.5	-1.5	-1.11273~	-1.3	-15.2	-1.4	-1.4	-1.5	-1.8
AA674270	major urinary protein 1	1.1	-1.1	-6.01013*	-2.7	1.0	1.09942~	1.5	-16.7	-1.5	-1.6	-1.6	-1.4
AA822106	ESTs, Weakly similar to CO8A_HUMAN_COMPLEMENT_COMPONENT_C8 ALPHA_CHAIN_PRECURSOR [H.sapiens]	2.7	-1.7	2.2	-1.0	1.1	2.60798~	-1.8	-20.2	-1.5	-1.3	-1.4	-2.7
AA822027	ATPase, Cu++ transporting, beta polypeptide	1.2	-1.9	1.2	-1.4	-1.0	1.17594~	-1.2	-21.9	-1.5	-1.5	-1.8	-1.7
A1386058	serum albumin variant	2.9	-1.7	2.0	1.1	-1.1	1.66348~	-1.3	-23.1	-1.4	-1.5	-1.3	-2.9
AA822105	major urinary protein 1	-1.1	-2.4	-28.7649*	-7.8	-1.1	1.43224~	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2

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TABLE 2

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brain	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL- 4B_BDEnor	PL- 2B_BDEnor	PL- 6B_BDEnor	PL- 9B_BDEnor	PL- 9B_BDEnor	PL-5B_BDEnor	1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
AA068763 hemoglobin_beta_adult_major_chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.8	-1.1	-1.3	1.5	-1.8	-2.0
W16809 hemoglobin_beta_adult_major_chain	1.5	-1.2	1.2	-2.9	1.3	-3.7	3.4	-1.2	-1.0	1.8	-1.7	-1.6
W14953 kinase-associated protein_3	-1.0	-1.0	1.4	3.2	-1.2	-3.932~	3.3	-1.2	-1.2	1.3	-1.5	-1.5
AA106071 hemoglobin_beta_adult_major_chain	1.3	-1.4	1.2	-3.0	-1.1	-4.3	3.2	1.1	-1.3	1.8	-1.7	-2.0
AB14738_RIKEN_cDNA_261030115_gene	1.3	2.07881+	1.1	2.4	1.5	1.2409+	2.9	1.4	1.5	1.8	1.5	1.6
AI447957_ESTs	1.1	1.7	1.0557+	2.5	1.85853+	-1.08065+	2.8	1.6	1.7	1.8	2.1	2.1
AI551391_ESTs_Weakly_similar_to_FY1_MOUSE_FRIEND_VIRUS_BU	1.2	1.71031+	-1.05799+	2.7	1.7	1.39433+	2.5	1.67563+	1.6	1.5	1.8	1.8
AA289586_protein_kinase_C_beta	-1.5	1.2	-1.6	1.3	1.1	-1.16438+	2.4	1.01996+	-1.1	-1.1	1.1	1.1
AA821884_amylase_2_pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.3	-1.2	-4.4	-1.1	-1.1	-1.2
AA588976_ESTs	1.1	1.8	-1.5	2.6	1.7	1.17361+	2.3	1.88668+	1.7	1.4	1.9	2.1
W57281_Mest-linked_imprinted_transcript_1	1.3	1.2	1.1	1.3	1.1	-1.43302+	2.3	1.5	1.4	1.1	1.7	1.2
AI549687_RIKEN_cDNA_573040615_gene	1.3	1.7	-1.0	1.1	-1.0	1.01531+	2.3	1.0	1.1	1.3	1.1	1.1
AA002994_ESTs_Moderately_similar_to_No_similarities_to_any_reported_protein_s_[H.sapiens]	1.1	1.0	-1.3	2.5	-1.1	-1.28021+	2.3	1.0	-1.2	1.2	-1.2	-1.0
AI529513_ESTs_Moderately_similar_to_F26L_MOUSE_8PF-2-KIFRU-2,6-P2ASE_LIVER_ISOZYME_[M.musculus]	-1.2	1.1	1.1	-1.6	1.1	-2.6	2.2	1.3	-1.1	1.4	-1.3	-1.3
AI605734_septin_3	1.0	-1.4	1.0	1.2	-1.7	1.78421+	2.1	1.2	1.1	-1.2	1.3	1.1
AI484803_RIKEN_cDNA_0740001E13_gene	1.1	1.1	1.0	2.0	1.4	-1.08185+	2.1	1.08953+	1.4	1.2	1.4	1.4
AA717025_Mus_musculus_10_day_old_male_pancreas_cDNA_RIKEN_full-length_enriched_library_clone:1810009A17_full_insert_sequence	1.8	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.8	-2.9	1.2	-1.1	-1.4
AA117355_RIKEN_cDNA_1190006L01_gene	-1.0	1.8	-1.0	1.7	1.0	1.23278+	2.1	1.2	1.2	-1.0	1.3	1.4
AA287673_ESTs	-1.18/24+	1.5	1.37787+	1.3	1.2	-1.28358+	2.1	1.15552+	1.1	1.3	1.2	1.2
AI594945_RIKEN_cDNA_6330408P08_gene	1.05631+	1.20985+	-1.07584+	1.2	1.09763+	-1.02044+	2.1	-1.01366+	-1.02153+	1.4	-1.1	1.0976+
AA119984_liver-specific_bHLH-Zip_transcription_factor	1.5	1.3	1.0	-1.0	1.5	1.31112~	2.1	1.1	1.2	1.4	1.1	1.1
AA522311_RIKEN_cDNA_0610038P07_gene	1.2	1.7	-1.1	1.8	1.2	-1.08749+	2.0	1.3	1.6	1.4	1.5	1.5
AA987657_brain_protein	1.0	-1.0	-1.1	-1.2	-1.5	1.00533~	2.0	1.1	1.0	-1.5	1.2	1.1
AA253844_ESTs	1.4	1.3	1.0	1.8	1.1	-1.54029~	2.0	1.3	1.48945*	1.2	1.4	1.24284*
AI122516_microtubule-associated_protein_6	1.1	1.0	-1.6	1.4	1.4	1.28845+	2.0	1.1	-1.0	-1.1	-1.2	-1.1
AI430438_RIKEN_cDNA_3110023G01_gene	1.0	1.2	-1.4	1.8	1.5	1.34987+	2.0	1.2	-1.0	1.1	1.1	-1.0
AI505996_stearoyl-Coenzyme_A_desaturase_2	1.4	1.2	-1.3	2.1	1.4	-1.5	2.0	1.5	1.5	1.2	1.4	1.3

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TABLE 2

BRAIN

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PCT/US02/41825

AA200457_ESTs	-1.4	1.2	-1.6	-1.1	1.19151*	1.03839+~	2.0	-1.2	-1.1	1.1	-1.3	-1.1
AA324398_glycosylphosphatidylinositol_specific_phospholipase_D1	1.1	-1.3	1.2	-3.4	2.3	-1.5	2.0	-1.2	-1.3	1.2	-1.6	-1.6
AA828696_peptidyl_arginine_deiminase_type_II	-1.4	1.0	-1.5	-1.3	1.1	-1.10637+~	2.0	-1.2	-1.3	1.0	-1.4	1.1
AA123314_ESTs_Highly_similar_to_S68176_TOG_protein_H.sapiens	1.1	-1.0	-1.2	-1.0	1.1	-1.0657~	2.0	1.3	-1.1	-1.0	-1.1	-1.2
AA473684_RIKEN_cDNA_C030002017_gene	1.22138+	1.56183+	-1.02182+	2.3	1.37779+	-1.21258+~	2.0	1.50959+	1.3697+	1.62061+	2.24475+	1.7053+
AA518686_ESTs	1.2	1.4	-1.3	2.0	1.5	-1.5	2.0	1.4	1.4	1.2	1.5	1.6
AA412921_RIKEN_cDNA_4921514120_gene	1.4	1.6	1.0	2.1	1.4	-1.23027~	1.9	1.7	1.6	1.4	1.6	1.5
AA051041_potassium_voltage-gated_channel_subfamily_Q_member_2	1.1551+	1.9792+	1.21255+	-1.0	1.71234+	1.50089+~	1.9	-1.0726+	1.10775+	-1.1	-1.21672+	-1.20296+
AA604587_ESTs	1.2	1.3	-1.1	3.3	1.5	-1.02494+~	1.9	1.5	1.6	1.3	1.5	1.6
AA059783_Public_domain_EST	1.14965+	-1.05364+	1.39958+	1.1	1.05655+	-1.18682+~	1.9	1.19474+	1.1	1.2	1.1	-1.1
AA466153_ESTs	1.0	-1.11378+	1.02861+	1.2	-2.4	-1.16147+~	1.9	1.09478+	1.2	1.3	1.1	-1.33715+
AA222952_zuotin_related_factor_2	1.0	-1.16406+	1.12995+	-1.34277+	-1.48418+	-1.47865+~	1.9	1.03133+	-1.14619+	1.0	1.0	-1.0
AA552958_RIKEN_cDNA_1110003E08_gene	1.0	1.0	-1.1	1.9	1.4	-1.16793~	1.9	1.1	1.1	1.1	1.2	1.2
AA416143_ESTs	1.08986+	-1.2	-1.0032+	1.4	1.2	-1.04633+~	1.9	1.00503+	-1.1	1.0	-1.1	1.2
AA58253_RIKEN_cDNA_1500015J03_gene	1.26047+	1.92377+	-1.04077+	1.8417+	1.58234+	1.32632+~	1.9	1.37534+	1.4	1.5	1.4	1.39535+
AA553232_ribosomal_protein_S6	1.2	1.5	1.0	2.2	1.2	-1.20532+~	1.9	1.8	1.6	1.4	2.1	1.7
AA511234_ESTs	-1.1	1.1	-1.3	1.1	-1.6	-1.6533+~	1.9	1.0	-1.2	-1.1	-1.1	1.0
AA50872_RAS11a_member_RAS_oncogene_family	-1.1	1.3	-1.6	1.6	1.6	-1.31004+~	1.9	1.3	1.2	1.3	1.2	1.4
AA839604_ESTs	-1.6	-1.1	-1.55245+	-1.2	1.0	-1.36963+~	1.9	1.0	-1.3	1.2	-1.1	-1.3
AA120302_ESTs	-1.2	1.1	-1.2	1.3	1.4	-1.30774+~	1.9	1.1	-1.1	1.1	1.0	1.2
AA412912_ESTs	1.2	1.5	-1.4	2.2	1.5	-1.07075+~	1.9	1.6	1.7	1.2	1.5	1.8
AA003144_ESTs	-1.00111+	-1.05949+	1.0939+	1.1	1.00927+	1.05326+~	1.9	-1.02885+	1.1	1.4	1.1	1.0
AA387339_ESTs	-1.2	1.0	1.1	-1.5	-1.7	-1.14348~	1.9	-1.1	-1.1	-1.1	-1.0	-1.1
AA738833_solute_carrier_family_1_member_7	1.2	-1.2	-1.5	-1.7	-1.2	1.0	-1.9	1.2	-1.1	-1.0	1.1	-1.5
AA893895_cytochrome_P450_2d9	1.2	-1.7	1.3	-1.4	1.7	1.1	-1.9	-3.7	1.1	-1.0	1.1	1.1
W30045_eukaryotic_translation_initiation_factor_4E_binding_protein_1	1.0	1.3	1.1	-1.2	1.0	-1.0	-1.9	-1.2	1.0	-1.0	-1.1	-1.2
W59510_elastin	-1.2	-1.4	-1.3	-1.7	-1.2	1.1	-1.9	-1.0	-1.1	-1.3	1.0	-1.3
AA68219_intelectin	-1.0	-1.3	-1.1	1.7	2.0	2.2	-1.9	1.3	1.2	-1.0	1.5	1.8
AA822098_apolipoprotein_A-I	-1.9	-1.5	1.1	-2.4	2.1	2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.6
AA326604_cyclin_F	-1.1	1.0	1.2	1.0	-1.0	1.1	-1.9	-1.1	1.1	1.1	-1.1	1.1
AA671135_myosin_heavy_chain_cardiac_muscle_adult	-1.1	-1.7	1.3	1.2	1.1	2.1	-1.9	-1.3	-2.1	1.4	-1.2	-1.3
AA930278_ESTs	1.1	-1.3	1.1	-1.2	-1.1	1.36967~	-1.9	1.1	1.0	-1.0	-1.1	-1.0
AA156185_cystic_fibrosis_transmembrane_conductance_regulator_homolog	1.2	-1.42323+	-1.16278+	-1.4	-1.9	-1.16394~	-1.9	1.2	1.17519+	-1.1	1.0	-1.4
AA792001_RIKEN_cDNA_4931400A14_gene	-1.3	1.2	1.1	-1.1	-1.2	-1.06494+~	-1.9	1.1	-1.0	1.0	1.0	1.1
AA672765_Niemann_Pick_type_C1	1.1	-1.3	1.3	-1.5	-1.0	1.27447~	-1.9	-1.1	1.0	-1.3	-1.1	-1.2

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BRAIN

TABLE 2

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AA792268_solute_carrier_family_4_(anion_exchanger)_member_1	1.0	-1.5	1.1	-1.1	-1.1	1.2	-1.9	-1.5	-1.1	-1.2	-1.6	-1.7
W53917_serine_hydroxymethyl_transferase_1_(soluble)	1.0	-1.1	1.3	1.1	-1.1	-1.6	-1.9	-1.2	1.1	-1.2	1.0	-1.1
AA464601_ESTs	-1.06043+	-1.40465+	-1.02444+	1.02571+	-1.14202+	-1.23593+	-1.9	1.2	-1.12881+	-1.0	-1.07024+	1.06265+
AA096815_Public_domain_EST	1.2	-1.3	1.2	1.5	1.2	-2.2907	-1.9	-1.2	1.3	1.0	1.0	1.4
W80245_ESTs	-1.2	1.4	-1.1	-1.4	-1.3	1.3	-1.9	-1.5	-1.2	-1.3	-1.2	1.0
AA51578_RIKEN_cDNA_1600013P15_gene	-1.3	-1.4	1.3	1.0	-1.6	-1.7	-1.9	-1.1	-1.0	-1.2	1.0	1.0
AA880295_immunoglobulin_joining_chain	1.2	-1.5	-1.4		-2.2	-2.4	-1.9	-1.1	1.3	1.5	1.4	-1.3
AA871838_phospholipase_A2_group_IIA_(platelets_synovial_fluid)	-1.1	-1.0	-1.2	1.7	2.8	1.9	-1.9	-1.3	1.5	1.2	1.3	1.1
AA529474_carbohydrate_(N-acetylglucosamine_6-O)_sulfotransferase_5	1.0	1.4	-1.1	1.3	1.2	1.07225+	-1.9	1.2	-1.1	1.0	1.0	1.1
AA277642_ESTs_Weakly_similar_to_A53399_LB_antigen_-_mouse_[M.musculus]	-1.2	-1.1	1.4	-1.1	-1.3	3.61228+	-1.9	-1.1	1.1	1.2	1.1	1.7
AA667906_cysteine-rich_protein_2	1.2	1.1	1.5	-1.6	-1.3	-1.3	-1.9	-1.5	-1.2	-1.1	-1.2	-1.3
AA444443_immunoglobulin_heavy_chain_6_(heavy_chain_of_igm)	-1.2	-1.8	-1.4	1.1	1.2	-2.1	-1.9	1.1	1.0	-1.0	1.2	1.0
AA065522_RIKEN_cDNA_1700029G01_gene	-1.2	-1.4	-1.0	-1.1	-1.3	1.2	-1.9	-1.2	-1.1	-1.1	-1.1	-1.1
AA656407_troponin_T1_skeletal_slow	1.1	-1.2	1.3	-1.1	1.2	1.85435+	-1.9	-1.1	-1.0	1.1	1.1	-1.5
W18463_thioether_S-methyltransferase	1.0	-1.5	2.0	-1.3	-1.6	-1.6	-1.9	-1.0	-1.7	1.2	-1.0	-1.2
AA065551_Mus_musculus_clone IMAGE:3489758_mRNA_partial_cds	-1.0	-1.2	1.2	1.1	1.1	1.82438+	-1.9	-1.2	1.0	-1.2	1.0	-1.0
AA571365_Mus_musculus_MRP56_mRNA_for_mitochondrial_ribosomal_protein_S6_partial_cds	-1.2	-1.1	1.3	1.3	1.3	2.9	-1.9	-2.2	-1.2	-1.0	-1.4	-1.3
AA146546_ESTs	-1.2	-1.4	-1.4	-1.5	-1.1	-1.03444+	-1.9	-1.1	-1.3	-1.2	-1.3	-1.2
AA028420_small_proline-rich_protein_1A	1.3	-1.7	-1.4	-1.5	-1.9	-1.2	-1.9	-1.2	1.0	-1.1	1.3	1.3
AA718431_RIKEN_cDNA_1700020B19_gene	1.0	-1.2	1.2	1.0	1.2	1.46773+	-1.9	-1.2	-1.1	-1.1	-1.2	-1.3
AA109757_solute_carrier_family_22_(organic_cation_transporter)-like_2	-1.2	-1.0	-1.1	-1.3	-1.3	1.2	-1.9	-1.0	-1.1	1.2	-1.1	-1.1
AA65613_RIKEN_cDNA_2210401F01_gene	1.1	-1.2	1.1	-1.2	-1.7	1.4	-1.9	1.8	-1.0	-1.1	1.0	1.1
AA671264_troponin_T2_cardiac	1.0	-1.7	-1.3	-1.1	-1.2	-1.0	-1.9	-1.6	1.1	1.4	-1.2	-1.2
AA64912_ESTs_Weakly_similar_to_A53583_testosterone-resistant_1_immunity-associated_protein_AP38_-_mouse_[M.musculus]	-1.2	-1.2	1.1	-1.1	1.3	1.56425+	-1.9	-1.1	-1.2	-1.4	-1.1	-1.4
AA181090_cytochrome_P450_subfamily_IV_B_polypeptide_1	1.0	-1.4	-1.1	-1.1	1.1	1.9	-1.9	-1.2	-1.2	1.1	-1.1	-1.1
AA764455_Mus_musculus_clone MGC:8241_mRNA_complete_cds	1.3	-1.4	-1.3	-1.5	-1.4	-1.32023+	-1.9	1.2	-1.1	-1.1	-1.1	1.1
AA117605_cytotoxic_granule-associated_RNA-binding_protein_1	1.3	-1.1	1.1	-1.0	1.1	-1.1	-1.9	1.0	-1.0	-1.2	1.0	-1.0
AA544749_myosin_Ic	-1.1	-1.1	1.0	-1.2	-1.4	1.0	-1.9	1.1	-1.1	1.0	-1.1	-1.2
AA754656_immunoglobulin_heavy_chain_6_(heavy_chain_of_igm)	1.3	-1.5	1.0	-1.2	-1.9	-3.2	-1.9	-1.0	-1.2	-1.0	-1.1	-1.4
W53837_mitogen_activated_protein_kinase_13	1.0	1.1	-1.0	-1.2	-1.0	-1.5	-1.9	-1.1	-1.0	-1.1	-1.0	1.1
AA800430_myeloblastosis_oncogene-like_2	-1.1	-1.2	1.1	-1.1	-1.2	1.24314+	-2.0	-1.1	-1.1	-1.1	-1.3	1.0
AA982280_N-myc_(and_STAT)_interactor	-1.2	-1.2	1.5	1.0	-1.2	1.0219+	-2.0	-1.2	1.1	-1.3	-1.0	1.2
AA798953_transformation_related_protein_63	1.0	-1.5	-1.3	1.1	1.2	1.35181+	-2.0	-1.1	-1.2	-1.2	-1.0	-1.0
AA046576_testis_specific_gene_1	1.4	-1.3	-1.4	1.5	1.2	-1.05001+	-2.0	1.3	1.2	-1.1	1.5	-1.6

TABLE 2

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AA681032_Mus musculus ETL1 mRNA, complete cds	-1.2	-1.0	1.3	1.1	1.1	1.1	-1.2	-1.1	-1.3	-1.2	-1.1
AA771566_tropoin_C_fast_skeletal	1.1	-1.6	1.4	-1.1	1.0	1.0	-2.0	-3.0	-1.3	-1.3	-1.3
AA545451_gamma-glutamyl_transpeptidase	1.0	1.4	-1.8	1.4	1.4	1.4	-2.0	-1.5	1.4	1.3	1.1
AA458072_adipocyte complement related protein of 30 kDa	1.3	-1.2	-1.0	-1.3	1.0	1.0	-2.0	-1.1	-1.5	1.1	1.3
AA047912_Mus musculus_DNA_segment_Chromosome_1_Pasteur_institute_1_(D1Pas1)_mRNA	1.07563+	-1.57658+	-1.09024+	-1.13529+	-1.21199+	-1.5955+	-2.0	1.30571+	-1.08385+	1.1837+	-1.0
AI385784_plectrin_2	-1.1	-1.1	-1.0	1.2	1.1	1.1	-2.0	1.0	-1.1	1.0	-1.1
AA671573_chemokine (C-C) receptor_5	1.0	-1.1	1.1	-1.5	-1.1	-1.1	-2.0	-1.2	-1.4	-1.3	1.0
W16358_mucin_1_transmembrane	1.5	1.4	-1.2	-2.2	-1.3	-1.1	-2.0	1.0	1.1	-1.2	1.0
AI227408_lyosomal trafficking regulator	-1.2	-1.25843+	-1.02071+	-1.01518+	-1.22397+	1.08155+	-2.0	1.5	-1.0	-1.2	-1.2
AA711611_RIKEN cDNA_1110015E18_gene	1.0	-1.2	1.4	1.3	1.1	1.1	-2.0	1.1	-1.1	-1.3	-1.2
AA760185_carbonic anhydrase_6	-1.2	-1.7	-1.0	-1.2	-1.2	-1.2	-2.0	1.8	-1.6	-1.2	-1.4
AI552705_NADPH oxidase_4	-1.0	-1.0	1.3	-1.0	1.4	1.4	-2.0	1.1	-1.0	-1.4	1.1
AA667824_arginine vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-1.4	-2.0	-1.4	1.4	-1.2	-2.3
AI098411_Public domain_EST	-1.3	-1.0	1.3	-1.2	-1.1	1.0	-2.0	-1.2	-1.1	-1.1	-1.2
AI594906_ESTs	-1.28447+	-1.28228+	1.1	1.4	-1.1	1.1	-2.0	-1.2	-1.3	-1.0	-1.00617+
AA414490_RIKEN cDNA_1200014D15_gene	1.3	-1.4	1.4	-1.2	1.0	1.0	-2.0	-1.8	-1.1	-1.1	1.0
W13870_amino-terminal enhancer of split	1.1	-1.0	-1.0	1.0	-1.0	-1.2	-2.0	-1.1	1.1	1.1	1.1
AA771229_ESTs_Weakly similar to zinc finger protein 95 [M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.2	-2.0	-3.3	-2.2	-1.4	-1.4
AA760220_RIKEN cDNA_2300002G24_gene	1.1	-1.0	1.2	-1.1	1.3	1.3	-2.0	-1.3	-1.0	-1.2	-1.1
AI385961_cAMP responsive element modulator	-1.1	-1.1	-1.0	1.1	1.2	1.2	-2.0	-1.2	-1.1	-1.1	1.2
AI152670_ESTs	1.16789+	-1.54754+	-1.28954+	-1.39621+	-1.48435+	-1.01746+	-2.0	-1.03099+	1.06908+	-1.1	-1.38695+
AA739040_lipoprotein lipase	1.1	-1.4	1.1	-1.3	-1.0	1.2	-2.0	1.1	-1.6	1.3	-1.3
AA004134_centromere autoantigen A	1.0	-1.1	1.2	1.1	1.1	1.1	-2.0	-1.6	-1.1	-1.2	1.0
AA105999_B-cell src-homology tyrosine kinase	-1.4	1.08091+	1.5	1.2	1.0	1.0	-2.0	-1.4	-1.0	-1.3	1.0
AA874245_RIKEN cDNA_1810047J07_gene	1.2	-1.3	-1.1	-1.2	-1.1	-1.1	-2.0	1.2	-1.0	1.1	1.1
AA756749_submaxillary_gland_androgen regulated protein_1	-1.1	-1.6	1.0	-1.3	-1.2	-1.2	-2.0	1.3	-1.2	-1.2	-1.8
AI894035_proteinase convertase subtilisin/kexin type 5	1.1	-1.49699+	-1.0	-1.2	1.3	1.3	-2.0	-1.0	1.0	-1.1	-1.2
AI450453_ESTs_Weakly similar to T33424_hypothetical protein_M01G5.4_-Caenorhabditis elegans [C.elegans]	1.1	1.1	-1.3	1.1	1.2	1.2	-2.0	-1.0	-1.0	1.1	-1.6
AA840053_actinin_alpha_2_associated LIM protein	1.1	-1.3	1.0	-1.3	1.1	1.0	-2.0	-1.0	-1.2	-1.4	-1.7
AA497592_ets variant gene 6 (TEL oncogene)	-1.3	1.0	1.1	-1.1	1.2	1.2	-2.0	-1.4	-1.4	-1.2	-1.1
AA687301_tropoin_L_cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.3	-2.0	-2.0	-2.2	3.55728+	1.3
AA517353_nuclear_factor_of_kappa_light_chain_gene_enhancer_in_B-cells_inhibitor_alpha	-1.0	1.2	1.1	-1.1	1.1	1.1	-2.0	-1.3	-1.2	-1.2	-1.0
AI120822_serine_(or_cysteine)_proteinase_inhibitor_clade_G_(C1_inhibitor)_member_1	1.1	-1.4	-1.1	-1.5	1.2	1.2	-2.0	-1.0	1.0	-1.0	-1.1



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AA06016_RIKEN_cDNA_1190002H23_gene	-1.6	1.2	1.2	1.5	1.5	1.5	3.33219++	-2.0	-2.4	-1.4	-1.6	-2.0	-1.3
AA061920_phospholipase_A2_group_IIc	-1.3	1.05115+	1.3	1.1	1.1	1.1	1.55314+	-2.0	-1.2	1.1	1.0	-1.2	1.3
AA821953_paraoxonase_1	1.0	-1.6	1.5	-1.0	1.3	1.3	1.30398~	-2.1	-1.4	-1.1	-1.2	-1.0	-1.1
AA416441_gene_rich_cluster_C8_gene	1.1	-1.3	1.3	1.2	1.1	1.1	1.4	-2.1	-1.3	1.1	1.3	-1.1	1.0
W55995_hemoglobin_X_alpha-like_embryonic_chain_in_Hba_complex	1.1	-1.6	-1.3	-1.2	-2.2	-2.2	1.11232~	-2.1	-2.0	1.0	-1.2	-4.0	-1.6
AA771396_4-hydroxyphenylpyruvic_acid_dioxygenase	1.1	-1.4	1.2	1.1	1.4	1.4	1.1	-2.1	-6.2	1.3	-1.2	1.1	1.5
AA760223_epithelial_membrane_protein_3	-1.1	-1.1	1.4	-1.0	1.2	1.2	1.0434~	-2.1	-1.3	-1.1	-1.3	-1.2	-1.4
W55649_vasodilator-stimulated_phosphoprotein	1.0	-1.1	1.1	-1.3	1.1	1.1	-1.1	-2.1	-1.3	-1.2	-1.2	-1.2	-1.3
AI019668_prostaglandin_I_receptor_(IP)	1.01606+	-1.10471+	1.08277+	-1.3	-1.31076+	-1.3	-1.49409++	-2.1	-1.11103+	1.5	-1.1	1.29004+	1.11434+
AA674177_cytochrome_P450_2a4	1.2	-1.6	2.8	1.1	1.3	1.3	1.72563~	-2.1	1.2	-1.0	-1.1	-1.1	-1.2
AA437572_inner_centromere_protein	1.1	-1.4	1.1	-1.3	-1.2	-1.2	1.23932~	-2.1	-1.1	1.2	1.1	-1.0	1.1
AI020539_secretory_leukocyte_protease_inhibitor	1.1	-1.5	1.1	-1.1	1.0	1.0	1.1	-2.1	1.1	-1.0	-1.1	-1.1	-1.4
W83739_DNA_segment_Chromosome_2_Brigham_and_Women's_Genetics_1423_expressed	-1.2	-1.0	-1.5	-1.5	1.0	1.0	-1.66255++	-2.1	-1.2	-1.3	-1.2	1.1	1.0
AA198236_kit_ligand	1.0	1.10758+	1.00332+	-1.28916+	-1.5351+	-1.5351+	-1.09631++	-2.1	1.1	1.1	-1.1	1.3	-1.1
AI451780_prostate_specific_ets_transcription_factor	-1.1	1.4	1.1	-1.5	-1.1	-1.1	-2.44752~	-2.1	-1.0	-1.1	1.0	1.0	1.0
W11251_Fc_receptor_IgE_high_affinity_I_gamma_polypeptide	1.2	1.3	1.3	1.1	1.1	1.1	-1.02621++	-2.1	1.1	1.1	-1.1	-1.1	-1.1
AA981355_Mus_musculus_DNA_cytosine_methyltransferase_mRNA	-1.4	-1.3	1.2	1.0	1.0	1.0	1.51303~	-2.1	-1.8	-1.2	-1.1	-1.4	-1.02751+
A324400_transforming_growth_factor_beta_receptor_II	-1.1	-1.1	1.5	1.0	1.6	1.6	1.3	-2.1	1.1	1.3	1.1	1.0	1.0
AA733479_syndecan_1	1.1	1.1	1.1	-1.2	1.1	1.1	-1.4	-2.1	1.1	-1.1	-1.1	1.0	-1.2
AA617316_TEA_domain_family_member_2	-1.3	1.1	-1.1	-1.1	-1.2	-1.2	1.50814~	-2.1	-1.5	-1.3	-1.3	-1.3	-1.1
AA049060_inter_alpha-1(I) collagen_inhibitor_heavy_chain_4	1.5	1.3	1.2	-1.2	-1.0	-1.0	1.05302~	-2.1	-2.2	1.7	1.1	1.4	1.3
AA759995_procollagen_type_XVII_alpha_1	1.1	-1.2	1.5	-1.2	1.4	1.4	1.30837~	-2.1	-1.2	1.2	-1.1	1.0	-1.2
AA028578_keratin_complex_2_basic_gene_4	1.2	-1.9	-1.3	-1.0	-1.0	-1.0	1.44671~	-2.1	-1.8	1.4	-1.1	1.5	1.3
AA755961_insulin-like_growth_factor_2_receptor	-1.1	-1.1	1.2	-1.1	-1.1	-1.1	1.4	-2.1	-1.1	-1.3	-1.1	-1.1	-1.1
AA727051_myeloid_leukemia_factor_1	1.1	-1.2	1.4	1.1	1.3	1.3	1.33554~	-2.1	-1.1	-1.1	-1.3	1.1	-1.4
AA288467_glycosylation_dependent_cell_adhesion_molecule_1	-1.0	-1.8	1.2	1.2	-1.1	-1.1	1.2	-2.1	-1.3	-1.0	-1.1	1.2	1.0
AA444639_sialyltransferase_7_((alpha-N-acetylneuraminyl_2,3-beta-galactosyl-1,3)-N-acetyl_galactosaminide_alpha-2,6-sialyltransferase)_B	1.4	-1.2	-1.0	1.0	-1.2	-1.2	-1.2	-2.2	-1.1	-1.1	-1.3	1.2	1.5
AA545691_thymidine_kinase_1	1.2	-1.2	1.6	-1.2	-1.1	-1.1	1.24271~	-2.2	-1.1	1.3	1.0	-1.1	1.1
AA106072_Public_domain_EST	1.0	-1.7	1.7	-1.1	1.0	1.0	2.39593~	-2.2	-1.9	1.0	1.3	-1.3	1.1
AA414110_ESTs	-1.2	-1.5	-1.3	-1.2	1.0	1.0	1.02832~	-2.2	-1.0	-1.0	-1.1	1.1	1.1
AA414112_phosphatidylinositol_glycan_class_A	1.1	-1.6	1.1	-1.1	-1.6	-1.6	1.15321++	-2.2	1.0	-1.0	-1.0	1.2	1.2
AI045662_lactate_dehydrogenase_3_C_chain_sperm_specific	1.2	-1.6	-1.3	1.5	1.3	1.3	1.27823~	-2.2	-1.0	-1.1	1.0	1.1	1.4
AI120958_RIKEN_cDNA_2700018N07_gene	-1.2	1.2	1.2	-1.4	-1.5	-1.5	1.0	-2.2	-1.2	-1.2	-1.3	-1.1	1.0
W16012_uteroglobin	1.3	-1.6	1.2	-1.4	-1.6	-1.6	1.0	-2.2	-1.3	-1.2	1.1	-1.2	-1.3

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AA152940	immunoglobulin_kappa_chain_variable_28_V28)	1.3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	-1.1	-2.5
AI326527	preprocrasolin	-1.3	-1.2	-1.0	-1.2	1.0	1.59773~	-2.2	-1.3	-1.1	-1.2	1.2
AA267626	mitogen_activated_protein_kinase_kinase_kinase_2	1.0	1.19439+	1.08191+	1.10045+	-1.00411+	-1.21849+~	-2.2	1.2	-1.00036+	1.1	-1.1
AA607483	proteoglycan_secretory_granule	1.2	-1.4	1.1	1.3	1.2	1.1	-2.2	-1.2	1.1	-1.2	1.4
AA982227	glutathione_S-transferase_alpha_3	1.3	-1.0	1.4	-1.3	-1.0	2.2	-2.2	1.2	1.8	1.3	-1.2
AA200024	trophoblast_specific_protein	1.5	-2.0	-1.2	1.5	1.1	-1.0	-2.2	-1.2	1.4	1.1	1.2
AA106793	plasminogen	1.1	-1.6	1.3	1.0	1.1	2.40205~	-2.2	-3.6	1.0	1.0	-1.4
W08947	non-catalytic_region_of_tyrosine_kinase_adaptor_protein_2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.2
AI050373	RIKEN_cDNA_4921524P20_gene	-1.3	1.2	-1.3	-1.40942*	1.0	-1.22069+~	-2.2	-1.2	-1.7	-1.1	-1.2
AA612413	chitinase_acidic	-1.1	-1.3	1.8	-1.2	1.2	3.09734~	-2.3	1.2	2.5	-1.2	-1.0
AI327450	phospholipase_A2_group_IB_pancreas	1.3	1.8	1.1	-1.8	-6.7	1.01624~	-2.3	-1.6	-1.4	-1.4	-1.0
AA117554	growth_arrest_specific_2	1.1	-1.4	1.4	1.1	1.3	3.96148~	-2.3	-1.3	1.0	-1.3	-1.4
AA529824	fatty_acid_binding_protein_2_intestinal	-1.5	-1.5	-1.7	1.7	-1.1	2.6	-2.3	1.0	1.4	1.1	1.7
W36635	carbonyl_reductase_2	1.2	-1.9	-1.4	1.4	1.0	1.3	-2.3	1.1	1.0	1.2	1.5
AI154217	poliovirus_sensitivity	-1.2	1.0	1.8	-1.1	1.2	1.3	-2.3	-1.4	-1.3	-1.1	-1.1
AA237607	pyruvate_kinase_liver_and_red_blood_cell	-1.4	-1.2	1.9	-1.2	1.5	1.3	-2.3	-1.2	1.2	-1.1	1.1
AA600553	claudin_7	-1.1	1.1	-1.2	-1.1	1.2	-1.3	-2.3	-1.2	-1.1	1.0	-1.3
AI019575	secreted_frizzled-related_sequence_protein_4	1.2	-1.3	-1.4	-1.2	-1.2	1.30118~	-2.3	-1.3	1.0	-1.2	1.3
W18281	RIKEN_cDNA_2310012115_gene	1.1	1.1	-1.1	1.1	1.1	-1.1	-2.3	1.1	1.0	1.1	1.2
AA028346	keratin_complex_1_acidic_gene_19	-1.4	-1.6	-1.9	-1.5	1.0	-1.2	-2.3	-1.1	-1.1	-1.3	-1.2
AA061047	secreted_frizzled-related_sequence_protein_2	1.9	-1.2	-1.3	1.1	1.1	-1.08865~	-2.3	1.3	-1.1	-1.0	1.1
AA220582	cytochrome_P450_212	1.4	-1.6	1.7	-1.0	1.1	1.1	-2.3	1.5	-1.2	-1.1	1.2
AA108495	deoxyribonuclease_I	1.1	-1.8	-1.1	1.2	1.4	2.1	-2.3	-1.2	1.7	-2.4	1.3
AA655921	neural-salient_serine/arginine-rich	-1.1	-1.4	1.1	-1.0	-1.1	1.5	-2.3	-1.1	-1.1	-1.3	-1.1
AI159406	casein_gamma	1.1	-1.7	-1.5	1.2	1.3	1.7	-2.3	-1.3	1.0	-1.1	1.6
AI326575	glucose-6-phosphatase_catalytic	1.3	-1.6	1.4	1.9	1.4	1.97895~	-2.3	-1.2	1.5	1.1	1.2
AI162792	aquaporin_5	1.3	-1.1	-1.0	-1.6	-1.8	1.03979~	-2.3	1.1	1.0	1.2	-1.6
AA062457	RIKEN_cDNA_0610006F02_gene	1.2	-1.1	1.3	1.1	1.1	-1.4	-2.3	-1.9	1.1	-1.3	1.3
AA286306	ESTs	-1.18303+	-1.52374+	-1.22332+	-1.2	-1.3	-1.22297+~	-2.4	1.1	1.1	1.09912+	1.1
AA549040	histone_acetyltransferase	-1.1	-1.2	-1.3	-1.8	-1.1	-1.10371+~	-2.4	-1.2	-1.0	-1.1	-1.2
AA656712	myosin_heavy_polypeptide_1_skeletal_muscle_adult	1.0	-1.6	1.1	1.2	1.2	2.1	-2.4	-1.4	-1.3	1.1	-1.2
AI256668	deleted_in_azoospermia-like	1.1	-1.2	-1.1	1.0	-1.1	-1.06147+~	-2.4	-1.2	-1.1	-1.0	1.1
AA106125	cytochrome_P450_2a4	1.3	-1.3	3.0	1.3	1.4	1.0	-2.4	1.3	1.1	2.3	1.1
AA064494	Public_domain_EST	1.0	-1.5	-1.1	1.8	1.3	2.47455~	-2.4	1.2	1.3	1.0	1.4
AA066835	corticosteroid_binding_globulin	1.0	1.2	1.8	-1.1	1.2	1.4	-2.4	-2.3	1.1	-1.0	-1.3

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AA106167 Public domain_EST	-1.2	-1.4	-1.2	-1.1	-1.1	-1.8	-2.4	-1.6	-1.2	-1.1	-1.1	-1.2
AI878995 immunoglobulin-associated_alpha	-1.1	-1.8	-1.2	-1.8	-1.1	-2.1	-2.4	-1.2	-1.5	-1.3	-1.2	-1.2
AA681602 enolase_3_beta_muscle	1.1	-1.7	-1.0	-1.4	1.3	-1.5	-2.5	-1.3	-1.9	1.1	1.2	-1.4
W17866 uterine-specific_proline-rich_acidic_protein	-1.4	-1.7	-1.2	-1.4	-1.2	1.61144	-2.5	-1.0	-1.3	-1.3	-1.5	2.8
AI060394 ESTs	-1.6	1.3	1.4	1.3	1.3	1.64091	-2.5	-1.49757+	-1.6	-1.0	-1.6	-1.0
AA864136 lectin_galactose_binding_soluble_7	1.1	-1.2	1.3	-1.0	1.2	1.6	-2.5	-1.5	1.1	1.0	1.0	-1.0
AI552711 creatine_kinase_muscle	1.1	-1.2	1.1	-1.2	1.3	1.7	-2.5	-1.2	-1.4	-1.0	-1.1	-1.2
AA980349 glutathione_peroxidase_2_pseudogene_1	-1.3	-1.0	1.2	-1.9	1.1	-2.4	-2.5	-1.5	1.1	-1.1	-1.5	1.5
AA756171 cysteine-rich_protein_3	1.1	-1.7	1.0	1.1	1.3	2.04467	-2.5	-1.6	-1.2	1.0	-1.1	-1.2
AA822346 odorant-binding_protein_la	-1.2	-1.8	-1.2	-1.0	-1.2	1.72207	-2.6	-1.6	-1.8	-1.4	-1.2	-3.01254*
AA276747 ESTs	1.14674+	1.07209+	1.11618+	1.0	-1.5	-1.10511+	-2.6	1.1	1.0	1.2	1.1	1.2
AI390909 gap Junction_membrane_channel_protein_alpha_4	-1.1	1.1	1.1	-1.1	1.1	-1.26782+	-2.6	1.1	-1.1	-1.2	-1.0	-1.0
AV496194 immunoglobulin_kappa_chain_variable_20_V20_family	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.6	-1.0	1.4	-1.0	-2.7
W92497 ubiquitin-like_1	1.3	-1.8	-1.0	1.1	-1.0	-1.1	-2.7	-1.5	-1.6	1.3	-1.2	-1.2
AI425461 ESTs_Moderately_similar_to_1615347A_ras_p21_GTPase_activating_protein_[M.musculus]	1.1	1.1	1.2	1.1	1.2	1.17621+	-2.7	1.1	-1.2	-1.2	-1.2	-1.1
AA198997 ESTs	1.1	1.03128+	1.03168+	1.0	-1.2	-1.30212+	-2.7	1.23177+	1.1	-1.1	1.2	-1.00032+
AI664286 tumor_necrosis_factor_receptor_superfamily_member_9	1.3	-2.3	-1.1	-1.3	-1.3	1.2	-2.7	-1.3	-1.1	-1.2	1.1	1.7
AA823639 RIKEN_cDNA_A930018B01_gene	1.1	-1.0	1.4	-1.1	1.0	1.37539-	-2.7	1.0	1.0	-1.1	-1.0	-1.1
AI594276 transcription_factor_AP-2_alpha	-1.5	-1.1	-1.1	-1.4	1.2	1.30517-	-2.7	-1.4	-1.2	-1.2	-1.1	-1.1
AA122791 histocompatibility_2_Q_region_locus_7	1.3	-1.4	1.3	-3.0	1.6	-1.2	-2.8	-1.2	-1.3	-1.0	-1.3	-1.2
AA759679 Ia-associated_invariant_chain	-1.0	-1.8	-1.6	-1.9	1.5	-3.7	-2.8	-1.0	-1.9	-1.0	-1.3	-1.4
AA681596 procollagen-lysine_2-oxoglutarate_5-dioxygenase_1	1.2	-1.2	-1.0	-1.1	-1.1	-1.3	-2.8	-1.0	-1.0	1.1	-1.0	-1.1
AA538511 histocompatibility_2_D_region_locus_1	1.4	-1.2	1.2	-1.5	1.5	-1.5	-2.8	1.1	-1.0	-1.0	1.0	-1.1
AA273374 RIKEN_cDNA_1810008K20_gene	-1.0	-1.0	-1.3	1.4	1.1	1.06792+	-2.8	1.0	-1.2	-1.1	1.1	1.1
AA413953 ESTs_Weakly_similar_to_KIAA0661_protein_[H.sapiens]	-1.2	-1.1	1.1	-1.4	-1.2	1.05059-	-2.8	-1.0	-1.0	-1.2	-1.1	1.1
W11170 small_inducible_cytokine_A21a_(taucine)	-1.2	-1.0	1.1	1.0	1.3	-2.7	-2.8	-1.1	-1.1	-1.1	-1.3	1.0
AA717019 ATPase_Cav+ transporting_cardiac_muscle_fast_twitch_1	-1.2	-2.1	-1.1	-1.5	-1.3	1.2	-2.8	-1.4	-1.8	-1.2	1.1	-1.1
AA016759 mini_chromosome_maintenance_deficient_5_(S.cerevisiae)	-1.4	1.1	1.1	1.1	1.3	1.9	-2.9	-2.0	-1.4	-1.3	-1.6	-1.1
W54403 ATPase_Cu++ transporting_beta_polypeptide	1.2	-2.1	1.1	-1.0	1.2	1.3	-2.9	-7.9	1.1	-1.1	-1.1	1.2
AA145479 ESTs	-1.2	-1.3	-1.3	-1.2	-1.0	1.16703+	-2.9	-1.2	-1.3	-1.3	-1.2	-1.3
AI603969 sarcoglycan_beta_(43kD_dystrophin-associated_glycoprotein)	1.035+	-1.0	-1.2	-1.4	1.0	-1.42644+	-2.9	1.1	-1.3	-1.4	1.0	-1.2
AI282835 gap Junction_membrane_channel_protein_beta_4	1.1	-1.3	1.1	-1.0	1.1	1.49281-	-3.0	-1.6	-1.3	-1.1	-1.1	-1.0
AA795319 myosin_light_chain_phosphorylatable_cardiac_ventricles	-1.1	-1.9	-1.2	-1.4	-1.3	1.3331	-3.0	-1.8	-1.3	1.1	1.1	1.0
AI638807 ESTs_Weakly_similar_to_E6-AP_ubiquitin_protein_ligase_[M.musculus]	1.3	-1.14976+	1.09866+	-1.53665+	-1.1162+	-1.6245+	-3.0	1.11591+	1.1408+	-1.2	1.1	1.2

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AA212144 forkhead box A2	-1.2	3.7	1.2	-1.2	-1.7	1.16246+	-3.1	-1.3	1.1	-1.4	-1.5	-1.1
AA871285 Public domain EST	1.3	-1.4	-2.0	1.4	-1.7	-3.0	-3.1	-1.3	1.2	1.3	1.4	-1.7
AA270904 nuclear receptor subfamily 1, group H, member 4	1.23141+	1.21202+	1.5	1.0	1.20848+	-1.53218+-	-3.1	-1.09991+	-1.00129+	1.1	1.1	1.29189+
AA738672 Mus musculus mRNA for thymopsin, complete cds	-1.1	-1.2	1.2	1.1	1.2	2.27473-	-3.1	-1.3	-1.2	-1.1	-1.3	-1.5
W36421 McInerney leukemia virus 10	-1.1	1.0	1.1	1.2	1.0	-1.09155-	-3.3	1.1	1.1	-1.1	-1.1	1.1
AI550101 ESTs	-1.13885+	-1.00093+	-1.00993+	1.0	1.06911+	1.21429+-	-3.4	-1.15513+	-1.3	-1.3	-1.2	-1.2
AA008393 phosphodiesterase 6D, cGMP-specific, rod, delta	1.2	-1.03596+	-1.5	1.0	1.1	-1.1258+-	-3.4	1.0	1.1	-1.1	1.0	-1.2
AI609041 Mus musculus Rep-8 mRNA for reproduction 8, complete cds	-1.0	1.1	1.7	-1.0	-1.3	-1.17893+-	-3.4	-1.1	1.0	-1.1	1.1	-1.0
AA549705 ESTs	1.1	1.2204+	1.2	1.2	-1.0	1.0769+-	-3.5	-1.3	-1.0	-1.3	-1.2	-1.4
W18330 tropomyosin 2, beta	1.2	-1.3	1.0	-2.0	1.2	-1.1	-3.5	-1.5	1.1	-1.1	-1.3	-1.4
AA815777 RIKEN cDNA_1110007F23 gene	1.0	-1.1	1.2	-1.3	1.2	1.1	-3.5	1.0	1.0	1.1	-1.2	-1.5
W15612 desmin	-1.0	-1.4	-1.3	-1.3	1.1	-1.8	-3.6	-1.7	-1.1	-1.1	-1.3	-1.0
AI695315 ESTs	1.0	-1.12188+	-1.08667+	-1.4	-1.21568+	-1.29621+-	-3.7	1.03263+	-1.2	-1.1	1.1	1.19019+
AA549305 RIKEN cDNA_4833427P12 gene	-1.11812+	1.22912+	-1.03061+	-1.19208+	-1.1371+	1.02682+-	-3.7	-1.05244+	-1.0	-1.0	1.1	1.05066+
AA114721 RIKEN cDNA_5830475I06 gene	-1.5	1.3	-1.4	-1.27884*	1.3	-1.8	-3.7	-1.2	-1.4	-1.1	-1.16457*	-1.1
AA089188 uromodulin	-1.2	-2.0	-1.0	1.1	-1.3	1.0	-4.0	-1.4	-1.7	1.1	-1.2	-1.4
AA839138 CD8 antigen, alpha chain	-1.3	-1.08773+	-1.3	-1.8	1.2	-2.63867+-	-4.0	1.0	-2.0	1.1	1.0	-1.1
AA763276 smail muscle protein, X-linked	-1.7	-1.4	1.1	1.6	1.2	1.9	-4.6	-2.5	-1.6	-1.2	-2.0	-1.5
AA474047 ESTs	-1.2	-1.6	-1.1	-1.1	-1.8	1.1	-6.0	1.0	-1.2	-1.3	-1.0	-1.2

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colon	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL- 4B_BDError	PL- 2B_BDError	PL- 6B_BDError	PL- 8B_BDError	PL- 3B_BDError	PL- 5B_BDError	PL- 1B_BDError	PL- 7B_BDError	PL- 9B_BDError	PL- 10B_BDError	PL- 11B_BDError	PL- 12B_BDError
AA666894 cytochrome P450, 2b9, phenobarbital inducible, type 1	-1.1	-1.4	1.9	1.3	2.8	3.8	-1.3	1.1	1.3	1.2	1.1	1.2
AA231099 necln	-1.8	1.3	1.1	2.3	1.7	3.6	1.0	-2.0	-1.3	-1.2	-1.7	1.0
AA610906 Mus musculus Cyp4b3 mRNA for family 4 cytochrome P450, complete cds	-1.0	-1.6	1.4	-1.1	1.7	1.5	-1.2	-1.1	1.0	1.0	1.2	1.1
AA606610 RIKEN cDNA 2610002G21 gene	1.1	-1.1	1.0	-1.8	1.1	3.3	-1.1	-1.0	1.4	-1.2	-1.0	-1.1
AA107035 quanylate cyclase activator 2b (retina)	-1.2	-1.3	1.1	-1.1	3.1	3.2	-1.5	-1.9	-1.2	1.2	-1.3	6.5
AA224053 forkhead box D3	-1.5	1.0	1.4	1.0	1.2	3.0	-1.4	-2.1	-1.5	-1.3	-1.7	-1.3
AA671366 Mus musculus MRPS8 mRNA for mitochondrial ribosomal protein S8, partial cds	-1.2	-1.1	1.3	1.3	1.3	2.9	-1.9	-2.2	-1.2	-1.0	-1.4	-1.3
AA822473 DNA segment, Chr 8, Brigham 6 Women's Genetics 1320 expressed	-1.0	-1.6	1.3	-1.0	-1.1	2.9	-1.7	-1.7	-1.2	1.2	-1.2	-1.3
AA062403 ESTs, Moderately similar to proteasome inhibitor Np121 subunit [Hsapens]	-1.3	1.2	1.8	1.1	1.3	2.7	-1.7	-2.0	-1.3	-1.2	-1.5	-1.1
AA671395 Mus musculus, Similar to ectonucleotide pyrophosphatase ephosphodiesterase 3, clone IMAGE3486323, mRNA, partial cds	1.1	-1.0	1.3	1.1	-1.3	2.6	-1.59207+	-1.3	1.0	-1.1	1.0	1.2
AA518917 slug, chicken homolog	-1.6	-1.0	1.1	1.2	1.1	2.6	-1.0	-1.8	-1.4	-1.2	-1.8	-1.3
AA619789 methylglutathionylhydrofolate dehydrogenase [NAD+ dependent], methyltetrahydrofolate cyclohydrolase	-1.1	1.2	1.4	1.1	1.1	2.8	-1.8	-1.7	-1.3	1.1	-1.3	-1.1
AA629824 fatty acid binding protein 2, intestinal	-1.5	-1.5	-1.7	1.7	-1.1	2.6	-2.3	1.0	1.4	1.1	1.7	2.1
AA660691 RIKEN cDNA 2710003F10 gene	-1.4	-1.1	-1.8	-1.5	1.2	2.5	1.2	-1.6	-1.3	-1.5	-1.2	-1.1
AA669473 defensin related cryptidin 5	-1.2	1.1	-1.2	1.8	1.7	2.6	-1.3	1.5	1.1	1.0	1.9	1.5
AA623172 defensin related cryptidin 6	-1.0	1.1	-1.1	1.1	1.8	2.5	-1.2	-1.2	-1.1	-1.2	-1.2	-1.5
AA693944 forkhead box G1	-1.7	-1.0	1.7	1.5	1.5	2.6	1.1	-1.7	-1.5	-1.1	-1.6	-1.1
AA619963 ESTs, Weakly similar to T2802, hypothetical protein D3.6 - Caenorhabditis elegans (Ca elegans)	-1.0	1.2	1.4	1.3	-1.0	2.5	-1.5	-1.4	-1.3	-1.2	-1.5	-1.0
AA034676 Protein	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4

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AA067003 glutathione S-transferase, mu 1	1.1	1.2	1.0	-2.0	1.5	1.4	1.0	1.2	1.4	-1.3	-1.2
AA591707 DNA polymerase epsilon, subunit 2	-1.1	1.1	1.05228*	2.0	1.4	-1.6	1.1	1.1	1.1	-1.1	1.1
AA546945 lysine_3-monooxygenase/typtophan_5-monooxygenase activation protein, zeta polypeptide	-1.3	1.3	1.4	-1.1	1.2	1.3	-2.0	-1.5	-1.2	-1.8	-1.1
AA066225 selenoprotein P, plasma_1	1.2	1.4	1.2	-1.7	2.3	1.0	-1.2	-1.1	1.2	-1.6	-1.1
AI365457 retinol binding protein 2, cellular	-2.0	-2.1	-1.6	-1.9	1.5	1.3	-1.9	-1.6	-1.9	-1.5	-1.7
AA795264 ubiquitin-like 1	-1.0	-1.8	1.3	1.1	1.1	1.0	-1.6	-1.3	1.1	-1.1	-1.2
AA070943 phosphatidic acid phosphatase 2a	1.1	-1.1	1.4	1.2	1.3	1.0	-1.1	1.0	1.0	1.1	-1.0
AI181090 cytochrome P450, subfamily IV B, polypeptide_1	1.0	-1.4	-1.1	-1.1	1.1	1.0	-1.2	-1.2	1.1	-1.1	-1.1
AA071638 phospholipase A2, group IIA (platelets, synovial fluid)	-1.1	-1.0	-1.2	1.7	2.3	1.0	-1.3	1.5	1.2	1.3	1.7
AA763276 small muscle protein, X-linked	-1.7	-1.4	1.1	1.8	1.2	1.0	-2.5	-1.6	-1.2	-2.0	-1.5
AI385503 cysteine rich intestinal protein	1.3	1.1	-1.0	-1.6	2.3	1.0	-1.1	1.0	-1.0	-1.0	1.1
AA120401 A kinase (PKA) anchor protein 10	1.1	1.1	-1.1	-1.0	1.3	1.0	1.2	1.1	1.1	1.2	1.1
AI595611 aquaporin 7	-1.0	-1.2	-1.0	1.6	1.3	1.0	-1.3	1.1	1.1	1.0	-1.0
AI892208 protamine 2	-1.4	-1.8	1.3	1.4	-1.2	1.0	-1.5	-1.7	-1.2	-1.3	-1.3
AA799873 ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 42kD	-1.5	1.4	1.3	1.0	1.4	1.0	-1.9	-1.5	-1.0	-1.9	-1.2
AA268059 troponin related homeobox 3 (Drosophila)	-1.3	-1.2	-1.7	-1.5	-1.1	1.2	-1.4	-1.2	-1.2	-1.2	-1.0
AA711681 transaldolase 1	1.0	1.1	1.1	-1.3	-1.2	-1.0	-1.3	-1.0	1.0	-1.1	-1.0
AA145254 SEC61, gamma subunit (S. cerevisiae)	1.4	1.1	1.1	-1.4	-1.7	-1.8	-1.2	1.1	-1.0	-1.1	-1.0
AA794074 aldo-keto reductase family 1, member B1 (aldose reductase)	1.1	-1.1	-1.2	-1.5	-1.0	-1.9	-1.1	1.0	1.0	1.1	-1.2
AI036487 ESTs	-1.0	1.1	-1.1	-1.3	-1.9	-1.9	1.0	-1.0	-1.3	1.1	1.0
W21012 timeless homolog (Drosophila)	-1.2	1.1	1.0	-1.8	-1.1	-1.9	-1.3	-1.2	-1.0	-1.3	-1.1
AA138265 RIKEN cDNA 2010309G21 gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	-1.3	-1.0	-1.0	-2.4
AI121690 RIKEN cDNA 1300007C21 gene	-2.0	-1.7	-1.4	-1.4	-1.4	-1.9	-1.2	-1.1	-1.7	-1.5	1.2
AI676997 carboxyl ester lipase	1.5	1.6	-1.4	-2.3	-8.9	-1.9	-1.3	-1.4	1.1	2.0	2.2
AA106894 carbonic anhydrase 4	-1.2	-1.5	-1.2	-1.4	1.3	-1.9	-1.5	1.0	-1.2	-1.2	1.2
AI158565 guanine nucleotide binding protein (G protein), gamma_10	-1.0	-1.0	-1.1	-1.3	-1.6	-1.9	1.2	-1.5	-1.3	-1.1	-1.3
AI693892 interferon regulatory factor 2	-1.4	-1.0	-1.3	-1.5	1.1	-1.9	-1.3	-1.2	-1.3	-1.1	-1.1
AA238062 CD52 antigen	1.1	-1.6	-1.3	1.0	-1.1	-1.9	-1.6	-1.3	-1.1	-1.2	-1.1
W33651 platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	1.2	-1.7	-1.1	1.2	1.3	-1.9	-1.1	1.2	1.4	1.3	1.1
AA794055 cysteine rich protein	1.0	1.4	-1.9	-1.3	1.7	-2.0	1.3	-1.0	-1.4	-1.3	1.1
AI036381 ninturin 1	1.1	1.1	1.1	-1.2	1.1	-2.0	1.1	-1.4	-1.1	-1.2	-1.2
AI326722 lymphocyte antigen 6 complex, locus E	-1.1	-1.2	-1.2	-3.5	-1.1	-2.0	1.1	-1.1	-1.1	-1.4	-1.2

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AA245754 lysosomal membrane glycoprotein 2	1.2	-1.2	1.1	-1.5	-1.6	-2.0	-1.7	-1.0	1.2	-1.1	1.1	-1.0
AA145895 heat shock protein, 70 kDa 1	1.1	-1.1	-1.0	1.2	-1.8	-2.0	-1.7	1.1	1.1	1.1	-1.0	-1.1
AI594243 CD8beta opposite strand	-1.4	-1.0	-2.0	-1.7	1.1	-2.0	1.2	-1.2	-1.1	-1.2	-1.1	-1.2
AI390138 RIKEN cDNA 3830401B19 gene	-1.4	-10.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1
AI120876 CD24a antigen	1.3	1.2	-1.5	-2.8	-1.7	-2.1	1.1	-1.2	-1.0	-1.0	-1.4	1.1
AI552004 ESTs, Highly similar to H-REV_107 PROTEIN [R.norvegicus]	1.4	1.2	1.5	-1.1	-1.3	-2.1	1.5	1.0	-1.0	-1.0	1.0	-1.2
W15990 guanylate cyclase activator 2 (guanylin 2, intestinal, heatstable)	1.0	1.0	-1.3	1.2	-2.8	-2.1	-1.5	-1.1	-1.2	-1.0	1.1	1.4
AA444443 immunoglobulin heavy chain 6 (heavy chain of IgM)	-1.2	-1.8	-1.4	1.1	1.2	-2.1	-1.9	1.1	1.0	-1.0	1.2	1.0
AI894018 complement component 1, q subcomponent, c polypeptide	1.1	-1.4	1.3	1.0	1.3	-2.1	1.1	-1.1	-1.1	1.1	-1.2	-1.2
AA414831 hypoxia induced gene 1	1.4	1.1	1.2	-1.3	-1.4	-2.1	1.1	-1.1	1.3	-1.1	1.1	-1.2
AI892299 RIKEN cDNA 583049B15 gene	1.0	-1.3	1.1	1.8	1.3	-2.1	-1.8	-1.0	1.5	1.2	1.2	1.9
AI322733 2'-5' oligoadenylate synthetase 1A	1.1	1.2	-1.1	-2.6	1.1	-2.1	-1.1	1.0	-1.2	1.1	-1.2	1.1
AA688795 ESTs	-1.0	1.4	-1.3	-1.1	1.1	-2.1	-1.1	1.3	-1.0	-1.1	1.1	1.2
AI325323 myocyte enhancer factor 2C	-1.3	-1.0	1.2	-1.3	-1.7	-2.1	1.2	1.2	-1.1	-1.0	-1.1	-1.2
AA138854 ESTs, Weakly similar to lysophospholipase 1 [M.musculus]	-1.4	-1.6	-1.1	-1.0	-2.3	-2.1	1.1	-1.7	-1.0	1.4	-1.1	1.2
AI876995 immunoglobulin-associated alpha	-1.1	-1.8	-1.2	-1.6	-1.1	-2.1	-2.4	-1.2	-1.5	-1.3	-1.2	-1.2
AI060720 T-cell specific GTPase	1.0	-1.3	-1.2	-1.8	-1.1	-2.1	1.2	-1.4	-1.4	-1.2	-1.0	-1.0
AA675084 elastase 2	2.3	1.4	-1.2	-2.7	-2.1	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA123007 2'-5' oligoadenylate synthetase-like	1.1	-1.4	-1.3	-2.2	-1.1	-2.2	-1.1	1.3	-1.1	-1.1	-1.1	-1.1
AA237793 rat regenerating islet-derived mouse homolog 1	2.5	1.4	-1.3	-3.9	-1.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA688697 distal intestinal serine protease	1.1	1.3	-1.2	-1.7	1.7	-2.2	1.3	1.5	1.2	1.0	1.5	1.3
AI037523 transgelin	1.1	-1.1	-1.2	-1.5	1.1	-2.2	-1.6	-1.2	-1.4	1.0	-1.7	-1.1
AI325697 lymphocyte antigen 6 complex	1.8	-1.1	1.6	-1.3	1.1	-2.2	-1.3	-1.1	1.4	1.1	1.1	-1.1
AA237943 sperm specific antigen 1	1.0	-1.0	1.1	-1.1	-1.2	-2.2	1.0	1.0	1.1	1.1	1.0	1.0
AI058616 ESTs	-1.2	-1.1	1.3	-1.5	-1.9	-2.3	-1.4	-1.4	-1.2	-1.2	-1.5	-1.1
W82520 thiosulfate sulfurtransferase, mitochondrial	1.1	-1.0	1.3	-1.7	-1.3	-2.3	-1.2	-1.3	-1.0	-1.3	-1.2	-1.2
AI036082 histocompatibility 2, class II, locus DMA	-1.3	1.2	-1.2	1.2	1.1	-2.3	1.0	-1.1	-1.3	-1.0	-1.0	-1.1
AA939788 caspase 7	-1.1	-1.0	1.0	-1.0	-1.0	-2.3	-1.4	-1.2	-1.2	1.0	-1.0	-1.1
AA097896 0.6-methylguanine-DNA methyltransferase	-1.2	1.2	-1.6	-1.9	1.3	-2.3	1.0	-1.1	-1.1	-1.2	-1.1	-1.1
AI481911 Mus musculus, clone MGC-6727, mRNA, complete cds	-1.1	-2.0	-1.8	1.0	-1.8	-2.3	-1.5	-2.4	-1.4	1.1	-1.4	-1.4
AA498574 kallikrein 6	1.8	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	2.2	2.2	1.1	1.0	1.3
W15001 CD52 antigen	1.1	-1.7	1.2	1.1	1.1	-2.3	-1.2	-1.2	-2.5	1.1	-1.1	-1.0
AA619407 pancreatitis-associated protein	1.7	19.5	-1.9	1.2	4.4	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1

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AA575501 ESTs	-1.4	2.2	1.0	-1.3	1.2	-2.4	1.3	-1.6	-1.5	-1.2	-1.3	-1.1
AA684403 ESTs	-1.4	1.7	-2.3	-2.0	2.0	-2.4	1.5	-1.0	-1.3	-1.3	-1.1	-1.1
AA458072 adipocyte complement related protein of 30 kDa	1.3	-1.2	-1.0	-1.3	1.0	-2.4	-2.0	1.1	-1.5	1.1	1.3	-1.5
AA980349 glutathione peroxidase 2, pseudogene 1	-1.3	-1.0	1.2	-1.9	1.1	-2.4	-2.5	-1.5	1.1	-1.1	-1.5	1.5
W09198 calcium binding protein A6 (calyculin)	1.2	-1.2	-1.2	-1.6	-1.9	-2.4	1.1	1.1	1.0	1.2	-1.2	1.0
A1386062 carbonic anhydrase 3	1.1	-1.3	-2.1	-1.5	1.1	-2.4	-1.7	-2.1	-1.3	-1.2	-1.6	-1.5
AA980295 immunoglobulin joining chain	1.2	-1.5	-1.4	1.7	-2.2	-2.4	-1.9	-1.1	1.3	1.5	1.4	-1.3
AA068624 hydroxyacid oxidase (glycolate oxidase) 3	1.3	1.3	-1.2	2.2	1.32102*	-2.4	1.2	1.4	1.3	1.1	1.3	1.5
AA146478 M.musculus mRNA (3C10) for IgA V-D-J-heavy chain	-1.3	1.0	-1.6	2.7	-2.0	-2.4	-1.1	-1.4	1.5	2.0	1.1	1.6
AA050168 proteasome (prosome, macropain) subunit, beta type 10	-1.1	1.2	1.2	-1.1	-1.1	-2.5	-1.0	-1.3	-1.1	-1.2	1.1	-1.2
A1451862 RIKEN cDNA 0910001A18 gene	1.8	1.3	-1.1	-2.5	-14.7	-2.6	1.2	-1.3	-2.4	-1.3	-1.1	-1.3
A1386046 trypsin 4	1.7	1.8	1.1	-1.8	-15.9	-2.6	1.8	-1.5	-2.5	-1.1	-1.3	-1.2
AA386807 RIKEN cDNA 2310002A12 gene	-1.0	1.1	-1.7	-1.3	-1.2	-2.6	-1.2	-1.2	1.1	1.0	1.1	-1.1
AA822485 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)	1.0	-1.3	1.3	-1.1	-1.1	-2.6	-1.1	-1.1	-1.1	1.1	-1.0	-1.3
AA880322 calpain 1	-1.2	-1.4	-1.1	-1.1	1.1	-2.6	-1.7	-2.1	-1.5	-1.2	-1.4	-1.0
AA212405 dihydrofolate reductase	-1.2	-1.6	-1.2	-1.0	-2.5	-2.6	1.1	-1.4	-1.2	1.1	-1.1	-1.7
A1529513 ESTs, Moderately similar to F26L_MOUSE_6PF-2/KFRU-2,6-P2ASE LIVER ISOZYME [M.musculus]	-1.2	1.1	1.1	-1.6	1.1	-2.6	2.2	1.3	-1.1	1.4	-1.3	-1.3
AA762277 lymphocyte antigen 8 complex, locus C	1.4	1.1	1.1	1.0	-1.2	-2.6	1.2	-1.3	1.1	1.1	-1.1	-1.1
A1048040 claudin 4	-1.6	1.5	-2.1	-1.9	1.7	-2.7	1.5	-1.1	-1.2	-1.3	-1.2	-1.2
A1326566 histocompatibility 2, class II, antigen E, alpha	1.4	-1.5	1.2	1.1	1.5	-2.7	-1.1	1.2	-1.6	1.1	-1.1	-1.4
W11170 small inducible cytokine A21a (leucine)	-1.2	-1.0	1.1	1.0	1.3	-2.7	-2.8	-1.1	-1.1	-1.1	-1.3	1.0
AA967824 arginine vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-2.7	-2.0	-1.4	-1.3	1.4	-1.2	-2.3
W06321 inhibitor of DNA binding 1	1.1	-1.1	1.1	-2.0	-1.1	-2.7	-1.6	-1.1	-1.0	1.0	-1.0	1.2
A1157238 histocompatibility 2, class II, locus Mb1	-1.2	-1.1	-1.1	1.1	1.2	-2.8	-1.2	-1.2	-1.4	-1.1	1.1	-1.2
AA272836 aquaporin 8	-1.1	1.2	-1.1	1.4	1.4	-2.8	1.2	1.0	1.0	1.2	-2.4	1.3
AA496194 immunoglobulin kappa chain variable 20 (V20 family)	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.6	-1.0	1.4	-1.0	-2.7
AA782785 histocompatibility 2, class II, antigen E, beta	1.2	-1.7	-1.1	1.5	1.6	-2.9	-1.2	1.2	-1.7	1.1	1.0	-1.1
A1428626 ESTs	-1.4	1.1	-2.1	-1.8	1.3	-3.0	1.2	-1.2	-1.1	-1.3	1.0	-1.2
AA871265 Public domain EST	1.3	-1.4	-2.0	1.4	-1.7	-3.0	-3.1	-1.3	1.2	1.3	1.4	-1.7
AA152940 immunoglobulin kappa chain variable 28 (V28)	1.3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	-1.1	-1.1	-2.5
AA754696 immunoglobulin heavy chain 6 (heavy chain of IgM)	1.8	-1.5	1.0	-1.2	-1.9	-3.2	-1.9	-1.0	-1.2	-1.0	-1.1	-1.4
AA790398 ribonuclease 1, pancreatic	1.7	2.3	-1.2	-5.8	-16.8	-3.3	1.0	-1.9	-4.1	-1.1	-1.2	-1.1
AA072834 RIKEN cDNA 9030418M05 gene	1.1	1.2	-1.1	-2.1	1.13744*	-3.3	-1.1	1.1	-1.1	1.1	1.1	1.3

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W17930 small inducible cytokine A21a (leucine)	-1.2	1.0	-1.4	-1.2	1.2	-3.3	-1.3	-1.0	-1.2	-1.2	-1.5	-1.2
AA242406 CEA-related cell adhesion molecule_1	-1.1	-1.1	1.0	1.4	1.5	-3.4	1.2	-1.0	-1.1	-1.0	1.2	1.1
AI627143 ESTs	-1.0	-1.1	1.1	-1.3	-2.5	-3.6	1.2	-1.1	-1.2	-1.1	-1.1	-1.0
AA250087 proteosome (prosome, macropain)_subunit_beta_type_8 (large multifunctional protease 7)	1.1	-1.5	1.1	-1.9	1.0	-3.6	-1.5	-1.2	-1.1	1.2	-1.0	-1.2
W15909 hemoglobin, beta adult major chain	1.5	-1.2	1.2	-2.9	1.3	-3.7	3.4	-1.2	-1.0	1.8	-1.7	-1.6
AA759679 Ia-associated invariant chain	-1.0	-1.8	-1.6	-1.9	1.5	-3.7	-2.8	-1.0	-1.9	-1.0	-1.3	-1.4
AA790409 sialyltransferase_7 ((alpha-N-acetylneuraminyl_2,3-beta-galactosyl)-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) F	-1.0	-1.1	1.0	1.2	1.3	-3.9	1.2	-1.1	-1.4	1.0	-1.1	-1.1
AI605648 small proline-rich protein_2A	-1.0	-1.1	-1.4	-1.3	-5.5	-3.9	1.0	-1.2	-1.2	-1.1	-1.5	-1.1
AA821884 amylase_2, pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.3	-1.2	-4.4	-1.1	-1.1	-1.2
AI386257 calbindin-D9K	-2.2	-1.3	1.2	1.5	-53.5	-4.1	1.0	-1.2	-1.1	-1.2	-1.2	1.4
AA066763 hemoglobin, beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.8	-1.1	-1.3	1.5	-1.8	-2.0
AA106071 hemoglobin, beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	-4.3	3.2	1.1	-1.3	1.8	-1.7	-2.0
AA199011 histocompatibility_2, class II, antigen_A_alpha	-1.1	-1.3	1.1	1.0	1.3	-4.5	1.2	1.1	-1.9	1.3	-1.0	-1.2
AA497618 crp-ductin	1.7	1.8	-1.1	-1.6	-6.1	-5.0	1.5	-1.2	-1.3	-1.2	1.5	1.2
AA717025 Mus_musculus_10_day_old_male_pancreas_cDNA_RIKEN_full-length_enriched_library_clone:161009A17, full insert sequence	1.9	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1	-1.4

COLON

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TABLE 2

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intestine	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL- 4B_BDEnor	PL- 2B_BDEnor	PL- 6B_BDEnor	PL- 8B_BDEnor	PL- 3B_BDEnor	PL- 9B_BDEnor	PL- 1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
AA619407_pancovallitis-associated_protein	1.7	19.6	-1.9	1.2	4.4	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1
AA227986_cytochrome_P450_3a25	1.5	-1.2	1.3	-1.1	4.0	2.35798	-1.1	-2.2	1.2	1.1	1.0	1.3
W56303_peripher_myelin_protein_22_kDa	1.5	1.05393+	1.4	1.1	3.3	-1.4304-	1.2	1.1	1.3	1.2	1.1	-1.2
AA107035_guanylate_cyclase_activator_2b_(rodina)	-1.2	-1.3	1.1	-1.1	3.1	3.2	-1.5	-1.9	-1.2	1.2	-1.3	6.6
AA110886_amnionless	-1.1	1.06508+	1.1	1.2	3.0	1.27917+	-1.2	1.0	1.1	1.1	-1.1	1.5
AA108873_RIKEN_cDNA_0610010E05_gene	-1.1	-1.1	1.1	-1.0	2.8	1.8	1.0	1.0	1.3	1.8	-1.1	1.0
AI323162_dipeptidase_1_(rebat)	1.3	-1.3	-1.4	1.3	2.9	1.1	-1.5	-1.3	-1.1	1.0	1.0	-1.3
AA871838-phospholipase_A2_group_IIA_(platelets_synovial fluid)	-1.1	-1.0	-1.2	1.7	2.8	1.9	-1.9	-1.3	1.5	1.2	1.3	1.7
AA565394_RIKEN_cDNA_1110026D15_gene	1.6	1.3	1.1	-1.4	2.7	1.4	-1.1	1.1	-1.0	1.3	-1.2	-1.2
AA565694_cytochrome_P450_2b9_phenobarbital_inducible_type_2	-1.1	-1.4	1.9	1.3	2.6	3.9	-1.3	1.1	1.3	1.2	1.1	1.2
W16890_guanylate_cyclase_activator_2_(guanylin_2_intestinal_heatstable)	1.0	1.0	-1.3	1.2	2.8	-2.1	-1.5	-1.1	-1.2	-1.0	1.1	1.4
AI325330_cytochrome_P450_2b13_phenobarbital_inducible_type_2	1.4	-1.1	2.0	1.0	2.6	2.82616+	1.0	1.1	1.2	-1.2	1.1	1.4
AA242201_serine_protease_inhibitor_Kazal_type_3	1.5	1.8	-1.4	1.1	2.5	-1.0	-1.8	1.2	-9.2	-1.0	1.0	2.6
AA516927_sphingosine_phosphate_lyase_1	1.1	1.1	1.4	1.2	2.4	1.7	1.3	1.2	-1.0	1.3	1.0	-1.0
AA638765_metallothionein_1	1.0	1.1	2.5	1.2	2.4	1.8	1.2	-1.6	-1.3	1.3	-1.9	-1.2
AA422098_apolipoprotein_A1	-1.9	-1.5	1.1	-2.4	2.1	2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.6
AA871663_defensin_related_cryptidin_related_sequence_7	1.2	-1.4	-1.6	1.7	2.3	1.3	-1.2	-1.5	-1.1	-1.5	1.1	1.2
AA793433_glutaryl_aminopeptidase	1.3	1.1	1.1	1.3	2.3	-1.0	1.3	1.1	1.5	1.0	1.2	-1.1
AA889168_defensin_related_cryptidin_related_sequence_10	-1.0	-1.1	-1.7	2.0	2.3	1.5	1.2	1.2	1.6	1.1	1.6	1.2
AI324398_glycosylphosphatidylinositol_specific_phospholipase_D1	1.1	-1.3	1.2	-3.4	2.3	-1.5	2.0	-1.2	-1.3	1.2	-1.6	-1.6
AA066225_selenoprotein_P_plasma_1	1.2	1.4	1.2	-1.7	2.3	1.9	1.5	-1.2	-1.1	1.2	-1.6	-1.1

TABLE 2

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AA024217	Public domain EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AA082450	RIKEN cDNA 1200011D11 gene	-0.0	1.1	-1.1	-1.1	2.3	1.60563~	-1.4	-1.0	1.1	-1.2	-1.2	1.1
AI385503	cysteine rich intestinal protein	1.3	1.1	-1.0	-1.6	2.3	1.8	-1.3	-1.1	1.0	-1.0	-1.0	1.1
AA162211	guanine nucleotide binding protein, alpha_11	-1.0	1.0	-1.0	1.3	2.3	1.2	1.2	1.0	1.2	1.1	1.0	1.0
AA415344	histone deacetylase 7	1.2	1.3	1.8	-1.2	2.2	1.28947~	1.7	1.5	1.0	1.4	-1.2	1.0
AA230419	P glycoprotein 2	1.0	-1.2	-1.0	-1.1	2.2	1.0	1.0	1.0	1.1	-1.0	-1.2	1.3
AA105528	ESTs_Weakly similar to CA1C_MOUSE_COLLAGEN_ALP HA_1(XII)_CHAIN_PRECURSOR [M.musculus]	-1.1	-1.1	-1.0	-1.1	2.2	1.78648~	-1.5	1.0	-1.2	1.4	-1.1	1.0
AA770902	actin, alpha_1, skeletal muscle	-1.0	-1.1	-1.1	-1.1	2.2	1.1	-1.5	1.1	1.1	1.1	-1.1	-1.2
AA647336	cytochrome P450, steroid inducible 3a11	1.5	-1.4	1.7	1.1	2.2	3.84011~	-1.3	-8.0	-1.0	-1.1	1.2	1.1
AA386758	ESTs	-1.3	-1.3	1.0	-1.3	2.1	2.9254~	1.1	1.3	1.1	1.1	1.1	-1.0
AA871641	defensin related cryptdin, related sequence 2	-1.0	1.3	-1.4	1.8	2.1	2.0	1.2	1.4	1.2	1.1	1.8	1.6
AA871410	defensin related cryptdin 5	-1.5	-1.1	-1.0	1.8	2.1	1.8	-1.0	-1.2	1.2	-1.1	1.1	1.0
AA210237	Mus musculus, clone MGC:8377, mRNA, complete cds	-1.1	1.0	1.0	-1.0	2.0	1.5	1.3	1.3	1.2	1.4	1.0	-1.0
AI552087	IQ motif containing GTPase activating protein 1	-1.3	-1.1	1.3	1.1	2.0	1.2	-1.2	1.4	1.0	-1.0	1.0	1.1
AA166427	Mus musculus, germline immunoglobulin gamma_constant_1 region. (IgG3) mRNA	-1.3	1.0	-1.0	1.1	2.0	-1.2153+~	1.3	1.0	1.2	-1.1	1.1	-1.5
AA756138	actin, gamma_2, smooth muscle, enteric	1.1	-1.2	1.1	-1.1	2.0	-1.3	1.0	1.2	1.1	1.1	-1.3	1.1
AA230727	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.0	-1.1	-1.1	-1.0	2.0	1.4	1.2	-1.1	-1.0	-1.2	-1.4	1.8
AA465630	choline kinase	1.7	1.9	-1.4	3.1	2.0	1.31548+~	1.3	2.3	2.0	1.8	2.2	2.1
AI594147	beta-2 microglobulin	1.8	1.1	1.2	-2.1	2.0	-1.8	-1.0	-1.1	-1.0	1.3	-1.1	-1.2
AA684403	ESTs	-1.4	1.7	-2.3	-2.0	2.0	-2.4	1.5	-1.0	-1.3	-1.3	-1.1	-1.1
AA869219	Intelectin	-1.0	-1.3	-1.1	1.7	2.0	2.2	-1.9	1.3	1.2	-1.0	1.5	1.8
AA073925	ESTs	1.3	1.8	-1.4	2.5	2.0	-1.27077~	1.1	1.9	1.9	1.2	1.8	1.9
W54383	glutathione S-transferase, mu_2	1.3	1.7	-1.0	-1.5	2.0	1.2	-1.4	1.1	1.2	1.3	1.2	1.0
AA013726	calthepsin J	-1.0	-1.0	-1.2	1.8	1.9	-1.4	-1.2	1.8	1.2	1.1	-2.1	1.5
AI549624	RIKEN cDNA 0810041E09 gene	1.8	1.9	-1.3	3.6	1.9	-1.01549+~	1.1	2.2	2.1	1.9	2.5	2.3
AI552598	ESTs_Weakly similar to MIA_MOUSE_MELANOMA_DERIVED_GROWTH REGULATORY PROTEIN PRECURSOR [M.musculus]	-1.2	1.2	1.1	1.1	1.9	1.7	1.1	-1.2	-1.0	-1.1	-1.5	1.1
AA450725	membrane metallo endopeptidase	1.3	-1.3	1.1	-1.1	1.8	1.48772~	-1.2	1.2	-1.4	1.1	1.0	1.3
AA870247	mitogen regulated protein, proliferin_3	-1.0	1.0	-1.3	2.0	1.9	-1.0	-1.8	1.7	1.1	1.0	-1.8	1.4
AI892437	transglutaminase 2, C polypeptide	-1.1	-1.2	1.0	1.3	1.9	-1.3	-1.0	1.1	-1.2	1.1	-1.1	-1.1
AI036411	angiotensin converting enzyme	-1.1	-1.0	1.2	1.4	1.8	3.92701~	1.1	-1.2	1.1	1.8	1.2	-1.3
AA619767	ornithine decarboxylase antizyme	1.3	1.8	-1.0	-1.6	1.8	-1.0	-1.2	-1.2	-1.1	1.1	-1.3	-1.2
AA106623	hexosaminidase B	1.1	-1.0	1.3	1.1	1.8	1.4	1.3	-1.1	1.1	1.0	-1.1	-1.1

TABLE 2

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W14224_N-myc downstream regulated 1	1.1	1.0	1.0	1.1	1.1	1.2	1.1	1.6	1.0	1.3	2.1
AA624460 actin_alpha_2_smooth_muscle_aorta	-1.0	1.2	-1.3	-1.1	-1.9	-1.3	1.1	1.1	1.0	-1.2	1.0
W36474_metallothionein_2	-1.2	-2.2	2.1	1.2	1.6	1.3	1.1	-1.1	1.8	-1.9	1.0
AA821963 aspartyl aminopeptidase	1.0	1.0	1.1	-1.2	1.9	1.3	1.1	1.0	1.3	1.0	-1.2
W13521_cytochrome_P450_2f6	1.4	-1.0	1.1	-1.4	1.3	2.58949+-	1.3	1.2	-1.0	1.4	1.2
AA413490 transferrin receptor	1.4	-1.3	1.2	-1.0	1.3	-1.1	1.2	1.2	-1.3	1.5	1.5
AI594093_Mus_musculus putative CAMP protein (Camp)_mRNA_com plete cds	-1.1	-1.3	1.1	1.4	-1.9	-1.14409+-	1.5	1.2	-1.0	1.2	-1.3
AA028420_small proline-rich protein 1A	1.3	-1.7	-1.4	-1.5	-1.9	-1.2	-1.9	1.0	-1.1	1.3	1.3
AA245987 ESTs	-1.01124+	-1.30375+	1.1	1.29885+	-1.9	1.12110+-	-1.46943+	-1.02333+	-1.00306+	1.2	1.28207+
AI390129_proteasome_(prosome_macropain) subunit_alpha_type_2	1.1	1.0	1.3	-1.4	-1.9	-1.6	1.1	1.2	1.0	1.0	-1.3
AI156982_nuclear_receptor_subfamily_5_group_A_member_2	-1.3	1.2	-1.1	-1.1	-1.9	-1.40144+-	-1.0	-1.4	-1.2	-1.5	-1.2
AA548964_ESTs_Weakly_similar_to_TLM_MOUSE_TLM_PROTEIN_[M. musculus]	1.0	-1.4	-1.1	-1.1	-1.9	1.1	1.4	1.2	-1.4	1.2	-1.0
AI605616 ESTs	-1.2	-1.1	1.3	-1.5	-1.9	-2.3	-1.4	-1.2	-1.2	-1.5	-1.1
AA561934 ESTs	-1.5	-1.5	-1.4	1.1	-1.9	-1.03655+-	1.3	-1.2	-1.1	-1.5	1.0
AI157093_RIKEN_cDNA_2700094F01_gene	-1.0	-1.6	-1.0	-1.1	-1.9	-1.1	1.2	1.1	-1.3	-1.4	1.0
AA794319 ESTs	-1.1	-1.1	1.3	-1.7	-1.9	-1.7378-	-1.2	-1.4	-1.0	-1.1	-1.1
AA433804 ESTs	-1.1	-1.1	-1.1	-1.2	-1.9	-1.0	-1.0	-1.2	-1.4	1.0	-1.1
AA754696_immunoglobulin_heavy_chain_6_(heavy_chain_of_IgM)	1.6	-1.5	1.0	-1.2	-1.9	-3.2	-1.8	-1.0	-1.2	-1.1	-1.4
W09198_calcium_binding_protein_A6_(calyculin)	1.2	-1.2	-1.2	-1.6	-1.9	-2.4	1.1	1.1	1.2	-1.2	1.0
AA967824_arginine_vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-2.7	-2.0	-1.4	-1.3	-1.2	-2.3
AA496194_immunoglobulin_kappa_chain_variable_20_(V20_family)	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.6	-1.0	-1.4	-2.7
AA647876 ESTs	-1.3	-1.3	-1.0	1.3	-1.9	1.14107+-	-1.0	-1.2	-1.2	-1.3	-1.0
AA780455_RIKEN_cDNA_3110001120_gene	1.1	-1.1	1.2	-1.1	-1.9	-1.50429-	1.2	-1.1	1.0	1.2	1.3
AA068562_RIKEN_cDNA_2810417H13_gene	-1.0	-1.5	-1.1	-1.1	-1.9	-1.0	-1.0	-1.2	-1.5	-1.1	-1.2
AI627033 ESTs	-1.3	-1.1	-1.1	1.1	-1.9	-1.03772+-	1.3	-1.0	-1.1	-1.4	1.1
AI607043_ESTs_Weakly_similar_to_S12207_hypothetical_protein_[M.mu sculus]	1.2	-1.2	-1.1	-1.2	-1.9	1.1	1.0	1.1	-1.3	1.1	-1.2
AI536309_RIKEN_cDNA_2210410L06_gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-1.5	-2.1
AA166386_transducer_of_ErbB-2.1	-1.0	-1.2	1.3	-2.0	-1.9	-1.1	1.1	-1.2	-1.0	-1.2	1.2
AA414465 ESTs	-1.2	-1.3	-1.0	1.0	-1.9	1.2	1.0	-1.0	-1.3	1.0	-1.1
AA529377_heat_shock_protein_86_kDa_1	1.4	1.0	-1.3	-1.9	-1.9	-1.5	1.4	1.3	1.2	-1.0	1.3
AA562129_ESTs_Weakly_similar_to_T26899_hypothetical_protein_M04 B2.4 - Caenorhabditis elegans [C.elegans]	-1.0	-1.4	1.1	-1.2	-1.9	1.1	1.1	1.1	-1.0	1.0	-1.1
AI428592_Public_domain_EST	1.0	-1.5	-1.1	-1.3	-1.9	1.2	1.3	1.2	-1.1	-1.1	-1.1

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AA738642 proteasome (prosome, macropain) subunit, alpha type 3	1.2	-1.0	1.4	-1.3	-1.9	-1.5	1.1	-1.1	1.2	-1.1	1.1	-1.1	1.1	-1.2
AI596504 t-complex testis expressed 1	1.1	-1.6	-1.0	1.3	-1.9	1.4	1.1	1.4	-1.0	-1.1	1.3	-1.0	1.3	-1.0
AI036487 ESTs	-1.0	1.1	-1.1	-1.3	-1.9	-1.9	1.0	1.0	-1.0	-1.0	1.1	-1.0	1.1	1.0
AI386181 gamma-glutamyl carboxylase	-1.1	-1.3	-1.0	-1.2	-1.9	1.0	-1.0	1.1	-1.2	-1.3	-1.0	-1.2	-1.0	-1.2
AA422743 ESTs_Highly similar to AF091622.1_PHD_finger_protein_3 [H.sapiens]	-1.5	-1.3	-1.2	1.1	-1.9	-1.4	-1.2	1.1	-1.1	-1.2	-1.1	-1.2	-1.1	-1.1
AA289639 ESTs	-1.2	-1.2	-1.1	1.1	-1.9	-1.27388~	1.1	1.1	-1.1	-1.1	1.1	-1.2	1.1	-1.1
W84257 interferon (alpha and beta) receptor	-1.0	-1.4	-1.1	-1.2	-1.9	1.1	-1.1	1.1	-1.1	-1.1	-1.3	-1.1	1.1	-1.1
AI429064 ESTs_Weakly similar to S12207_hypothetical_protein [M.musculus]	1.0	-1.5	1.0	-1.1	-1.9	1.3	1.1	1.2	-1.0	-1.2	1.0	-1.3	1.0	-1.3
AA197547 RIKEN cDNA 2310031L18 gene	-1.1	-1.4	-1.1	-1.1	-1.9	-1.05207+~	1.1	-1.0	-1.1	-1.4	1.0	-1.1	1.0	-1.1
AA563376 DNA segment, Chr 8, ERATO Doi 233, expressed	-1.2	-1.1	1.1	-1.0	-1.9	1.12124~	-1.6	-1.1	-1.1	-1.3	1.1	1.0	1.1	1.0
AA414730 NCK-associated protein 1	1.2	-1.1	1.0	-1.8	-1.9	-1.2	1.2	1.1	1.2	1.1	1.1	1.1	1.1	1.1
AA276909 ESTs_Weakly similar to GRBA_MOUSE GROWTH FACTOR RECEPTOR-BOUND PROTEIN 10 [M.musculus]	-1.3	-1.8	-1.2	-1.1	-1.9	-1.29386~	-1.3	1.2	1.1	-1.1	1.3	1.3	1.3	1.3
AA538300 ESTs_Moderately similar to S12207_hypothetical_protein [M.musculus]	1.0	-1.2	-1.2	-1.1	-1.9	1.1	-1.2	1.1	-1.1	-1.3	1.0	-1.1	1.0	-1.1
W34620 kallikrein 26	1.2	1.1	-1.1	-1.4	-1.9	-1.2	-1.5	2.8	10.1	1.1	-1.1	-1.4	-1.1	-1.4
AI592338 ESTs	1.08777+	-1.50505+	-1.48731+	-1.6	-1.9	-1.40845+~	-2.12716+	-1.39471+	-1.0	-1.1	-1.0	1.1524+	-1.0	1.1524+
AA727388 ESTs_Moderately similar to S12207_hypothetical_protein [M.musculus]	-1.0	-1.1	1.0	-1.1	-1.9	1.0	-1.1	-1.0	-1.1	-1.4	-1.0	-1.2	-1.0	-1.2
AA437755 tnymus expressed acidic protein	-1.3	-1.5	-1.0	-1.1	-1.9	-1.49997+~	-1.4	-1.2	-1.5	-1.5	-1.0	1.1	-1.0	1.1
AA981354 cyclin T1	-1.4	-1.2	-1.2	-1.6	-1.9	-1.2	-1.4	-1.1	-1.3	-1.3	-1.1	-1.2	-1.1	-1.2
AI465828 ESTs	-1.2	-1.4	-1.3	-1.2	-1.9	-1.24163+~	-1.0	-1.1	-1.2	-1.3	1.2	-1.3	1.2	-1.3
AA467531 double C2, gamma	-1.2	-1.3	-1.3	-1.4	-1.9	-1.42692~	-1.0	-1.1	-1.2	-1.0	-1.0	1.1	-1.0	1.1
AA656528 ESTs_Highly similar to S12207_hypothetical_protein [M.musculus]	1.0	-1.1	1.0	-1.3	-1.9	-1.1	-1.2	-1.1	-1.2	-1.4	-1.0	-1.2	-1.0	-1.2
AI100100_02002_norvegicus_ventromedian_nerve_regeneration_factor g	1.2	-1.42323+	-1.16278+	-1.4	-1.9	-1.16394~	-1.9	1.2	1.17519+	-1.1	1.0	-1.4	1.0	-1.4
AA673741 DNA segment, Chr 12, ERATO Doi 604, expressed	1.3	-1.0	-1.1	-1.4	-1.9	-1.5707+	-1.1	-1.5	-1.2	-1.4	-1.3	-1.3	-1.3	-1.3
AA619869 RIKEN cDNA 5730534O06 gene	1.1	-1.0	1.1	-1.2	-1.9	-1.1	1.3	-1.0	1.0	-1.5	1.0	-1.2	1.0	-1.2
AI390319 ESTs_Weakly similar to apolipoprotein F [H.sapiens]	-1.1	-1.5	1.2	-1.1	-1.9	1.3	-1.4	1.0	-1.1	-1.2	1.1	-1.3	1.1	-1.3
AI614000 ESTs	-1.1	-1.2	1.0	-1.1	-2.0	1.2	-1.2	1.1	-1.1	-1.2	-1.0	-1.1	-1.0	-1.1
AA794176 ESTs_Moderately similar to SPA-1 like protein p1294 [R.norvegicus]	-1.0	-2.0	-1.2	-1.2	-2.0	1.2	1.2	1.3	-1.3	-1.3	1.1	-1.1	1.1	-1.1
AI156378 ESTs	-1.1	-1.7	-1.2	-1.1	-2.0	-1.02813~	-1.3	-1.4	1.3	1.4	-1.0	1.1	-1.0	1.1
AA656612 RIKEN cDNA 4631416G20 gene	-1.1	-1.3	1.1	-1.1	-2.0	-1.2	1.1	1.0	-1.2	-1.4	-1.0	-1.1	-1.0	-1.1
AA177238 ESTs	-1.2	-1.2	1.0	1.1	-2.0	-1.31702+~	1.3	1.0	1.0	-1.2	1.2	-1.1	1.2	-1.1
AA023331 adenosine deaminase	1.1	1.1	-1.1	1.1	-2.0	-1.4	1.2	1.2	1.3	1.1	-1.1	1.4	-1.1	1.4

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AA415510 ESTs	-1.0	-1.4	-1.1	-1.3	-2.0	-1.1	1.2	1.1	-1.2	-1.2	-1.1	-1.1
AA47943 EST	-1.1	-1.3	-1.2	-1.2	-2.0	1.0	-1.2	1.1	-1.2	-1.5	-1.0	-1.2
AA623448 ESTs_Weakly similar to NED4_MOUSE_NEDD-4_PROTEIN [M.musculus]	1.3	-1.2	-1.0	-1.1	-2.0	1.2	1.0	1.3	-1.1	-1.3	1.1	-1.2
AA120315 splicing factor, arginine/serine-rich 5 (SRP40, HRS)	1.8	-1.4	1.2	-1.1	-2.0	-1.0	-1.3	-1.0	1.1	-1.2	-1.1	-1.4
AA509560 ESTs	-1.1	-1.3	1.2	-1.1	-2.0	1.0	1.2	1.1	-1.2	-1.2	-1.0	-1.3
AA692960 ESTs_Weakly similar to AF089896_1_topoisomerase-related function protein [H.sapiens]	1.1	-1.5	1.0	-1.1	-2.0	1.1	-1.1	1.1	-1.1	-1.2	1.0	-1.3
AA459667 tumor rejection antigen gp96	1.3	1.4	-1.5	-1.9	-2.0	-1.4	1.2	-1.1	1.2	-1.1	1.1	-1.0
AA982569 ESTs	-1.1	-1.5	-1.1	-1.2	-2.0	1.0	1.12345*	1.1	-1.2	-1.5	-1.0	-1.2
AA14153 ESTs_Moderately similar to_S12207_hypothetical_protein [M.musculus]	-1.0	-1.1	1.1	-1.1	-2.0	-1.1	-1.2	1.1	-1.1	-1.4	1.0	1.0
AA598800 ESTs	-1.4	-1.3	-1.1	-1.3	-2.0	-1.42466~	-1.0	-1.1	-1.3	-1.4	-1.1	-1.2
AA638908 ESTs	1.0	-1.6	-1.0	-1.1	-2.0	-1.0	1.0	-1.1	-1.2	-1.4	-1.0	-1.1
AA605657 serine/arginine-rich protein specific kinase 2	-1.1	-1.0	1.0	1.1	-2.0	1.0	-1.4	-1.1	-1.0	-1.0	-1.2	-1.1
AA795130 ESTs_Moderately similar to_S12207_hypothetical_protein [M.musculus]	1.0	-1.3	-1.0	-1.1	-2.0	1.1	-1.1	-1.0	-1.1	-1.3	-1.1	-1.2
AA146478 M.musculus mRNA (3C10) for IgA V-D-J-heavy chain	-1.3	1.0	-1.8	-1.7	-2.0	-2.4	-1.1	-1.4	1.5	2.0	1.1	1.8
AA397221 ESTs_Weakly similar to NED4_MOUSE_NEDD-4_PROTEIN [M.musculus]	-1.1	-1.2	-1.0	-1.0	-2.0	-1.0	-1.2	1.1	1.0	-1.2	1.1	1.0
AA717269 ESTs_Weakly similar to_146456_hypothetical_protein_DKF Zp434L132.1 [H.sapiens]	1.1	-1.7	1.0	-1.1	-2.0	1.0	1.0	1.1	-1.1	-1.2	1.1	-1.2
AA666289 ESTs	-1.1	-1.4	-1.0	-1.1	-2.0	-1.0	-1.2	1.1	-1.2	-1.2	-1.0	-1.1
AA552745 Mus_musculus_clone_MGC-6888_mRNA_complete_cds	1.1	1.1	1.1	-2.0	-2.0	1.1	-1.2	-1.5	-1.2	-1.4	-1.3	-1.1
WA0608 anterior gradient 2 (Xenopus laevis)	1.4	1.1	-1.4	-1.7	-2.0	-1.4	1.4	-1.0	-1.0	-1.0	-1.0	-1.2
AA692534 ribosomal protein S24	1.3	1.1	1.3	-2.1	-2.0	-1.1	1.3	-1.2	1.2	-1.4	-1.1	-1.2
AA450438 Mus_musculus_mRNA_for_erythroid_differentiation_regulator, partial	-1.0	-1.0	-1.2	-1.5	-2.0	-1.3	-1.7	-1.3	-1.3	-1.6	-1.2	-1.2
AA619114 solute_carrier_family_11 (proton-coupled divalent metal ion transporters), member 2	1.1	1.0	1.0	-1.2	-2.0	-1.4	-1.5	1.4	1.1	-1.0	1.1	-1.0
AA608285 ubiquitin fusion degradation 1 like	-1.2	-1.4	-1.0	-1.3	-2.0	1.0	-1.1	-1.1	-1.2	-1.3	-1.1	-1.1
AA549540 ESTs	1.1	-1.4	-1.0	-1.0	-2.0	1.0	1.4	1.3	-1.1	-1.4	1.2	1.1
AA066867 RIKEN cdNA_3010002H13 gene	1.3	-1.1	1.0	-1.1	-2.0	1.48546~	1.4	-7.9	-1.1	-1.1	-1.7	-1.2
AA608085 ESTs	-1.1	-1.5	-1.1	-1.3	-2.0	-1.0	-1.0	-1.0	-1.3	-1.4	1.0	-1.2
AA474446 ESTs	-1.3	-1.5	-1.1	1.3	-2.0	1.01705+-	1.3	1.1	-1.1	-1.3	1.2	-1.1
AA444672 RIKEN cdNA_2510001A17 gene	-1.1	-1.0	1.1	-2.3	-2.0	-1.1	1.3	-1.1	1.2	-1.4	1.0	-1.2
AA473972 heterogeneous nuclear ribonucleoprotein H1	1.5	-1.2	1.2	-1.8	-2.0	-1.17495~	-1.2	1.0	1.1	-1.5	-1.1	1.1
AA287106 ESTs	-1.1	-1.3	1.1	-1.1	-2.0	-1.2	1.3	1.1	-1.1	-1.1	1.1	-1.2

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AA638929 ESTs, Moderately similar to S12207_hypothetical_protein_1 [M.musculus]	1.0	-1.3	-1.0	-1.1	-2.0	1.95911~	-1.1	1.1	-1.1	-1.3	-1.0	-1.2
AI391001_Pubic domain_EST	-1.2	-1.3	-1.0	1.0	-2.0	-1.1	-1.0	1.1	-1.1	-1.4	1.2	-1.0
AA575047 ESTs	-1.3	-1.4	-1.1	1.1	-2.0	1.3	-1.2	-1.1	-1.4	-1.1	1.0	-1.0
AI450530 ESTs	-1.1	-1.3	1.1	-1.3	-2.0	1.2	1.0	-1.1	-1.3	-1.4	-1.1	-1.1
AA536789_RIKEN_cDNA_1110002B05_gene	1.2	1.0	1.5	-1.3	-2.0	1.3	1.1	-1.2	1.0	-1.1	-1.1	1.0
AA684191_CDC-like_kinase	1.5	-2.1	-1.3	-1.1	-2.0	-1.4	-1.3	1.3	1.4	-2.1	1.4	1.2
AA549591 ESTs, Highly similar to CRM1 [H.septiens]	-1.2	-1.7	-1.1	-1.4	-2.0	1.4	-1.2	-1.0	-1.4	-1.4	-1.0	-1.1
AI536183_Pubic domain_EST	1.0	-1.1	1.0	1.1	-2.0	1.0	-1.4	1.1	-1.0	-1.2	1.1	-1.1
AA674133 ESTs	-1.2	-1.6	1.1	-1.2	-2.0	1.3	-1.1	-1.1	-1.2	-1.4	-1.0	-1.2
AA684092 ESTs, Moderately similar to S12207_hypothetical_protein_1 [M.musculus]	1.0	-1.4	1.0	-1.2	-2.0	-1.0	1.1	1.0	-1.2	-1.4	-1.1	-1.2
AA672766_Mouse mRNA for TI-227	-1.5	-1.3	-1.0	-1.1	-2.1	1.12734~	-1.1	-1.1	-1.0	-1.3	-1.1	-1.2
AA164064 ESTs	-1.1	-1.7	-1.1	-1.0	-2.1	-1.14579~	-1.37792~	1.2	1.0	-1.1	1.1	1.0
W15606_Ornithine, axon, heavy chain_11	1.3	-1.3	-1.1	-2.5	-2.1	-1.8	-1.1	1.0	-1.1	-1.2	-1.2	-1.1
AA450917_RIKEN_cDNA_1810005K14_gene	-1.1	-1.0	-1.06093~	-1.4	-2.1	-1.1	1.4	-1.1	-1.1	1.1	1.1	-1.1
AA696036 ESTs, Highly similar to GUANINE_NUCLEOTIDE-BINDING_PROTEIN_BETA.SUBUNIT-LIKE_PROTEIN_123 [M.musculus]	-1.2	-1.2	-1.1	1.0	-2.1	2.19728~	1.1	-1.1	-1.0	-1.1	-1.1	-1.2
AA514844_Pubic domain_EST	1.3	-1.5	1.0	-1.2	-2.1	1.0	1.0	1.2	-1.1	-1.3	1.1	-1.1
AA059886_protein_phosphatase_EF_hand_calcium-binding_domain_2	1.1	-1.6	-1.1	-1.1	-2.1	1.1	1.02202~	1.2	-1.1	-1.3	1.1	-1.1
AA067797_heat_shock_protein_cognate_70	1.0	-1.1	-1.0	-2.1	-2.1	-1.5	-1.1	1.3	1.5	1.3	1.0	1.2
AI530648 ESTs	-1.6	-1.1	1.7	-1.2	-2.1	2.39808~	1.8	-1.2	1.0	-1.1	-1.0	-1.1
AA619915_RIKEN_cDNA_1110015M06_gene	1.2	-1.3	1.1	1.3	-2.1	-1.0	1.8	1.3	1.1	-1.1	1.2	-1.0
AA000282_naked_cuticle_1_homolog_(Drosophila)	-1.0	-1.3	-1.0	1.0	-2.1	1.0	1.0	1.3	-1.1	-1.3	1.2	-1.1
AA607713_Mus_musculus_10_day_old_male_pancreas_cDNA_RIKEN_full-length_enriched_library_clone:1810009A17_full_insert_sequence	1.1	1.5	-1.2	-1.5	-2.1	-1.5	-1.7	1.4	-1.0	-1.1	1.5	1.4
AA152940_immunoglobulin_kappa_chain_variable_28_(V28)	1.3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	-1.1	-1.1	-2.5
AI640116 ESTs	-1.6	-1.02516+	1.3	-1.1	-2.1	1.37809~	1.3	-1.2	-1.1	1.1	-1.0	1.3
AA260035 ESTs	-1.1	-1.3	1.0	1.0	-2.1	-1.1	-1.2	1.2	-1.0	-1.2	1.1	-1.1
AA444576_heat_shock_protein_60_kDa	1.1	-1.1	1.4	-1.8	-2.2	-1.2	1.1	1.0	1.1	1.0	-1.1	-1.2
AI451754 ESTs	1.0	-1.3	-1.0	1.1	-2.2	1.3	-1.1	1.3	1.0	-1.1	1.2	-1.1
AI019837_laminin_beta_3	1.1	1.4	-1.1	-1.5	-2.2	-2.16452~	1.21089+	1.5	-1.1	1.1	1.1	1.4
AA068404_topoisomerase_(DNA)_II_beta	1.1	-1.2	1.2	-2.2	-2.2	1.0	-1.2	-1.5	-1.2	-1.5	-1.3	-1.2
AA680295_immunoglobulin_joining_chain	1.2	-1.5	-1.4	-1.4	-2.2	-2.4	-1.9	-1.1	1.3	1.5	1.4	-1.3
AA200306 ESTs	-1.5	-1.3	-1.5	-1.0	-2.2	1.06091~	1.1	-1.2	-1.3	-1.3	1.1	-1.1

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AI645264 ESTs Weakly similar to S29170 annexin VII - mouse [Musculus]	-1.1	-1.1	-1.1	-1.2	-2.2	-1.19222~	1.5	-1.1	1.3	1.5	-1.1	-1.1
W56995 hemoglobin X, alpha-like embryonic chain in Hba complex	1.1	-1.6	-1.3	-1.2	-2.2	1.11232~	-2.1	-2.0	1.0	-1.2	-4.0	-1.6
AA288278 ESTs	-1.3	-1.5	-1.3	1.3	-2.2	-1.01004+~	1.4	-1.0	-1.2	-1.4	1.2	1.0
AI463733 ESTs Moderately similar to S14234 hypothetical protein_- mouse [Musculus]	1.0	-1.3	-1.0	-1.2	-2.2	-1.1	1.2	1.1	-1.1	-1.3	1.0	-1.2
AA152636 integrin alpha 4	1.2	-2.2	-1.3	1.1	-2.2	-1.1	-1.0	1.3	-1.3	-1.4	1.2	-1.0
AA138854 ESTs Weakly similar to lysophospholipase I [Musculus]	-1.4	-1.6	-1.1	-1.0	-2.3	-2.1	1.1	-1.7	-1.0	1.4	-1.1	1.2
AI117296 Paneth cell enhanced expression	1.3	-1.2	1.1	1.1	-2.3	-1.28142~	-1.6	1.2	-1.0	-1.8	1.0	-1.0
AI592114 molybdenum cofactor synthesis 2	1.1	-1.7	-1.0	1.2	-2.3	1.2	-1.1	1.3	1.0	-1.3	1.3	1.0
AA435317 ESTs	-1.2	-1.7	1.1	-1.0	-2.3	1.1	1.1	-1.1	-1.5	-1.4	1.1	-1.2
AA105092 Bruton agammaglobulinemia tyrosine kinase regulated protein, 78kD	-1.4	1.0	1.2	-1.4	-2.3	1.05832~	-1.53017+	-1.4	1.0	-1.2	-1.2	-1.2
AA466153 ESTs	1.1	1.6	-2.4	-2.2	-2.4	-1.6	1.0	-1.3	1.2	-1.1	-1.1	-1.2
AA466153 ESTs	1.0	-1.11378+	1.02861+	1.2	-2.4	-1.16147+~	1.6	1.03478+	1.2	1.3	1.1	-1.33715+
AA718596 ESTs	-1.6	-1.3	-1.2	-1.3	-2.4	-1.2	-1.2	-1.4	-1.3	-1.4	-1.1	1.2
AA212405 dihydrofolate reductase	-1.2	-1.6	-1.2	-1.0	-2.5	-2.6	1.1	-1.4	-1.2	1.1	-1.1	-1.7
AA727065 ESTs	1.1	-1.2	1.2	-2.1	-2.5	1.2	-1.2	-1.6	-1.2	-1.4	-1.4	-1.3
AI464865 ESTs	-1.3	1.1	1.0	1.3	-2.5	-1.21294+~	-1.1	-1.4	-1.2	-1.2	-1.4	1.1
AI627143 ESTs	-1.0	-1.1	1.1	-1.3	-2.5	-3.6	1.2	-1.1	-1.2	-1.1	-1.1	-1.0
AA065764 AXL receptor tyrosine kinase	-1.3	1.0	1.1	1.0	-2.6	1.01582~	1.6	-1.1	1.1	-1.1	-1.1	-1.1
AI390861 retinoic acid induced 1	-1.5	1.0	-1.3	-1.2	-2.6	1.01684+~	-1.1	-1.3	-1.3	-1.1	-1.2	-1.5
AA619964 nuclear receptor coactivator 4	1.4	-1.3	1.4	-1.7	-2.7	-1.0	1.1	1.1	1.2	1.3	-1.1	-1.1
AA498574 kallikrein 6	1.8	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	2.8	7.2	1.1	1.0	1.3
AI596527 ribosomal protein L26	1.2	1.1	1.3	-1.8	-2.7	-1.2	1.2	-1.2	1.1	-1.1	-1.2	-1.5
AA521693 Public domain EST	-1.8	-1.3	-1.6	-1.5	-2.7	-1.5	-1.2	-1.0	-1.5	-1.1	-1.3	1.2
AA210505 Public domain EST	1.4	-1.5	1.2	-2.1	-2.7	-1.7	-1.1	1.1	1.3	1.1	1.1	1.2
AA242360 cytochrome P450, 1a2, aromatic compound inducible	1.3	-1.5	1.4	-1.1	-2.8	-1.33495~	-1.37353+	-2.4	1.6	1.1	1.2	1.2
AI536352 G protein-coupled receptor, family C, group 5, member B	-1.3	-1.7	-1.4	-2.1	-2.9	-1.3	-1.6	-1.1	-1.3	-1.1	-1.1	-1.0
AA693081 alkaline phosphatase 5	1.14857+	-1.15714+	1.35347+	-1.05793+	-2.9	1.52048+~	1.07417+	-1.01637+	-1.07118+	-1.16957+	1.08192+	-1.03494+
AA105866 glutathione S-transferase, alpha 4	1.1	1.0	1.8	-2.4	-3.0	1.3	1.2	1.0	1.3	1.3	-1.1	-1.2
AI425738 ESTs Weakly similar to ACRO_HUMAN_ACROSIN_PRECU RSO [H.sapiens]	-1.3	-1.6	-1.3	-1.1	-3.2	1.0	-1.0	-1.1	-1.3	-1.3	-1.2	-1.3
AA790247 RIKEN cDNA 2210407P13 gene	1.01667+	-1.39059+	-1.0	1.2	-3.5	-1.03402+~	-1.06819+	1.2	-1.0	1.1	1.1	1.3
AI614443 3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.2	-1.2	1.5	1.2	-3.7	-1.4	-1.3	1.4	1.5	1.3	2.1	1.7
AA839435 cathepsin E	-1.0	-1.5	1.0	-1.6	-4.1	-1.6	-1.5	-1.1	-1.1	-1.3	1.1	1.0
AI605648 small proline-rich protein 2A	-1.0	-1.1	-1.4	-1.3	-5.5	-3.9	1.0	-1.2	-1.2	-1.1	-1.5	-1.1

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TABLE 2

AI327450 phospholipase A2_group IB_pancreas	1.3	1.8	1.1	-1.8	-5.7	1.01624~	-2.3	-1.6	-1.4	-1.4	-1.1	-1.0
AA674409 pancreatic lipase related protein 1	2.0	1.7	-1.4	-1.7	-5.9	-1.0	1.2	1.0	-1.1	-1.1	1.6	1.3
AA497618 crp-ductin	1.7	1.8	-1.1	-1.6	-6.1	-5.0	1.5	-1.2	-1.3	-1.2	1.5	1.2
AA107101 prostate stem cell antigen	-1.1	-1.4	-1.3	-2.1	-6.1	1.51614~	-1.8	-2.1	-1.0	-1.1	-1.4	-1.4
W12985 annexin A10	1.5	-1.7	-1.1	-2.3	-8.5	-1.03567~	-1.3	-1.1	1.1	-1.0	1.0	-1.9
AI876997 carboxyl ester lipase	1.5	1.6	-1.4	-2.3	-8.9	-1.9	-1.3	-1.4	-1.1	1.1	2.0	2.2
AA582254 RIKEN cDNA 2210010C04 gene	2.3	1.6	-1.3	-2.0	-9.5	-1.3	1.8	1.5	-2.0	-1.4	-1.1	-1.1
AA237783 rat regenerating islet-derived mouse homolog 1	2.5	1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA675111 RIKEN cDNA 1610007A24 gene	1.4	1.3	-1.0	-2.1	-14.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	2.0
AI451862 RIKEN cDNA 0910001A18 gene	1.8	1.3	-1.1	-2.5	-14.7	-2.6	1.2	-1.3	-2.4	-1.3	-1.1	-1.3
AI386046 trypsin 4	1.7	1.8	1.1	-1.8	-15.9	-2.6	1.8	-1.5	-2.5	-1.1	-1.3	-1.2
AA790398 ribonuclease 1, pancreatic	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AA675084 elastase 2	2.3	1.4	-1.2	-2.7	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA717025 Mus_musculus_10 day old male pancreas cDNA_RIKEN full-length enriched library, clone:1810009A17, full insert sequence	1.8	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1	-1.4
AA821884 amylase 2, pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.3	-1.2	-4.4	-1.1	-1.1	-1.2
AI386257 calbindin-D9K	2.2	-1.3	1.2	1.5	-53.5	-4.1	1.0	-1.2	-1.1	-1.2	-1.2	1.4
AI894032 trefoil factor 2 (spasmolytic protein 1)	-1.1	1.8	-1.2	-2.0	-82.1	-1.89777~	-1.4	1.0	-1.4	-1.9	-1.0	1.4

INTESTINE

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TABLE 2

stomach	spl	panc	liv	stom	int	col	brain	lung	blad	kidn	p/ut	mam
Description	PL- 4B_BDEnor	PL- 2B_BDEnor	PL- 6B_BDEnor	PL- 8B_BDEnor	PL- 3B_BDEnor	PL- 5B_BDEnor	PL- 1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
A1598824_RIKEN_cDNA_0810041ED8_gene	1.6	1.2	-1.3	3.6	1.9	-1.01549+-	1.1	2.2	2.1	1.6	2.5	2.3
AA017112_ESTs	1.4	1.4	-1.2	3.3	1.7	-1.01971+-	1.3	1.6	1.7	1.3	1.8	1.9
A1804587_ESTs	1.2	1.3	-1.1	3.5	1.5	-1.02494+-	1.9	1.5	1.8	1.3	1.5	1.6
AA544433_dihydroorotate_dehydrogenase	1.2	1.5	1.0	3.2	1.7	1.2437+-	1.4	1.8	1.7	1.4	2.0	1.7
AA469630_choline_kinase	1.7	1.9	-1.4	3.1	2.0	1.31548+-	1.3	2.3	2.0	1.6	2.2	2.1
A1431982_EST	1.5	1.7	1.0	2.9	1.4283*	-1.60668+-	1.8	2.33182*	2.06474*	1.8	2.5	2.0
A1552802_RIKEN_cDNA_1706049J01_gene	1.35485+	1.07934+	1.02095+	2.9	1.17207+	-1.33509+-	1.73306+	1.18149+	1.29226+	1.4	1.2	1.13038+
AA607267_Public_domain_EST	1.4	1.7	-1.5	2.9	1.6	-1.07432+-	1.6	1.7	1.8	1.5	1.7	1.7
A1649854_programmed_cell_death_76	1.24627+	2.02725+	-1.0038+	2.8	1.6	1.10261+-	2.80284+	1.78399+	1.80094+	1.3	1.6	1.9
AA661920_RalBP1-associated_Eps_domain-containing_protein	1.4	1.7	-1.1	2.8	1.5	-1.1	1.2	1.8	1.9	1.7	2.0	1.7
A1036904_ESTs_Weakly_similar_to_X-LINKED_LYMPHOCYTE_REGULATED_PROTEIN_PM1_[M.musculus]	1.34106+	1.0	1.1	2.6	1.7	-1.23958+-	1.1	1.8	1.4	1.1	1.5	1.0
A1561391_ESTs_Weakly_similar_to_FV1_MOUSE_FRIEND_VIRUS_SUSCEPTIBILITY_PROTEIN_1_[M.musculus]	1.2	1.71031+	-1.05799+	2.7	1.7	1.69433+-	2.8	1.87693+	1.8	1.5	1.8	1.8
AA268406_nuclear_factor_I/B	1.4	1.1	-1.3	2.7	1.6	-1.28917+-	1.4	1.4	1.2	1.3	1.7	1.2
A1587825_RIKEN_cDNA_0710001D07_gene	1.4	1.3	-1.3	2.7	1.5	-1.20826-	1.4	1.5	1.7	1.3	1.6	1.5
AA146478_M.musculus_mRNA_(BC10)_for_IgA_V(D)-heavy_chain	-1.3	1.0	-1.6	2.7	-2.0	-2.4	-1.1	-1.4	1.5	2.0	1.1	1.6
A1158775_protein_tyrosine_phosphatase_receptor-type_11	1.02567+	1.1	-1.25592+	2.6	1.1	1.02178+-	1.2	1.3	1.0	1.1	1.1	1.3
AA002994_ESTs_Moderately_similar_to_No_similarities_reported_proteins_[H.sapiens]	1.1	1.0	-1.3	2.8	-1.1	-1.28021+-	2.3	1.0	-1.2	1.2	-1.2	-1.0
AA727914_ESTs	1.8	1.2	-1.1	2.6	1.5	-1.12264+-	1.7	1.8	1.8	1.3	1.6	1.5
AA036976_ESTs	1.1	1.3	-1.5	2.6	1.7	1.17381+-	2.3	1.88888+	1.7	1.4	1.8	2.1
AA162023_ESTs	1.3	1.5	-1.1	2.9	1.7	1.30792+-	1.3	1.7	1.8	1.2	1.7	1.6
AA073925_ESTs	1.3	1.6	-1.4	2.5	2.0	-1.27077-	1.1	1.9	1.9	1.2	1.8	1.9

TABLE 2

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AA688437 DNA polymerase epsilon	1.1	1.2	-1.4	2.5	1.8	1.12103+~	-1.0	1.6	1.4	1.3	1.8	1.3
AI651677 ESTs	1.2	1.3	-1.3	2.6	1.6	1.00205+~	1.6	1.3	1.5	1.5	1.3	1.6
AA624604 Public domain EST	-1.00414+	1.8	-1.1	2.5	1.1	1.06724+~	1.4	1.3	1.5	1.1	1.3	1.4
AA47967 ESTs	1.1	1.7	1.0557+	2.5	1.85593+	-1.08065+~	2.8	1.6	1.7	1.8	2.1	2.1
AA118029 RIKEN cDNA 2810018G03 gene	1.1	1.8	-1.5	2.8	1.8	1.22798+~	1.5	1.5	1.5	1.3	1.5	1.5
AA210486 ESTs	1.7	1.8	-1.1	2.4	1.5	1.2483+~	1.2	1.8	1.7	1.4	1.8	1.9
AA623587 ESTs	1.1	1.3	-1.3	2.4	1.5	-1.10185+~	1.2	1.8	1.6	1.2	1.5	1.7
AA623060 RIKEN cDNA 2410124L17 gene	1.5	1.5	1.1	2.4	1.36143*	-1.3	1.8	1.77425+	1.7	1.4	2.0	1.8
AI651943 ESTs Weakly similar to J02378 acyl-CoA C-acyltransferase (Hsapens)	1.2	1.1	-1.4	2.4	1.3	1.05496+~	1.4	1.8	1.7	1.7	1.7	1.6
AA470234 verine/threonine kinase 8	1.1	1.0	-1.3	2.4	1.3	1.3	1.5	1.4	1.5	1.2	1.2	1.3
AA412879 RIKEN cDNA C330006J08 gene	1.8	1.8	-1.0	2.4	1.2	-1.3	1.3	2.0	1.8	1.5	1.7	1.7
AA607883 zinc finger protein 101	1.23774+	1.9	-1.38204+	2.4	1.6	1.1254+~	1.85168+	1.432+	1.5	1.2	1.4	1.7
AI614738 RIKEN cDNA 2810301I35 gene	1.3	2.07881+	1.1	2.4	1.5	1.2409+~	2.8	1.4	1.5	1.8	1.5	1.6
AA489848 growth factor, ery1 (S. cerevisiae) like (augmenter of liver regeneration)	1.4	1.8	-1.4	2.4	1.6	1.35346+~	1.5	1.4	1.5	1.3	1.5	1.4
AA369264 ESTs	1.22008+	1.2	-1.28881+	2.4	1.48785+	-1.28488+~	1.45708+	1.48404+	1.53133+	1.7	1.57478+	1.32862+
AA623175 ESTs	1.5	1.5	-1.0	2.4	1.8	-1.30902+~	1.4	2.3	2.1	1.7	2.2885+	1.6
AI694170 ESTs	1.2	1.2	-1.2	2.4	1.5	-1.0	1.4	1.5	1.3	1.4	1.3	1.4
AI649645 RIKEN cDNA 1300017K15 gene	1.3	1.7	-1.1	2.4	1.4	1.0667+~	1.4	1.8	1.6	1.4	1.8	1.6
AA638805 Public domain EST	1.1	1.5	-1.2	2.3	1.5	-1.12759+~	1.4	1.6	1.6	1.3	1.8	1.7
AI650977 ESTs	-1.0	1.3	-1.1	2.3	1.3	-1.10355+~	1.5	1.8	1.4	1.2	1.5	1.5
AA663789 sirtuin_1_((silent_mating_type_information_regulation_2_homolog)_1_(S. cerevisiae))	1.1	1.3	-1.2	2.3	1.5	-1.22848+~	1.8	1.2	1.4	1.1	1.3	1.3
AI649694 ESTs Highly similar to P300_HUMAN_E1A-ASSOCIATED_PROTEIN_P300 [Hsapens]	1.0	1.1	-1.3	2.3	1.3	1.15359+~	-1.1	1.4	1.7	1.4	1.6	1.8
AI650200 SEC61, alpha subunit 2 (S. cerevisiae)	1.3	1.8	1.1	2.3	1.8	1.28243+~	1.2	1.8	1.8	1.5	1.4	1.7
AI645426 diaphanous homolog 3 (Drosophila)	1.2	1.8	-1.3	2.3	1.7	1.01107+~	1.8	1.5	1.3	1.2	1.3	1.4
AA231099 necdin	-1.8	1.3	1.1	2.3	1.7	1.8	1.0	2.0	-1.3	-1.2	-1.7	1.0
AA530026 ESTs	1.20192+	1.48056+	1.03838+	2.3	1.43226+	-1.18503+~	2.72586+	1.35485+	1.35148+	1.3	1.5	1.1

TABLE 2

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AI552219 ESTs	1.2087+	1.579+	-1.18563+	2.3	1.8	-1.26743~	2.14507~	1.53405+	2.1	1.8	1.85635+	1.8213+
AA517691 ESTs	1.3	1.8	-1.2	2.3	1.3	1.32145+	1.6	1.7	1.7	1.5	1.6	1.5
AA517337 WASP family 1	1.1	1.0	-1.6	2.3	1.4	1.40453~	1.5	1.1	1.4	1.2	1.2	1.3
AA543950 RIKEN cDNA 2900073G15 gene	1.1	1.4	-1.2	2.3	1.8	-1.09881~	-1.1	1.5	1.3	1.2	1.5	1.6
AA617362 low density lipoprotein receptor-related protein 2	1.1	1.4	-1.1	2.3	1.4	-1.17835~	1.53081+	1.1	1.5	1.4	1.0	1.7
AA473684 RIKEN cDNA C09002017 gene	1.22138+	1.53163+	-1.02182+	2.3	1.3	1.37779+	2.0	1.50959+	1.3697+	1.82061+	2.24475+	1.7053+
AA285337 deoxyguanosine kinase	1.1	1.1	-1.2	2.2	1.4	-1.04267~	1.1	1.4	1.7	1.3	1.6	1.5
AA588981 Mus musculus brain cDNA, clone MNCb-1820	1.0	1.1	-1.2	2.2	1.6	1.12888~	1.3	1.3	1.1	1.2	1.3	1.1
AI325781 ESTs, Weakly similar to S37771_ankyrin_erythrocyte-mouse [M.musculus]	1.4	1.3	-1.1	2.2	1.5	1.11463~	1.5	1.5	1.6	1.4	1.5	1.4
AI549656 RIKEN cDNA 3632413F13 gene	1.2	1.4	-1.22779*	2.2	1.4	-1.1	1.1	1.5	1.4	1.2	1.3	1.4
AI549656 ESTs	1.35481+	1.85118+	1.04863+	2.2	1.6	1.5167+	1.07014+	1.61878+	1.7	2.0	1.5	2.05047+
AI425572 ESTs, Highly similar to zygini [R.norvegicus]	1.3	1.2	-1.2	2.2	1.2	1.10985~	1.3	1.2	1.3	-1.1	1.2	1.3
AA210502 Public domain EST	1.1	1.7	-1.2	2.2	1.5	1.05245~	1.17392+	1.6	1.5	1.5	1.4	1.7
AI509664 RIKEN cDNA 2410174K12 gene	-1.0	1.1	-1.1864+	2.2	1.1	-1.19466~	1.7	1.0	1.1	1.1	1.1	1.1
AI587986 ESTs	1.0	1.1	-1.1	2.2	1.4	1.2339~	1.33244+	1.2	1.4	-1.1	1.3	1.5
AA606582 Public domain EST	1.13444+	1.5	-1.2	2.2	1.4	1.08581~	1.8	1.5	1.3	1.3	1.5	1.88536+
AI551955 RIKEN cDNA 6330415E02 gene	1.0	1.3	1.4	2.2	1.4	1.97213~	-1.2	1.2	1.1	1.3	1.2	1.6
AA823452 ESTs	1.44959+	1.3508+	-1.08198+	2.2	1.5	1.54682+	1.3	1.31484+	1.38275+	1.2	1.8	1.40132+
AW210270 ESTs, Weakly similar to T17254_hypothetical_protein_DKfZp585O1022.1 [H.sapiens]	1.1	1.3	-1.2	2.2	1.3	-1.1	1.4	1.4	1.4	1.2	1.27852*	1.4
AA412912 ESTs	1.2	1.5	-1.4	2.2	1.5	-1.07075~	1.9	1.6	1.7	1.2	1.5	1.8
AA068624 hydroxyacid oxidase (glycolate oxidase) 3	1.3	1.3	-1.2	2.2	1.3	1.32102*	2.4	1.2	1.4	1.3	1.1	1.5
AA096985 cytochrome P450, 2j5	1.0	-1.0	-1.0	2.2	1.6	1.57738~	1.4	-1.0	1.5	1.2	1.3	1.7
AA709576 ESTs	1.1	1.1	-1.44348+	2.2	1.5	-1.02969~	1.5	1.33339+	1.4	1.4	1.1	1.1
AA611551 Mes-linked imprinted transcript 1	1.27918+	1.1	-1.0	2.2	1.8	1.14544~	1.8	1.6	1.3	-1.1	1.4	1.3
AA000370 RIKEN cDNA 4933438K12 gene	1.3	1.1	-1.5	2.2	1.9	1.77642~	1.7	1.4	1.5	1.0	1.3	1.3
AA153231 Public domain EST	1.3	1.8	1.0	2.2	1.7	-1.56578~	1.3	1.8	2.0	1.5	1.8	1.8
AA288247 ESTs, Weakly similar to MRP5_MOUSE_MULTIDRUG_RESIS	1.1	1.4	-1.1	2.2	1.0	1.11973~	-1.5	1+	1.0	-1.1	1.3	1.4
TANCE-ASSOCIATED PROTEIN_5 [M.musculus]	1.2	1.2	-1.1503+	2.2	1.6	1.15298~	1.7	1.4	1.4	1.2	1.2	1.2
AA709668 ESTs	-1.0	1.0	-1.1	2.2	1.4	1.46574~	1.14559+	1.4	1.5	1.2	1.4	1.3
AA615213 ESTs, Moderately similar to unnamed_protein_product [H.sapiens]	1.2	1.5	1.0	2.2	1.2	-1.20582~	1.9	1.6	1.6	1.4	2.0	1.7
AI553232 ribosomal protein S6	1.2	1.6	-1.0	2.2	1.3	-1.17168~	1.8	1.65247+	1.5	1.4	1.5	1.3
AA210550 Mus musculus, Similar to RIKEN_cDNA_1500041N16_gene_c1one MGC:12066_mRNA_complete_cds	1.2	1.6	-1.0	2.2	1.3	-1.17168~	1.8	1.65247+	1.5	1.4	1.5	1.3
AI037649 transition protein_1	-1.1	1.2	-1.2	2.1	1.4	-1.3	-1.4	1.5	1.2	1.2	2.0	1.8
AA717167 cytotoxic T lymphocyte-associated protein 2_alpha	1.4	-1.8	-1.3	2.1	1.4	2.1	-1.8	-1.1	1.5	-1.4	-1.5	1.8

TABLE 2

AI53356 ESTs, Moderately similar to T00075_hypothetical_protein_KIAA0461 [H.sapiens]	1.1	1.8	1.0	2.1	1.5	1.06805+	1.3	1.4	1.2	1.6	1.3	1.3
AA710379 neuropilin	-1.08003+	1.2	1.3	2.1	1.4	-1.63768+	-1.1	1.1	1.2	-1.1	1.3	1.4
AI463731 ESTs	1.2	1.5	-1.4	2.1	1.3	-1.00785+	1.5	1.5	1.4	1.4	1.8	1.6
AA710200 ESTs	1.2	1.4	1.01548+	2.1	1.2	-1.28921+	1.3	1.2	1.2	1.1	1.1	1.1
AI464600 ESTs	1.2	1.0	-1.5	2.1	1.1	-1.07437+	1.4	1.4	1.2	1.3	1.4	1.4
AI643201 Mus_musculus TOB3 mRNA, complete cds	1.3	1.8	1.1	2.1	1.5	1.20006+	1.25034+	1.1	1.4	1.5	1.5	1.4
AA445667 RIKEN cDNA 4632401C08 gene	1.3	-1.2	-2.0	2.1	-1.0	1.1	1.3	-1.2	1.3	1.4	1.8	1.9
AA498760 syntaxin binding protein 1	-1.2	1.2	1.3	2.1	1.4	1.66943+	1.3	-1.2	-1.3	-1.1	-1.0	1.1
AI613926 twist gene homolog, (Drosophila)	-1.1	1.1	-1.17581*	2.1	1.4	2.1	-1.2	-1.3	1.1	1.0	-1.2	-1.0
AI549661 RIKEN cDNA 2410044K02 gene	1.2	1.5	-1.4	2.1	1.7	1.52602+	1.3	1.4	1.3	1.2	1.6	1.4
AA269742 RIKEN cDNA 1110065A22 gene	1.1	-1.0	-1.1	2.1	1.3	1.06169+	1.2	1.3	1.2	1.2	1.3	1.5
AI594144 DNA segment_Ch3_Brigham & Women's Genetics 0878_expressed	1.1	1.3	-1.2	2.1	1.4	-1.17655+	1.1	1.5	1.3	1.2	1.2	1.3
AI607675 Mus_musculus clone MGC:7865_mRNA, complete cds	1.3	1.3	1.0	2.1	1.1	-1.45989+	1.5	1.5	1.5	1.2	1.5	1.4
AA230591 myosin, heavy polypeptide 3, skeletal muscle, embryonic	1.4	1.5	-1.2	2.1	1.3	1.16035+	1.4	1.77332*	1.8	1.4	1.5	1.8
AA671408 core1_UDP-galactose:N-acetylgalactosamine-alpha_R_beta_1,3-galactosyltransferase	1.4	1.6	-1.3	2.1	1.6	1.14962+	1.8	1.7	1.5	1.3	1.6	1.5
AA450831 BCL2adenovirus E1B 19 kDa-interacting protein 1, NIP2	1.2	1.2	1.1	2.1	1.4	1.70102+	1.3	1.1	1.2	1.1	1.1	1.0
AA638776 matrix metalloproteinase 12	1.26422+	1.5439+	-1.11429+	2.1	1.63553+	1.01168+	1.84811+	1.29835+	1.4481+	1.4	1.2	1.48751+
AA110551 phospholipid scramblase 2	1.1	-1.1	-1.1	2.1	1.7	-1.1	-1.4	1.2	1.8	-1.0	1.2	1.2
AA833196 RIKEN cDNA 4932431F02 gene	1.4	1.5	-1.2	2.1	1.4	-1.0	1.4	1.8	1.6	1.4	1.5	1.5
AI505986 stearyl-Coenzyme A desaturase 2	1.4	1.2	-1.3	2.1	1.4	-1.5	2.0	1.5	1.5	1.2	1.4	1.3
AA655910 mast cell protease 2	1.12172+	-1.2816+	1.09121+	2.1	1.62532+	1.32118+	1.21826+	1.21528+	1.0051+	-1.07124+	-1.28511+	-1.1
AA412921 RIKEN cDNA 4921514I20 gene	1.4	1.6	1.0	2.1	1.4	-1.23027+	1.8	1.7	1.6	1.4	1.8	1.5
AI552048 ESTs	-1.04537+	1.2052+	-1.0	2.1	1.39436+	1.18278+	-1.03940+	1.19454+	1.2	-1.0	1.3	1.0
AA265101 RIKEN cDNA 1600021C16 gene	1.4	1.2	-1.1	2.1	1.1	1.03533+	-1.3	1.3	1.3	1.1	1.3	1.4
AA686687 ESTs, Weakly similar to Inv [M.musculus]	1.2	1.4	-1.35747+	2.1	1.5	1.18935+	1.4	1.3	1.2	1.0	1.3	1.1
AA516997 kinase suppressor of ras	1.1	1.2	-1.4	2.1	1.4	1.17949+	1.7	1.2	1.4	1.2	1.3	1.4
AA254235 complement receptor 2	1.1	1.5	-1.4	2.1	1.4	-1.02477+	1.5	1.4	1.2	1.1	1.4	1.3
AA450452 RIKEN cDNA 8430430L24 gene	1.2	1.5	-1.2	2.1	1.5	1.29003+	1.4	1.3	1.5	1.1	1.4	1.4
AA596430 galactose-1-phosphate uridylyl transferase	1.3	1.5	-1.0	2.1	1.4	-1.08755+	1.4	1.3	1.4	1.2	1.4	1.1
AA023720 ESTs	1.2	1.5	-1.1	2.0	1.2	1.07281+	1.5	1.5	1.3	1.7	1.5	1.3
AA267824 Public domain EST	1.3	1.6	-1.1	2.0	1.32119*	-1.13095+	1.3	1.5	1.5	1.3	1.5	1.5
AA607043 RIKEN cDNA 2400007G07 gene	1.1	1.4	-1.1	2.0	1.5	1.00337+	1.8	1.3	1.4	1.4	1.3	1.3
AA273401 Public domain EST	1.5	1.3	-1.0	2.0	1.40823*	-1.0	1.3	1.5	1.5	1.4	1.4	1.6

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AA68825	RIKEN cDNA A330103N21 gene	1.3	1.2	-1.2	2.0	1.4	1.1	1.9	1.4	1.3	1.6	1.4	1.3
AI64723	ESTs_Weakly similar to JH0494_alpha-1-antichymotrypsin-like protein EB22/4 - mouse [M.musculus]	1.2	1.4	1.1	2.0	1.2	-1.11434~	1.1	1.4	1.5	1.3	1.7	1.0
AA469724	WW domain binding protein_5	1.3	1.4	-1.1	2.0	1.5	1.0	1.1	1.7	2.0	1.3	1.8	1.8
AA474374	RIKEN cDNA 5730408C10 gene	1.6	1.5	1.0	2.0	1.3	-1.07742~	1.5	1.4	1.3	1.4	1.5	1.8
AA450453	Mus_musculus_Similar to hypothetical protein_clone_MGC7581_1_mRNA_complete cds	1.4	1.3	-1.2	2.0	1.4	1.02813~	1.7	1.3	1.3	1.2	1.5	1.3
AA79297	procollagen type V alpha 1	-1.2	1.0	-1.15089*	2.0	1.5	1.4	-1.4	1.0	1.2	1.1	-1.1	-1.3
AA105367	period homolog 3 (Drosophila)	1.2	1.1	-1.1	2.0	1.2	1.11211+~	-1.1	1.3	1.3	1.1	1.4	1.4
AA466199	RIKEN cDNA 2410056N02 gene	-1.04614+	1.41714+	-1.26081+	2.0	1.0	-1.03384~	1.7	1.2862+	1.2	1.75427~	1.6	1.2
AA823475	ESTs	-1.22121+	1.1	-1.7	2.0	1.9	-1.43639+~	1.3	1.5	1.4	1.2	1.3	1.3
AA638198	gap junction membrane channel protein_beta 3	1.2	1.5	-1.1	2.0	1.2	-1.31763~	1.5	1.6	1.3	1.49755+*	1.4	1.3
AA529248	Mus_musculus_Similar to phosphoprotein_regulated_by_mitogenic pathways_clone MGC11752_mRNA_complete cds	1.3	1.4	-1.1	2.0	1.4	-1.2	1.3	1.5	1.5	1.2	1.5	1.5
AA066256	Public domain EST	1.1	1.2	-1.1	2.0	1.4	1.46053+~	1.6	1.4	1.3	1.1	1.3	1.5
AA470294	DNA segment, Chr 2, ERATO Dcl 435, expressed	1.2	1.2	-1.1	2.0	1.4	-1.0	1.5	1.4	1.3	1.2	1.3	1.2
AA250545	ESTs_Weakly similar to SFRB_HUMAN_SPLICING_FACTOR_1 - C.elegans	1.3	1.2	1.2	2.0	1.1	-1.41089+~	1.5	1.5	1.40699*	1.3	1.7	1.5
AA869166	defensin related cryptidin, related sequence_10	-1.0	-1.1	-1.7	2.0	2.3	1.5	1.2	1.2	1.6	1.1	1.6	1.2
AI608071	RIKEN cDNA 2600017D14 gene	1.3	1.5	-1.1	2.0	1.2	-1.2	1.4	1.6	1.3	1.2	1.5	1.5
AA155097	ESTs	1.4	1.1	1.1	2.0	1.2	-1.2	1.4	1.6	2.0	1.2	1.7	1.8
AA518686	ESTs	1.2	1.4	-1.3	2.0	1.5	-1.5	2.0	1.4	1.4	1.2	1.5	1.6
AA616077	ESTs	1.2	1.2	-1.3	2.0	1.5	-1.10029+~	1.2	1.5	1.3	1.0	1.3	1.3
AA204045	Public domain EST	1.4	1.4	1.1	2.0	1.3	-1.2	-1.1	1.6	1.7	1.3	1.8	1.8
AA212102	ESTs	-1.1	1.3	-1.1	2.0	1.2	1.16314+~	1.7	1.1	1.3	1.1	1.1	1.3
AA058211	ESTs	1.3	1.3	-1.0	2.0	1.1	-1.0	1.8	1.3	1.1	1.3	1.2	1.2
AA870247	mitogen regulated protein_proliferin_3	-1.0	1.0	-1.3	2.0	1.8	-1.0	-1.8	1.7	1.1	1.0	-1.8	1.4
AA562544	RIKEN cDNA_1110035L05 gene	1.3	1.3	-1.1	2.0	1.3	1.0	1.4	1.5	1.4	1.3	1.5	1.4
AA210559	ESTs_Weakly similar to T34029_hypothetical protein_C32F10_1 - C.elegans	-1.1	1.3	1.0	2.0	1.3	-1.00634~	1.6	1.0	1.2	1.3	-1.0	1.2
AA684073	ESTs	-1.0	1.24976*	-1.3	2.0	1.7	1.12054+~	1.7	1.3	1.1	1.2	1.2	1.3
AA497627	intersectin (SH3 domain protein_1A)	-1.6	1.0	1.1	2.0	1.5	2.70772+~	-1.0	-1.8	-1.5	-1.2	-2.1	-1.2
AA717080	ESTs	1.0	1.2	-1.1	2.0	1.6	1.59321+~	-1.2	1.2	1.7	1.1	1.2	1.2
AA244813	calbindin 2	1.4	1.1	-1.5	2.0	1.7	-1.16196+~	1.0	1.4	1.2	1.3	1.5	1.7
AA265096	ESTs	1.2	1.3	1.1	2.0	1.3	-1.08802+~	1.5	1.5	1.4	1.3	1.5	1.5
AI464603	RIKEN cDNA 0710001E13 gene	1.1	1.1	1.0	2.0	1.4	-1.08185+~	1.6	1.08953+	1.4	1.2	1.4	1.4
AA254875	ESTs	1.1	1.1	1.0	2.0	1.1	-1.08064~	-1.11044+	1.4	1.3	1.3	1.2	1.3
AA646049	interleukin_13	1.2	1.4	-1.2	2.0	1.5	-1.02129+~	1.3	1.4	1.3	1.2	1.4	1.2

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AA290276 ESTs	1.5	1.4	-1.1	2.0	1.2	-1.29451+	1.0	1.5	1.2	1.8	1.6
AA211954 RIKEN cDNA 4930511A05 gene	-1.1	1.0	-1.2	2.0	1.2	1.1	1.3	1.1	1.4	1.2	1.1
A1530661 RIKEN cDNA 2810426N06 gene	1.5	1.7	1.2	2.0	1.2	-1.40231-	1.10197+	1.3	1.3	1.3	1.5
AA571416 RIKEN cDNA 1190004M21 gene	1.1	1.4	-1.2	2.0	1.4	1.07884-	1.3	1.4	1.3	1.3	1.3
A1627071 RIKEN cDNA 2310058A11 gene	1.3	1.4	-1.3	2.0	1.4	-1.21372+-	-1.1	1.5	1.2	1.3	1.5
A1597531 gap junction membrane channel protein beta 2	1.2	1.4	-1.1	2.0	1.2	1.17509+-	1.3	1.3	1.5	-1.2	1.1
AA591707 DNA polymerase epsilon, subunit 2	-1.1	1.1	1.05228*	2.0	1.4	1.9	-1.6	1.1	1.1	1.1	1.1
AA473562 ESTs, Moderately similar to alias DLC1 [H.sapiens]	1.3	1.5	1.2	2.0	1.6	-1.3061-	1.59994+	1.69984+	1.5	1.4	2.0
AA220774 ESTs	1.2	1.6	-1.0	2.0	1.3	-1.09803-	-1.0	1.5	1.3	1.3	1.5
A1117905 RIKEN cDNA 6530406M24 gene	-1.6	-1.1	1.5	2.0	1.4	2.33517+-	-1.3	-1.51658+	-1.3	-1.0	-1.3
AA395924 ESTs	1.3	1.4	-1.1	2.0	1.3	-1.07451-	1.3	1.5	1.3	1.3	1.8
AA869181 defensin related cryptidin 6	-1.8	-1.7	-1.5	2.0	1.5	2.3	-1.4	-1.2	1.1	-1.2	1.4
A1604192 RIKEN cDNA 4632433K11 gene	1.2	1.4	-1.1	2.0	1.2	1.13766+-	1.2	1.2	1.2	1.1	1.4
A1550560 ESTs	1.2	1.2	-1.2	2.0	1.2	-1.18773-	-1.2	1.3	1.4	1.3	1.5
AA473386 ESTs	1.2	1.5	-1.2	2.0	1.7	1.10149+-	1.0	1.5	1.4	1.3	1.6
AA591510 homeo box B1	-1.1	1.6	-1.4	2.0	1.7	1.90738+-	1.2	-1.0	1.2	1.1	1.3
A1587821 solute carrier family 22 (organic cation transporter), member 2	1.4	1.1	-1.3	1.9	1.5	-1.05076-	1.1	1.3	1.4	1.2	1.4
A1553220 ESTs	1.47614*	-1.0	1.3	1.9	1.2	-1.30242-	-1.1	2.14493*	2.0	1.8	2.57946*
AA209628 ESTs, Highly similar to T06741_hypothetical_protein_DKFZp586G0518.1 [H.sapiens]	1.2	1.3	1.1	1.9	1.2	-1.3	-1.0	1.4	1.3	1.1	1.3
AA067264 kinesin 1	-1.1	-1.0	-1.3	1.9	1.7	1.50139+-	1.6	1.1	1.3	1.0	-1.1
AA266331 ESTs	1.15878+	1.2	-1.1	1.9	1.3	1.00375+-	1.1	1.4	1.2	1.0	1.3
AA596525 chromodomain helicase DNA binding protein 1	-1.4	-1.07406+	1.0	1.9	1.1	1.34568+-	-1.59895+	1.0	1.2	1.3	1.0
AA209628 ESTs, Highly similar to T06741_hypothetical_protein_DKFZp586G0518.1 [H.sapiens]	1.1	-1.1	-1.0	1.9	1.3	1.1	-1.0	1.5	1.3	1.1	1.2
AA259281 LIM homeobox protein 2	1.4	1.6	-1.1	1.8	1.2	-1.2	1.6	1.4	1.4	1.3	1.6
A1549635 ESTs	1.1	1.1	-1.2	1.9	1.1	2.19723+-	-1.39628+	1.1	1.4	1.1	1.4
AA268913 flavin containing monooxygenase 5	1.2	1.2	-1.13647+	1.9	1.2	-1.15925+-	1.2	1.29569+	1.3	1.2	1.3
AA547242 undifferentiated embryonic cell transcription factor 1	-1.5	1.5	1.8	1.9	1.4	2.12+-	1.09749+	-1.90264+	-1.5	-1.1	-1.8
AA060731 nuclear factor interleukin 3, regulated	1.4	1.2	-1.1	1.9	1.3	1.16127+-	-1.0	1.4	1.5	1.3	1.3
A1596550 leukemia/lymphoma related factor	1.2	1.4	-1.2	1.9	1.5	-1.0536+-	1.4	1.5	1.5	1.2	1.4
AA822679 hematopoietic cell signal transducer	-1.0	1.1	-1.2	1.9	1.3	-1.79549+-	1.2	1.2	1.1	1.1	1.2
AA517193 unc119 homolog (C. elegans)	1.0	1.3	1.2	1.9	1.5	-1.01587+-	1.0	-1.0	1.1	1.0	-1.1
AA691755 RIKEN cDNA 1110068E08 gene	1.2	1.3	1.15501+	1.9	1.3	-1.29545+-	1.3	1.3	1.1	1.0	1.2
AA739464 killer cell lectin-like receptor subfamily A, member 9	1.4	1.2	-1.1	1.9	1.4	-1.0582*	1.1	1.5	1.5	1.3	1.3
AA413026 Public domain EST	-1.0	1.1	-1.4	1.9	1.3	1.32426+-	-1.1	1.4	1.5	1.2	1.4



AA510859 ESTs	1.3	1.3	1.0	1.2	1.2	1.2	-1.0865+-	1.5	1.5	1.4	1.3	1.4	1.3	1.3
AA798385 ESTs	-1.1	1.2	-1.1	1.2	1.2	1.2	-1.03504+-	1.1	1.7	1.3	1.1	1.4	1.4	1.3
AA438040 Public domain EST	-1.1	1.1	-1.1	1.0	1.5	1.5	1.38343-	-1.1	1.2	1.3	1.1	1.1	1.2	1.2
AA474160 ESTs	1.2	1.2	-1.1	1.0	1.8	1.8	1.31659-	1.5	1.4	1.3	1.1	1.5	1.3	1.3
AI614879 ESTs	1.2	1.2	-1.1	1.0	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.1	1.0	1.4
AI450469 ESTs	1.3	1.4	-1.1	1.3	1.3	1.3	-1.2	1.1	1.8	1.1	1.2	1.5	1.4	1.4
AI551472 ESTs	-1.6	1.02324*	-1.0	1.0	1.1	1.1	1.47107+-	-1.65524+-	-1.6	-1.2	-1.1	-1.6	-1.1	-1.1
AI594129 Mus_musculus_clone IMAGE:3494411_mRNA_partial_cds	1.1	1.2	-1.3	1.0	1.1	1.1	-1.16388+-	1.8	1.1	1.1	1.2	1.3	1.3	1.3
AI390609 ESTs	1.3	1.1881*	-1.0	1.0	1.5	1.5	1.06588+-	1.5	1.7	1.3	1.6	1.4	1.4	1.3
AA277192_RIKEN_cDNA_2900075A18_gene	1.0	1.5	-1.5	1.3	1.5	1.5	1.0011+-	1.4	1.3	1.1	1.2	1.6	1.7	1.2
AI604684_RIKEN_cDNA_4631422C13_gene	1.2	1.3	-1.1	1.0	1.3	1.3	1.17508+-	1.5	1.4	1.4	1.1	1.2	1.3	1.3
AI789680 ESTs	1.0429+	1.0	1.2	1.5	1.5	1.5	1.21987+-	1.1	1.2	1.1	-1.0	-1.0	1.2	1.2
AA270832 ESTs	1.3	1.6	-1.3	1.0	1.3	1.3	-1.02764+-	1.2	1.5	1.2	1.1	1.5	1.6	1.6
AA268472_RIKEN_cDNA_2410009C20_gene	1.1	1.3	-1.1	1.0	1.3	1.3	-1.17707+-	1.2	1.2	1.1	1.0	1.3	1.6	1.6
AA438136_nuclear_localization_signal_protein_absent_in_velo-cardio-facial_patients	1.2	1.5	1.2	1.2	1.3	1.3	-1.04778+-	1.3	1.5	1.5	1.3	1.3	1.3	1.3
AI592746 ESTs	-1.0	1.2	-1.1	1.0	1.2	1.2	1.00816+-	1.03689+	1.5	1.3	1.1	1.5	1.7	1.7
AA259871_hypothetical_protein_MNCb-4414	-1.0	-1.0	-1.2	1.0	1.2	1.2	-1.09183+-	1.1	1.5	1.3	1.3	1.2	1.2	1.2
AA710758_Mus_musculus_mRNA_for_b-b-carotene-9',10'-dioxygenase_(b-diox-II_gene)	1.5	1.5	1.0	1.0	1.0	1.0	-1.1	1.4	1.5	1.7	1.5	1.7	1.8	1.8
AI464636 ESTs	1.0	1.2	-1.5	1.0	1.5	1.5	-1.27046+-	1.5	1.1	1.2	1.2	1.39713*	1.1	1.2
AA895221 ESTs	1.1	1.1	1.0	1.0	1.2	1.2	1.32121-	-1.3	1.3	1.4	1.1	1.2	1.2	1.5
AI51957_RIKEN_cDNA_1810056J10_gene	1.3	1.4	-1.2	1.0	1.5	1.5	-1.2	-1.2	1.4	1.3	1.3	1.2	1.2	1.2
AI614440 ESTs_Moderately_similar_to_xylobkinnase_[H.sapiens]	1.5	1.0	1.1	1.1	1.4	1.4	1.2004-	-1.2	1.2	1.4	1.3	1.1	1.0	1.0
AI464729 ESTs	-1.2	1.2	-1.2	1.0	1.4	1.4	-1.14563+-	1.3	1.2	1.2	1.2	1.2	1.2	1.2
AI614454_reduced_in_osteosclerosis_transporter	1.7	-1.1	-1.8	1.0	1.7	1.7	1.11125-	1.3	1.2	1.2	2.2	1.5	1.9	1.9
AA185588 ESTs	1.21114+	1.1	-1.2	1.0	1.2	1.2	-1.11004+-	-1.15286+	1.6	1.1	1.3	1.3	1.2	1.2
AA680434_RIKEN_cDNA_2010305L05_gene	1.4	1.5	-1.2	1.0	1.3	1.3	1.1	1.3	1.4	1.3	1.1	1.4	1.3	1.3
AA615196 ESTs	-1.09609+	1.16002+	-1.07077+	1.0	1.49956+	1.49956+	1.824+-	1.51513+	1.10119+	1.175+	1.0364+	1.0	1.19102+	1.19102+
AA088280_ESTs_Weakly_similar_to_type_III_collagen_[M.musculus]	-1.3	-1.1	1.6	1.0	1.36708*	1.36708*	2.52341-	-1.3	-1.3	-1.0	1.2	-1.4	-1.3	-1.3
AA105069_ESTs	1.1	1.1	-1.2	1.0	1.5	1.5	-1.28705-	1.9	1.4	1.2	1.2	1.1	1.2	1.2
AA104537_c-fos_induced_growth_factor	1.1	1.5	-1.3	1.0	1.5	1.5	-1.3	1.3	1.3	1.5	1.5	1.4	1.6	1.6
AI323038_cathelin-like_protein	-1.8	1.3	-1.1	1.0	1.3	1.3	-1.00202+-	1.5	1.3	1.2	1.2	1.3	1.3	1.3
AI645164_RIKEN_cDNA_2510019N06_gene	1.1	1.5	-1.4	1.0	1.4	1.4	-1.01691+-	1.3	1.4	1.0	1.2	1.1	1.2	1.2
AI326575_glucose-6-phosphatase_catalytic	1.3	-1.6	1.4	1.0	1.4	1.4	-1.3163-	-2.3	-1.2	1.5	1.1	1.2	1.5	1.5
AI593604 ESTs	1.2	1.2	-1.2	1.0	1.5	1.5	-1.14398+-	1.6	1.5	1.2	1.1	1.1	1.1	1.3

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TABLE 2

AA386885 ESTs	1.5	1.2	1.1	1.9	1.4	-1.12144+	1.3	2.00574+	1.90013+	1.8	1.81382+	1.7
AA517175 Mus_musculus_pron_interactor_PINT1_mRNA_partial_cds	1.3	1.5	-1.1	1.9	1.4	-1.3	1.2	1.8	1.4	1.3	1.5	1.5
AA522311 RIKEN_cDNA_0610038P07_gene	1.2	1.7	-1.1	1.9	1.2	-1.08749+	2.0	1.3	1.8	1.4	1.5	1.5
AA330413 RIKEN_cDNA_1700020E22_gene	1.2	-1.4	-1.2	1.8	1.3	1.3	-1.1	-1.0	1.3	-1.2	1.1	-1.0
AA154791 calcitonin_receptor-like	-1.1	-1.3	-1.1	1.9	1.2	-1.12718+	-1.12138+	-1.3	1.1	-1.0	1.1	1.4
AA552958 RIKEN_cDNA_1110003E08_gene	1.0	1.0	-1.1	1.9	1.4	-1.16793~	1.9	1.1	1.1	1.1	1.2	1.2
AA037647 Public domain EST	1.4	1.7	-1.0	1.9	1.3	-1.1	1.1	1.7	1.8	1.4	1.8	1.4
AA68466 ESTs_Weakly_similar_to_T27880_hypothetical_protein_ZK520.1_Caenorhabditis_elegans [C.elegans]	-1.2	1.1	-1.4	1.9	1.6	1.52355+	1.3	1.2	1.3	1.0	1.0	1.3
AA709728 DNA segment, Chr 3, ERATO Dol 330, expressed	1.3	1.4	-1.0	1.9	1.5	1.07517+	1.0	1.8	1.5	1.3	1.5	1.2
AA734324 ESTs	1.25679+	1.3	-1.6	1.9	1.2	-1.06895+	-1.1	1.5	1.4	1.1	1.3	1.4
AA517891 ESTs_Weakly_similar_to_E64778_probable_membrane_protein_ybal_Escherichia_coli [E.coli]	1.1	1.1	-1.2	1.8	1.2	-2.00749~	1.1	1.4	1.2	1.1	1.2	1.5
AA509457 ESTs_Highly_similar_to_KIAA0169_protein [H.sapiens]	-1.3	-1.0	1.1	1.9	1.2	-1.28078+	-1.1	1.3	-1.1	-1.0	-1.0	1.1
AA432613 ESTs_Moderately_similar_to_1615347A_ras_p21_GTPase_activating_protein [M.musculus]	1.2	1.2	-1.4	1.9	1.8	1.4225~	1.7	1.3	1.3	1.1	1.2	1.2
AA079946 keratin associated protein_12-4	-1.1	1.4	-1.2	1.9	1.4	-1.07+	1.0	1.3	1.2	1.2	1.1	1.4
AA245063 ESTs	1.3	1.1	1.1	1.9	1.4	-1.0806+	1.3	1.04052+	1.1	1.1	1.2	1.4
AA386053 ESTs_Moderately_similar_to_CYP2C40 [M.musculus]	1.4	1.4	1.2	1.9	1.2	-1.0	1.2	1.4	1.5	1.2	1.7	1.5
AA154770 kinesin family member C2	1.4	1.1	-1.0	1.9	1.2	-1.07647+	1.8	1.2	1.4	1.3	1.3	1.3
AA020415 placental specific protein 1	1.2	1.06017+	-1.2	1.9	1.2	-1.16409+	-1.1	1.09682+	1.2	1.0	-1.4	1.3
AA414213 upstream binding protein 1	1.1	-1.5	-1.3	-1.9	-1.3	-1.0	-1.3	-1.3	-1.4	-1.3	-1.3	-1.2
AA414750 abi-interactor 1	-1.1	-1.2	-1.3	-1.9	-1.4	-1.1	1.2	-1.1	-1.2	-1.1	-1.1	-1.1
AA763355 small EDRK-rich factor 2	1.5	1.3	1.3	-1.9	1.8	1.2	-1.2	-1.2	1.0	1.2	-1.2	-1.2
AA413884 RIKEN_cDNA_1300014E15_gene	1.0	-1.1	1.8	-1.9	-1.4	1.25078+	-1.3	-1.1	-1.1	-1.1	1.1	1.2
AA414286 RIKEN_cDNA_1700016K02_gene	-1.0	-1.24129+	-1.7	-1.9	-1.1	1.0257+	-1.16076+	-1.62152+	-1.1	-1.2	-1.2	-1.3
AA606943 glutathione peroxidase 4	1.0	1.3	1.1	-1.9	1.8	1.4	-1.0	-1.7	-1.1	1.0	-1.3	-1.3
AA268171 protein phosphatase 2 (formerly 2A), regulatory subunit_A (PR 65), alpha isoform	1.0	-1.1	-1.0	-1.9	1.3	-1.1	1.1	1.1	1.1	1.2	-1.1	-1.1
AA759679 Ia-associated invariant chain	-1.0	-1.8	-1.6	-1.9	1.5	-3.7	-2.8	-1.0	-1.9	-1.0	-1.3	-1.4
W83121 legumain	1.2	-1.5	1.1	-1.9	-1.0	-1.7	-1.0	-1.3	-1.1	1.2	-1.3	-1.1
AA594339 nuclear factor I/C	-1.3	-1.2	-1.2	-1.9	1.0	1.1	-1.2	-1.0	-1.3	-1.2	-1.2	-1.4
AA116994 promyelocytic leukemia	-1.5	-1.1	-1.1	-1.9	-1.1	-1.6	-1.3	-1.2	-1.3	-1.3	-1.2	-1.1
AA671029 FK506 binding protein 4 (59 kDa)	-1.1	1.2	1.0	-1.9	-1.4	-1.4	-1.7	-1.0	-1.1	-1.1	-1.4	-1.2
AA415514 microtubule-associated protein, RPIEB family, member 1	1.0	-1.3	-1.1	-1.9	-1.2	-1.4	1.3	1.0	1.1	-1.1	1.0	-1.1
AA036489 cyclin G	-1.2	1.0	1.3	-1.9	-1.8	-2.26973~	1.2	-1.4	-1.4	-2.0	-1.0	-1.1
AA048040 claudin 4	-1.6	1.5	-2.1	-1.9	1.7	-2.7	1.5	-1.1	-1.2	-1.3	-1.2	-1.2

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TABLE 2

AA791819 annexin A5	1.3	-1.4	1.1	-1.9	-1.0	-1.0	1.0	1.2	1.1	-1.1	1.0	-1.1	-1.1
AA465997 RIKEN cDNA 2010103A03 gene	1.2	1.2	1.1	-1.9	-1.2	-1.5	1.1	1.2	1.0	-1.2	1.0	-1.2	-1.04125*
AA900349 glutathione peroxidase 2, pseudogene_1	-1.3	-1.0	1.2	-1.9	1.1	-2.4	-2.5	-1.5	1.1	-1.1	-1.5	1.5	1.5
AA415520 RIKEN cDNA 1810003N24 gene	1.2	1.2	-1.1	-1.9	-1.1	-1.42227+	1.3	1.1	1.3	1.2	1.0	-1.2	-1.0
AI120979 RIKEN cDNA 2410039E09 gene	1.2	1.3	1.1	-1.9	-1.6	-1.3	1.0	-1.3	1.0	-1.2	-1.5	-1.2	-1.2
AA106736 cytochrome c oxidase subunit VIIa 3	1.1	-1.0	1.5	-1.9	-1.2	-1.1	1.0	-1.3	1.0	1.0	-1.2	-1.1	-1.1
AA414844 emerlin	1.3	1.4	-1.0	-1.9	1.1	-1.0	-1.1	-1.1	-1.0	1.1	-1.1	-1.1	-1.2
AA716807 synaptophysin	-1.6	-1.3	-1.5	-1.9	-1.3	-1.3	1.4	-1.7	-1.5	-1.3	-1.2	-1.4	-1.4
AA154947 ESTs	-1.3	-1.5	-1.1	-1.9	-1.1	-1.0	-1.1	-1.1	-1.2	-1.1	-1.2	-1.3	-1.3
W15971 FK506 binding protein 2 (13 kDa)	-1.0	-1.0	-1.1	-1.9	-1.2	-1.4	-1.2	-1.4	-1.3	-1.0	-1.3	-1.3	-1.1
AA051479 Public domain EST	-1.2	-1.6	-1.1	-1.9	-1.6	-1.1	-1.1	-1.1	-1.3	-1.2	-1.3	-1.2	-1.2
AA008426 adaptor-related protein complex AP-3, sigma 2 subunit	-1.5	-1.3	-1.3	-1.9	-1.1	-1.2	-1.0	-1.1	-1.2	-1.1	-1.2	-1.1	-1.2
W34862 glutathione S-transferase, mu 6	1.2	1.1	1.5	-1.9	1.3	1.2	1.2	-1.1	1.1	1.3	-1.0	1.0	1.0
AI322387 insulin-like growth factor 2	-1.2	-1.8	-1.4	-1.9	-1.5	1.4	-1.5	-2.6	-1.2	-1.6	-1.2	-1.8	-1.8
AA727960 keratin complex 1, acidic, gene 18	1.0	1.5	-1.2	-1.9	-1.1	1.0	-1.7	-1.0	1.1	-1.2	-1.2	1.0	1.0
AI892334 ribosomal protein L5	1.3	1.4	1.1	-1.9	-1.2	1.1	1.2	1.1	1.3	-1.2	-1.1	-1.0	-1.0
AA529377 heat shock protein, 86 kDa 1	1.4	1.0	-1.3	-1.9	-1.9	-1.5	1.4	1.3	1.2	-1.0	-1.0	1.3	1.3
AA871749 ESTs, Weakly similar to I49759 Hrs - mouse [M.musculus]	-1.5	-1.2	-1.4	-1.9	-1.1	-1.4	1.3	-1.4	-1.4	-1.5	-1.1	-1.0	-1.0
AI645415 mini chromosome maintenance deficient (S. cerevisiae)	-1.3	-1.5	-1.3	-1.9	-1.4	-1.2	-1.8	-1.4	-1.2	-1.2	-1.3	-1.3	-1.3
AA415905 nucleolar and coiled-body phosphoprotein 1	1.1	1.4	1.3	-1.9	1.2	-1.0	-1.4	-1.0	-1.0	1.1	-1.1	-1.2	-1.2
AI428588 RIKEN cDNA 3110039B05 gene	-1.3	-1.5	-1.2	-1.9	-1.2	1.4	1.0	-1.3	-1.4	-1.1	-1.4	-1.4	-1.4
AA067069 histocompatibility 2, T region locus 9	1.2	-1.2	1.8	-1.9	1.4	-1.3	1.1	-1.1	-1.1	1.1	-1.0	-1.2	-1.2
AA674445 lectin, galactose binding, soluble 9	1.0	-1.0	1.5	-1.9	-1.2	-1.7	-1.4	-1.0	1.3	-1.2	-1.0	-1.0	-1.0
AA003005 CD151 antigen	-1.4	-1.5	-1.3	-1.9	-1.1	-1.3	-1.2	-1.2	-1.4	-1.1	-1.2	-1.3	-1.3
AI181662 RIKEN cDNA 3021401A05 gene	-1.2	-1.3	-1.3	-1.9	-1.4	-1.5	1.1	-1.1	-1.2	-1.4	-1.0	-1.0	-1.0
AI892472 RIKEN cDNA 0610011D08 gene	-1.1	1.1	1.2	-1.9	-1.6	-1.2	-1.5	-1.2	1.1	-1.2	-1.1	-1.1	-1.1
AI385457 retinol binding protein 2, cellular	-2.0	-2.1	-1.6	-1.9	1.5	1.9	-1.3	-1.9	-1.6	-1.9	-1.5	-1.7	-1.7
AI049439 torsin family 3, member A	-1.1	-1.2	-1.3	-1.9	-1.2	-2.24409+	-1.0	1.1	-1.3	-1.3	-1.1	-1.1	-1.1
AI000000 guanine nucleotide-binding protein, alpha 2, epsilon	-1.0	2.0	1.1	-1.9	1.1	-1.2	1.2	1.0	1.1	1.4	1.0	-1.0	-1.0
AA549280 Public domain EST	1.4	1.2	-1.0	-1.9	-1.56322+	-1.27908+	1.5	-1.1	1.0	-1.1	1.1	1.1	1.1
AA097896 0-6-methylguanine-DNA methyltransferase	-1.2	1.2	-1.6	-1.9	1.3	-2.3	1.0	-1.1	-1.1	-1.2	-1.1	-1.1	-1.1
AA824095 RIKEN cDNA 2610205H19 gene	-1.0	-1.2	1.3	-1.9	-1.3	1.2	-1.7	-1.9	-1.1	1.0	-1.4	-1.4	-1.4
AA619950 cyclin I	-1.1	-1.2	1.1	-1.9	-1.1	-1.1	1.5	-1.4	-1.3	1.1	-1.1	1.1	1.1
AA250057 proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7)	1.1	-1.5	1.1	-1.9	1.0	-3.6	-1.5	-1.2	-1.1	1.2	-1.0	-1.2	-1.2

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TABLE 2

AA030661 kinesin light chain 2	-1.3	-1.4	-1.4	-1.9	-1.1	-1.4	1.2	-1.4	-1.4	-1.2	-1.2	-1.2
AI536281 lorictn	1.2	-1.1	-1.3	-1.9	1.3	2.2332	-1.2	1.3	1.0	1.1	1.2	1.4
W10007 mast cell protease 6	-1.2	-1.4	-1.3	-1.9	-1.2	-1.2	-1.4	-1.2	-1.3	-1.4	-1.4	-1.4
AA469667 tumor rejection antigen gp96	1.3	1.4	-1.5	-1.9	-2.0	-1.4	1.2	-1.1	1.2	-1.1	1.1	-1.0
AA664319 protein tyrosine phosphatase 4a1	1.2	1.1	1.2	-2.0	-1.6	-1.2	1.3	1.1	1.0	-1.0	1.1	-1.1
AI553118 ESTs	-1.8	-1.2	-1.4	-2.0	1.1	-1.3	-1.1	-1.3	-1.5	-1.3	-1.2	1.0
AA500739 potassium channel, subfamily K, member 2	-1.1	-1.0	1.1	-2.0	-1.7	-1.24216~	1.4	-1.0	-1.0	-1.3	-1.0	-1.2
AA600581 ribosomal protein L44	1.3	1.4	1.3	-2.0	-1.7	-1.2	1.2	-1.4	-1.0	-1.2	-1.4	-1.0
AA684403 ESTs	-1.4	1.7	-2.3	-2.0	2.0	-2.4	1.5	-1.0	-1.3	-1.3	-1.1	-1.1
AA690387 inactive X specific transcripts	1.3	-1.04286+	1.3	-2.0	-1.3	1.15376+	-1.33094+	-1.2	-1.5	1.2	-1.3	-1.2
AA261440 lupus nephritis-associated peptide 1	1.2	1.0	1.7	-2.0	-1.4	-1.1	1.1	-1.6	-1.0	1.1	-1.0	-1.2
W08321 inhibitor of DNA binding 1	1.1	-1.1	1.1	-2.0	-1.1	-2.7	-1.6	-1.1	-1.0	1.0	-1.0	1.2
AA166386 transducer of ErbB-2.1	-1.0	-1.2	1.3	-2.0	-1.9	-1.1	1.1	-1.2	-1.1	-1.0	-1.2	1.2
AA437783 aplasia ras-related homolog B (RhoB)	-1.2	-1.6	-1.2	-2.0	-1.0	-1.5	-1.0	-1.2	-1.1	-1.4	-1.3	-1.2
AA067003 glutathione S-transferase, mu 1	1.1	1.2	1.0	-2.0	1.5	1.2	1.4	1.0	1.2	1.4	-1.3	-1.2
AA066634 lactate dehydrogenase 2, B chain	1.2	1.2	1.33999*	-2.0	-1.3	1.4	1.3	1.0	1.3	1.6	1.2	-1.1
AA606826 actin, gamma, cytoplasmic	1.1	-1.2	-1.1	-2.0	-1.0	-1.4	1.4	1.1	1.1	1.2	1.0	-1.0
AI121405 H2O-like homeo box gene	-1.7	-1.6	-1.2	-2.0	-1.1	-1.6	-1.2	-1.2	-1.5	-1.3	-1.3	-1.3
AA437457 methionine aminopeptidase	1.3	-1.0	1.2	-2.0	-1.1	-1.1	-1.4	-1.0	1.0	-1.0	-1.0	-1.1
W17766 spinocerebellar ataxia 10 homolog (human)	1.0	-1.1	-1.1	-2.0	-1.4	-1.3	1.2	1.0	1.0	1.0	-1.0	-1.2
AA619894 diazepam binding inhibitor	1.2	-1.1	1.1	-2.0	-1.0	-1.1	1.2	-1.7	-1.0	-1.1	-1.2	-1.0
AA185212 ESTs	-1.2	-1.3	-1.1	-2.0	-1.1	-1.3	-1.2	-1.2	-1.2	1.1	-1.2	-1.3
AI893237 RIKEN cDNA 0610009D10 gene	1.2	1.2	1.4	-2.0	-1.0	-1.3	1.4	-1.3	-1.0	-1.1	-1.2	-1.1
AA674592 ESTs	-1.7	-1.3	-1.4	-2.0	-1.1	-1.31126~	1.1	-1.6	-1.6	-1.7	-1.4	-1.6
AA420091 ESTs	-1.6	-1.7	-1.4	-2.0	-1.4	-1.4	-1.2	-1.4	-1.4	-1.4	-1.2	-1.2
AA874467 RIKEN cDNA 1110035G07 gene	-1.4	-1.4	-1.5	-2.0	-1.1	-1.3	1.1	-1.3	-1.5	-1.3	-1.1	-1.2
AA982254 RIKEN cDNA 2210010C04 gene	2.3	1.3	-1.3	-2.0	-9.5	-1.3	1.6	-1.5	-2.0	-1.4	-1.1	-1.1
AI552745 Mus musculus, clone MGC:6883, mRNA, complete cds	1.1	1.1	1.1	-2.0	-2.0	1.1	-1.2	-1.5	-1.2	-1.4	-1.3	-1.1
AA734030 opibid receptor, sigma 1	-1.6	-1.6	-1.1	-2.0	-1.1	-1.1	-1.2	-1.5	-1.4	-1.3	-1.4	-1.4
AA920158 max binding protein	-1.6	-1.2	1.06539*	-2.0	-1.2	1.3	-1.1	-1.1	-1.4	-1.1	-1.1	1.0
AA174675 ESTs	-1.8	-1.5	-1.4	-2.0	-1.3	-1.2	-1.1	-1.3	-1.6	-1.5	-1.5	-1.6
AA589092 ESTs	-1.8	-1.4	-1.2	-2.0	-1.1	-1.3	-1.3	-1.4	-1.4	-1.6	-1.3	1.1
W13098 natriuretic peptide receptor 1	-1.8	-1.6	-1.6	-2.0	-1.2	-1.4	-1.1	-1.1	-1.5	-1.3	-1.2	-1.3
AA210481 clusterin	1.1	3.0	1.2	-2.0	-1.8	-1.4	1.3	-1.1	1.1	1.4	-1.2	1.2

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TABLE 2

AA082452	ESTs, Moderately similar to C211 HUMAN PUTATIVE_SURF	1.1	1.1	1.3	-2.0	-1.1	1.1	1.3	-1.2	-1.2	1.4	-1.1	1.1
ACE	GLYCOPROTEIN C21ORF1 PRECURSOR [H.sapiens]	-1.4	-10.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1
A190138	RIKEN cDNA 3930401B19 gene	1.0	1.1693+	1.4	-2.0	-1.2	-1.16472+	1.31017+	-1.3034+	1.1	-1.3	-1.0	1.2
AA437424	Public domain EST	1.2	1.2	1.2	-2.0	1.1	-1.3	1.1	-1.1	1.0	1.1	-1.2	-1.0
W36498	amelogenin	-1.6	-1.5	-1.5	-2.0	-1.1	-1.36728-	-1.0	-1.3	-1.3	-1.5	-1.3	-1.4
A1930970	RIKEN cDNA 2310020F24 gene	-1.2	-1.2	1.4	-2.0	-1.1	1.0	-1.3	-1.7	-1.1	1.1	-1.2	-1.2
AA437633	RIKEN cDNA 2210401F17 gene	-1.3	1.4	1.1	-2.0	1.1	-1.08813-	-1.4	1.0	-1.2	-1.2	-1.1	-1.1
AA711419	POU domain, class 2, transcription factor 1	1.0334+	-1.48994+	-1.39873+	-2.0	-1.18242+	1.10979+	-1.06713+	1.1	-1.1	-1.1	1.1	-1.8
AA138836	myxovirus (influenza virus) resistance 1	-1.4	-1.3	-1.2	-2.0	-1.3	-1.2	-1.0	-1.1	-1.3	-1.2	-1.2	-1.2
AA422762	ESTs	1.5	1.1	1.3	-2.0	-1.5	1.0	1.2	-1.1	1.1	1.0	-1.2	-1.0
AA822609	ribosomal protein L27a	1.2	1.4	1.1	-2.0	1.1	1.00729+	-1.1	-1.2	-1.1	1.0	-1.3	-1.0
AA606665	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MUSV) ubiquitously expressed (fox derived)	-1.6	-1.5	-1.2	-2.0	-1.2	-1.0	-1.1	-1.1	-1.4	-1.3	-1.3	-1.2
AA469551	RIKEN cDNA 9130022E05 gene	1.3	1.0	1.2	-2.0	-1.8	-1.2	-1.1	-1.2	-1.2	-1.1	-1.1	-1.1
AA624488	prothymosin alpha	-1.4	-1.4	-1.2	-2.0	-1.4	-1.3	-1.1	-1.2	-1.4	-1.6	-1.1	-1.1
AA771675	run1 related transcription factor 2	1.2	-1.3	1.0	-2.0	1.2	-1.1	-3.5	-1.5	1.1	-1.1	-1.3	-1.4
W18330	tropomyosin 2, beta	1.1	1.4	-1.1	-2.0	1.5	-1.1	1.3	1.2	1.1	-1.0	-1.0	-1.2
A1606650	calmodulin	-1.1	1.8	-1.2	-2.0	-82.1	-1.8977-	-1.4	1.0	-1.4	-1.9	-1.0	1.4
A1894032	trefoil factor 2 (spasmolytic protein 1)	1.1	1.1	1.7	-2.0	1.3	-1.1	1.0	-1.1	1.2	1.2	-1.1	-1.0
AA106338	Public domain EST	-1.4	1.0	-1.2	-2.0	1.0	-1.29793+	-1.0	-1.3	-1.3	-1.2	-1.3	1.0
A1047049	ESTs	1.3	1.2	1.4	-2.0	-1.8	-1.2	1.1	-1.0	1.1	-1.1	1.0	-1.0
AA414427	RIKEN cDNA 9430015P09 gene	-1.3	1.02041+	-1.1	-2.0	-1.1	-1.20227+	1.05224+	1.08166+	-1.0	1.0	1.2	1.4
AA175784	ESTs	1.2	1.4	1.1	-2.0	-1.3	-1.4	-1.3	-1.4	1.0	-1.1	-1.2	1.0
AA414116	signal recognition particle 9 kDa	-1.4	-1.9	-1.3	-2.1	1.0	-1.1	-1.2	-1.2	-1.4	-1.0	-1.1	-1.2
AA008228	peroxisomal farnesylated protein	1.3	1.7	1.2	-2.1	1.1	-1.3	1.6	-1.1	1.2	1.3	-1.0	-1.0
AA444231	ribosomal protein S5	-1.7	-1.6	-1.3	-2.1	-1.1	-1.1	-1.0	-1.4	-1.2	-1.1	-1.3	-1.2
AA199056	Public domain EST	1.2	1.2	1.1	-2.1	1.1	-1.6	-1.0	1.1	1.1	1.0	-1.0	-1.0
AA819820	EST AA538654	1.1	-1.2	-1.0	-2.1	-1.2	1.1	1.1	1.0	1.1	1.1	-1.0	1.1
AA471862	myosin VI	-1.3	-1.7	-1.4	-2.1	-2.9	-1.3	-1.6	-1.1	-1.3	-1.1	-1.1	-1.0
A1596352	G protein-coupled receptor, family C, group 5, member B	-1.5	-1.4	-1.6	-2.1	1.20761*	-1.4	1.0	-1.5	-1.4	-1.4	-1.3	-1.2
A1604885	ubiquitin-like (sentrin) activating enzyme E1A	-1.2	-1.3	-1.2	-2.1	1.0	1.2	-1.0	-1.0	-1.1	1.1	-1.2	-1.3
W14484	Public domain EST	1.0	1.4	1.3	-2.1	1.1	-1.0	1.1	-1.3	1.0	1.1	-1.4	-1.0
AA065602	ribosomal protein L8	1.2	-1.1	1.5	-2.1	-1.2	-1.58973-	-1.5	-1.6	1.0	1.2	-1.2	1.1
AA595514	interferon gamma induced GTPase	1.6	1.1	1.2	-2.1	2.0	-1.8	-1.0	-1.1	-1.0	1.3	-1.1	-1.2
A1594147	beta-2 microglobulin	1.1	-1.3	1.5	-2.1	-1.1	1.0	1.1	-1.0	-1.3	1.2	-1.6	-1.5
A1326556	FMS-like tyrosine kinase 1	1.1	-1.3	1.5	-2.1	-1.1	1.0	1.1	-1.0	-1.3	1.2	-1.6	-1.5

TABLE 2

AI536309	RIKEN cDNA 2210410L06 gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5	-2.1
AA067797	heat shock protein cognate 70	1.0	-1.1	-1.0	-2.1	-2.1	-1.5	-1.1	1.3	1.5	1.3	1.0	1.2
V57231	protein kinase C and casein kinase substrate in neurons 2	-1.4	-1.2	-1.3	-2.1	1.2	-1.4	-1.6	-1.1	-1.3	-1.2	-1.3	-1.2
AI692534	ribosomal protein S24	1.3	1.1	1.3	-2.1	-2.0	-1.1	1.3	-1.2	1.2	-1.4	-1.1	-1.2
AA798766	selectin, lymphocyte	-1.7	-1.5	-1.2	-2.1	-1.0	-1.2	1.0	-1.5	-1.6	-1.5	-1.5	-1.4
AI182180	three prime repair exonuclease 1	-1.4	-1.1	1.1	-2.1	1.0	-1.24935+~	-1.4	1.2	-1.0	1.0	-1.0	-1.1
AA107101	prostate stem cell antigen	-1.1	-1.4	-1.3	-2.1	-6.1	1.51614~	-1.8	-2.1	-1.0	-1.1	-1.4	-1.4
AA437941	glutathione S-transferase, pi 2	1.1	1.5	1.2	-2.1	1.5	1.4	1.1	-1.6	1.1	1.1	-1.5	-1.2
AA276406	microsomal triglyceride transfer protein	-1.7	-1.4	-1.4	-2.1	1.0	1.2	1.0	-1.6	-1.3	-1.3	-1.4	-1.3
AA467239	RIKEN cDNA 1700008C22 gene	-1.4	-1.6	-1.5	-2.1	-1.2	-1.2	1.0	-1.5	-1.4	-1.1	-1.4	-1.3
AA065942	ATP synthase_H+transporting_mitochondrial_F0_complex_subunit c (subunit 9), isoform 1	-1.4	-1.6	-1.5	-2.1	-1.2	-1.2	-1.3	-1.4	-1.0	1.1	-1.2	-1.1
W12636	proteaseome (prosome, macropain) 28 subunit, 3	1.1	-1.3	-1.3	-2.1	1.1	-1.1	-1.0	-1.1	-1.1	1.0	-1.1	-1.3
AA212150	eukaryotic translation elongation factor 1 alpha 1	1.1	1.0	1.1	-2.1	-1.2	-1.2	1.2	1.1	1.2	1.2	-1.1	1.1
AI692747	glutathione S-transferase, alpha 1 (Ya)	-1.1	-1.3	-1.7	-2.1	-1.7	2.0	-1.2	-1.1	1.4	1.8	-1.1	1.1
AA667301	troponin I, cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.41297~	-2.0	-2.0	-2.2	3.55728+~	-1.0	1.3
AA072834	RIKEN cDNA 9030418M05 gene	1.1	1.2	-1.1	-2.1	1.13744*	-3.3	-1.1	1.1	-1.1	1.1	1.1	1.3
AA422639	ESTs	-1.6	-1.7	-1.4	-2.1	-1.3	-1.3	-1.2	-1.2	-1.5	-1.2	-1.3	-1.2
AI549639	RIKEN cDNA 2610301D06 gene	-1.1	1.6	1.2	-2.1	-1.1	-1.1	1.3	-1.1	1.0	1.1	-1.2	1.1
AA675111	RIKEN cDNA 1810007A24 gene	1.4	1.3	-1.0	-2.1	-1.4	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AI323199	tumor necrosis factor receptor superfamily, member 4	-1.3	1.2	1.1	-2.1	-1.2	-1.14522+~	1.1	-1.1	-1.2	-1.1	-1.3	-1.3
AA727065	ESTs	1.1	-1.2	1.2	-2.1	-2.5	1.2	-1.2	-1.6	-1.2	-1.4	-1.4	-1.3
AI536343	Public domain EST	-1.1	-1.1	-1.0	-2.1	1.2	1.0	1.8	1.4	1.1	1.1	1.7	1.4
AA066534	esterase 10	1.1	1.0	1.2	-2.1	1.0	1.1	1.1	-1.1	1.4	-1.2	-1.0	-1.2
AA674987	RIKEN cDNA 1110039G14 gene	-1.1	1.3	-1.1	-2.1	1.2	1.5	-1.3	-2.1	-1.4	-1.4	-1.8	-1.2
AA210505	Public domain EST	1.4	-1.5	1.2	-2.1	-2.7	-1.7	-1.1	1.1	1.3	1.1	1.1	1.2
AA123007	2'-5' oligoadenylate synthetase-like	1.1	-1.4	-1.3	-2.2	-1.1	-2.2	-1.1	1.3	-1.1	-1.1	-1.1	-1.1
AA607044	RIKEN cDNA 2700099C19 gene	-1.4	-1.3	-1.5	-2.2	-1.0	-1.4	-1.1	-1.4	-1.4	-1.3	-1.3	-1.9
AA047991	RIKEN cDNA 2700049I22 gene	-1.1	1.3	-1.1	-2.2	-1.0	-1.0	-1.3	-1.4	-1.4	-1.3	-1.4	-1.2
W11185	ribosomal protein S15	-1.1	1.1	-1.2	-2.2	-1.0	-1.2	1.2	-1.3	-1.3	-1.1	-1.2	-1.2
AI789568	potassium voltage-gated channel, subfamily Q, member 1	1.21639+	1.3	-1.42732+	-2.2	1.0	1.08585+~	-1.33325+	1.31433+	1.09021+	1.1	-1.01845+	-1.5
AA437994	hepatocellular carcinoma repeat-containing 4	-1.6	-1.5	-1.5	-2.2	-1.2	-1.39447~	1.2	-1.1	-1.7	-1.6	-1.3	-1.3
AA616180	RIKEN cDNA 2010004B12 gene	-1.2	1.2	1.2	-2.2	-1.4	-1.14572+~	1.1	-1.3	-1.3	-1.3	-1.1	-1.0
W16358	mucin 1, transmembrane	1.5	1.4	-1.2	-2.2	-1.3	-1.1	-2.0	1.0	1.1	1.1	-1.2	1.0
AA546625	ESTs_Weakly similar to SP62 MOUSE SPICEOSOME_ASS	-1.9	-1.6	-1.4	-2.2	-1.2	-1.4	1.2	-1.2	-1.7	-1.7	-1.4	-1.6

TABLE 2

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AA066685 villin 2	-1.0	-1.3	1.3	2.2	1.3	1.2	-1.2	-1.1	-1.2	1.1	-1.1	-1.0
AA674784 Mus musculus mosg protein (Mosg) gene, complete cds	-1.6	-1.9	-1.9	-2.2	-1.0	-1.1	-1.2	-1.4	-1.6	-1.6	-1.6	-1.6
AA450922 heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	1.1	1.6	-2.4	-2.2	-2.4	-1.6	1.0	-1.3	1.2	-1.1	-1.1	-1.2
AA060105 trefol factor 1	-1.5	-1.4	1.3	-2.2	-43.1146*	-1.06659~	1.0	-1.2	-1.6	1.0	-1.0	-1.5
W29311 peptidylprolyl isomerase C-associated protein	1.1	-1.0	1.6	-2.2	-1.2	-1.4	1.1	-1.0	1.3	1.1	-1.1	-1.1
W53728 carbonyl reductase 1	-1.1	1.2	1.1	-2.2	1.1	1.1	-1.2	-1.5	-1.1	1.4	-1.2	-1.2
AA066404 topoisomerase (DNA) II beta	1.1	-1.2	1.2	-2.2	-2.2	1.0	-1.2	-1.5	-1.2	-1.5	-1.3	-1.2
AA879946 RIKEN cDNA 1110015M06 gene	-1.8	-1.2	-1.3	-2.2	-1.2	-1.3	1.3	-1.6	-1.5	-1.2	-1.3	-1.3
AA667785 potassium_voltage-gated_channel_1sk-related_subfamily_member_1	-1.8	-1.9	-1.3	-2.2	-1.2	-1.0	-1.3	-1.4	-1.5	-1.2	-1.4	-1.5
AA437577 ESTs	-1.9	-1.8	-1.5	-2.2	-1.2	-1.47043~	-1.53147+	-1.5	-1.8	-1.5	-1.4	-1.5
AA260966 ATP synthase_H+_transporting_mitochondrial_F0_complex_subunit_g	1.1	-1.0	1.6	-2.2	-1.4	-1.2	-1.2	-1.7	-1.1	-1.3	-1.2	-1.3
AI551662 fcs-like antigen 2	-2.1	-2.0	-1.4	-2.2	-1.2	-1.1	-1.3	-1.4	-1.4	-1.4	-1.4	-1.5
AA066282 small inducible cytokine subfamily B (Cys-X-Cys)_member_14	-1.5	-1.7	-1.4	-2.3	-1.1	-1.0	-1.1	-1.4	-1.4	-1.5	-1.3	-1.2
AA426902 ESTs	-1.9	-1.3	-1.4	-2.3	1.0	-1.4	-1.1	-1.3	-1.6	-1.5	-1.3	-1.4
AA106618 RIKEN cDNA 0610007P06 gene	-1.0	1.1	1.4	-2.3	-1.3	1.21425~	-1.2	-1.1	1.2	1.1	-1.1	-1.0
W62007 neuron specific gene family member 2	-1.5	-1.5	-1.9	-2.3	-1.3	-1.0	1.4	-2.0	-1.6	-1.4	-1.3	-1.5
AA051655 somatostatin	1.0	1.0	-1.2	-2.3	1.2	-1.0	-1.3	-1.0	1.1	1.0	1.3	1.6
AI020170 semaphorin domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-1.4	-1.5	-1.6	-2.3	-1.1	-1.2	-1.2	-1.6	-1.5	-1.1	-1.2	-1.0
AA770808 pericentriolar material 1	-1.9	-2.1	-1.6	-2.3	-1.1	-1.2	-1.0	-1.5	-1.6	-1.5	-1.6	-1.6
AA062283 cytochrome c oxidase, subunit Va	1.1	1.0	1.3	-2.3	-1.2	-1.0	-1.2	-1.1	1.1	1.0	-1.1	-1.0
W36524 schlafen 2	-1.4	-1.3	-1.3	-2.3	-1.4	-1.4	-1.2	-1.1	-1.3	-1.5	-1.1	-1.1
AA106154 RIKEN cDNA 1300003O09 gene	-1.2	-1.2	1.5	-2.3	-1.3	1.2	1.1	-1.4	-1.1	1.1	-1.1	1.1
AI606037 Kruppel-like factor 2 (lung)	-1.3	-1.4	-1.4	-2.3	-1.1	-1.5	-1.1	1.1	-1.4	-1.4	-1.2	-1.2
AA049653 RAD51 like 3 (S. cerevisiae)	-1.7	-1.5	-1.5	-2.3	-1.1	-1.5	-1.3	-1.3	-1.5	-1.2	-1.3	-1.3
AA170469 interferon-induced protein with tetratricopeptide repeats 1	-1.1	-1.2	-1.1	-2.3	-1.6	-1.20626~	-1.4	1.0	-1.1	-1.2	1.1	-1.1
W12965 annexin A10	1.5	-1.7	-1.1	-2.3	-8.5	-1.03567~	-1.3	-1.1	1.1	-1.0	1.0	-1.9
AA413907 ATP synthase_H+_transporting_mitochondrial_F1F0_complex_subunit e	1.4	1.1	1.8	-2.3	-1.4	-1.0	1.0	-1.7	-1.1	1.1	-1.2	-1.4
AA014095 gene rich cluster, C9 gene	-1.7	-1.4	-1.5	-2.3	-1.1	-1.3	1.1	-1.5	-1.5	-1.2	-1.4	-1.3
AI876997 carboxyl ester lipase	1.5	1.6	-1.4	-2.3	-8.9	-1.6	-1.3	-1.4	-1.1	1.1	2.0	2.2
AA444672 RIKEN cDNA 2510001A17 gene	-1.1	-1.0	1.1	-2.3	-2.0	-1.1	1.3	-1.1	1.2	-1.4	1.0	-1.2
AA049003 heterogeneous nuclear ribonucleoprotein D	1.0	-1.6	-1.6	-2.3	-1.1	-1.2	-1.2	-1.3	-1.3	-1.2	-1.3	-1.5
AI325332 transglutaminase 3, E polypeptide	-2.0	-2.0	-1.4	-2.3	-1.2	-1.3	-1.2	-1.2	-1.7	-1.4	-1.5	-1.7
AA105866 glutathione S-transferase, alpha 4	1.1	1.0	1.8	-2.4	-3.0	1.3	1.2	1.0	1.3	1.3	-1.1	-1.2

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TABLE 2

AA922098 apolipoprotein A-I	-1.9	-1.5	1.1	-2.4	-2.4	-1.9	-2.1	-2.5	-1.6
AA619848 RIKEN cDNA 4430402G14 gene	1.5	-1.3	-1.1	-2.4	-1.1	-1.1	-1.1	1.0	-1.1
AA616014 ESTs	-1.8	-1.6	-1.4	-2.4	-1.2	-1.5	-1.4	-1.5	-1.3
AF593751 ESTs, Highly similar to AF091457_1 zinc finger protein_RIN_Z F [R. norvegicus]	1.5	-1.2	-1.0	-2.4	1.0	-1.0	-1.1	1.0	-1.1
AA718476 RIKEN cDNA 0610025G13 gene	1.2	1.6	1.3	-2.5	1.1	-1.1	1.1	1.2	-1.2
AA770709 aldehyde dehydrogenase family 3, subfamily A1	-1.1	1.1	-1.2	-2.4	1.3	-1.6108~	1.5	-1.0	1.1
AA437620 RIKEN cDNA 1810030E05 gene	-1.4	-1.6	-1.4	-2.5	-1.2	-1.0	-1.1	-1.3	-1.2
AA727627 ankyrin 1, erythroid	-1.8	-2.1	-1.6	-2.5	-1.3	-1.2	-1.4	-1.6	-1.7
AA451862 RIKEN cDNA 0910001A18 gene	1.8	1.3	-1.1	-2.5	-1.47	-2.6	1.2	-1.3	-1.3
W15806 dynein, axon, heavy chain 11	1.3	-1.3	-1.1	-2.5	-2.1	-1.8	-1.1	1.0	-1.1
AA437871 eukaryotic translation initiation factor 4, gamma 2	1.1	1.0	1.4	-2.5	-1.7	-1.0	1.2	-1.0	1.1
AI893971 zinc finger protein 57	-1.8	-1.8	-1.4	-2.5	-1.2	-1.2	-1.3	-1.5	-1.4
AI594148 ribosomal protein S19	1.2	1.1	1.2	-2.5	-1.4	-1.0	1.1	-1.4	-1.1
AA048952 solute carrier family 4 (anion exchanger), member 2	-1.0	1.1	1.1	-2.5	-1.1	-1.5	-1.4	-1.0	-1.0
AI117832 thymidylate kinase family LPS-inducible member	1.2	-1.10107+	-1.1	-2.5	1.3	-1.3814+~	1.4	1.1	1.1
AA444254 ornithine decarboxylase, structural	1.1	-1.3	-1.4	-2.5	-1.6	-1.2	-1.1	-1.8	-1.1
AI122517 interferon regulatory factor 7	1.3	-1.3	-1.1	-2.6	1.2	-1.86988~	-1.2	-1.0	-1.1
AI322733 2'-5' oligoadenylate synthetase 1A	1.1	1.2	-1.1	-2.6	1.1	-2.1	-1.1	1.0	-1.2
AA062440 quaking	1.3	1.3	1.4	-2.6	-1.2	-1.2	-1.0	-1.3	-1.1
AA245976 dihydrolipoamide dehydrogenase	1.0	1.5	1.1	-2.6	1.2	-1.1	1.4	-1.1	-1.1
AI551576 ESTs	-1.1	1.0	1.2	-2.6	-1.8	1.3	-1.1	-1.0	-1.2
AA717025 Mus_musculus_10_day_old_male_pancreas_cDNA_RIKEN_full-length_enriched_library_clone:1810009A17_full_insert_sequence	1.8	-1.1	-1.2	-2.7	-2.55	-5.2	-1.6	-2.9	-1.4
AI464778 ESTs	-1.9	-1.6	-1.6	-2.7	-1.1	-1.5	-1.0	-1.6	-1.5
AA674270 major urinary protein 1	1.1	-1.1	-5.01013*	-2.7	1.0	1.09942~	1.5	-1.67	-1.5
AA175695 RIKEN cDNA 5730455P16 gene	-1.3	-1.1	1.2	-2.7	-1.6	1.25121~	-1.0	-1.2	-1.1
AA675084 elastase 2	2.3	1.4	-1.2	-2.7	-2.17	-2.2	-1.7	-1.9	-1.4
AA555905 ribosomal protein L28	-1.3	1.8	-1.0793*	-2.7	1.0	1.1	1.1	-1.4	1.0
AI120876 CD24a antigen	1.3	1.2	-1.5	-2.8	-1.7	-2.1	1.1	-1.2	-1.0
AA414790 leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-1.8
AA821884 amylase 2, pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	-2.3	-4.4	-1.1
AA185052 RIKEN cDNA 2510004L01 gene	1.0	1.0	-1.1	-2.8	-1.0	-1.8914~	1.07838+	1.2	1.1
AA733740 ESTs	-2.0	-2.2	-1.6	-2.9	-1.3	-1.3	-1.2	-1.6	-1.7
W15809 hemoglobin, beta adult major chain	1.5	-1.2	1.2	-2.9	1.3	-3.7	3.4	-1.2	-1.6
AA122791 histocompatibility 2_Q region locus 7	1.3	-1.4	1.3	-3.0	1.6	-1.2	-2.6	-1.2	-1.3

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AA106071 hemoglobin, beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	-4.3	2.2	1.1	-1.3	1.8	-1.7	-2.0
W14953 kinesin-associated protein_3	-1.0	-1.0	1.4	-3.2	-1.2	-3.9332~	3.3	-1.2	-1.2	1.3	-1.5	-1.5
AA727519 interferon-induced protein with tetratricopeptide repeats_3	1.3	-1.1	1.1	-3.3	1.2	1.53884~	-1.2	1.2	-1.0	-1.3	-1.1	-1.2
A1324398 glycosylphosphatidylinositol specific phospholipase D1	1.1	-1.3	1.2	-3.4	2.3	-1.5	2.0	-1.2	-1.3	1.2	-1.6	-1.6
A1326722 lymphocyte antigen_6 complex, locus E	-1.1	-1.2	-1.2	-3.5	-1.1	-2.0	1.1	-1.1	-1.1	-1.4	1.1	-1.2
AA398056 ubiquitin specific protease 18	1.1	1.0	1.2	-3.6	1.1	-2.25663~	1.2	1.1	1.1	1.0	-1.1	-1.2
AA237793 rat regenerating islet-derived, mouse homolog_1	2.5	1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA066763 hemoglobin, beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.8	-1.1	-1.3	1.5	-1.8	-2.0
AA796818 interferon-stimulated protein (15 kDa)	1.0	-1.6	-1.2	-5.2	-1.0	-1.5	1.2	-1.2	-1.1	-1.2	-1.1	-1.2
AA790398 ribonuclease_1, pancreatic	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AA175618 interferon-induced protein with tetratricopeptide repeats_1	-1.1	-1.65103+	-1.2	-7.4	-1.3	-2.50237~	-1.96725+	-1.2	-1.0	-1.0	1.1	1.1
AA822105 major urinary protein_1	-1.1	-2.4	-28.7649*	-7.8	-1.1	1.43224~	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2

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liver	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL- AB_BDEnor	PL- 2B_BDEnor	PL- 8B_BDE nor	PL- 8B_BDEnor	PL- 3B_BDEnor	PL- 9B_BDEnor	PL- 1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
AA1892336-aminolevulinic acid synthase	-1.0	-1.1	3.6	-1.1	1.2	-1.2	-1.2	1.0	-1.0	1.6	-1.1	1.2
AA2766672 thyroid hormone responsive SPOT14 homolog (Rat iso)	1.2	-1.6	3.4	-1.4	-1.3	-1.6	-1.3	-1.8	-1.5	-1.3	1.1	-1.2
AA426346 hydroxysteroid_17-beta dehydrogenase_9	1.39696+	1.13053+	3.0	1.31173+	1.0	1.41016+	1.55284+	-1.10611+	-1.0531+	1.13851+	-1.05399+	-1.13526+
AA306125 cytochrome P450_2A4	1.3	-1.3	3.0	1.3	1.4	1.0	-2.4	1.3	1.1	2.3	1.1	1.1
AA617417 cytochrome P450_2A4	1.2	-1.6	2.8	1.1	1.3	1.72833	-2.1	1.2	-1.0	2.1	-1.1	-1.2
AA881013 cytochrome P450_2C37	1.0	-1.1	2.8	1.1	1.8	1.5	-1.2	-2.6	1.0	1.1	-1.1	1.5
AA507819 alcohol dehydrogenase_1 complex	1.2	-1.2	2.6	1.4	-1.2	1.3	-1.0	-1.4	1.1	1.1	-1.3	-1.3
AA552452 solute_carrier_family_27_fatty_acid_transporter member_5	1.7	-1.3	2.6	1.0	1.0	-1.19636~	-1.7	-1.7	1.1	1.0	1.3	1.2
AA474338 synaptonemal complex protein_3	-2.8	1.2	2.6	1.4	1.5	2.74133~	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA273737 solute_carrier_family_2_facilitated_glucose_transport er_member_2	1.09801+	1.21261+	2.5	1.1	1.4	1.79237~	-2.06124+	1.20289+	1.38263+	1.0	1.35503+	1.39713+
AA638765 metallothionein_1	1.0	1.1	2.5	1.2	2.4	1.8	1.2	-1.6	-1.3	1.8	-1.9	-1.2
AA162217 pre-B-cell colony-enhancing factor	1.2	-1.2	2.5	1.0	1.1	1.0	1.0	1.0	-1.1	1.0	1.0	1.0
AA274023 apoptosis_inhibitory_5	1.39098+	-1.01923+	2.5	1.0093+	-1.0148+	-1.52171+	-1.07118+	1.01954+	1.07528+	1.15311+	1.35956+	1.34836+
AA643982 interleukin_1_receptor_type_1	-1.00156+	-1.22244+	2.4	1.14256+	-1.0782+	-1.37095+	1.46647+	1.30476+	1.0216+	1.0616+	1.1	-1.03458+
AA245845 hydroxysteroid_dehydrogenase_3_delta<5>-3_beta	1.3	-1.3	2.4	-1.2	1.2	-1.52324~	-1.5	-1.3	1.2	1.2	-1.1	1.2
AA760070 Mus_musculus_triacetylglucol_hydrolase mRNA, no implet_cde	1.2	-1.4	2.4	1.1	1.1	1.4	-1.1	1.2	-1.5	1.1	-1.1	-1.3
AA027607 hydroxysteroid_17-beta dehydrogenase_2	1.26667+	-1.3006+	2.4	1.3	1.8774+	-1.29025+	-1.28348+	-1.02353+	1.3	1.3	-1.2	1.2
AA789876 fatty_acid Coenzyme_A ligase, long chain_2	1.0	-1.4	2.4	1.0	-1.0	-1.2	-1.6	-1.2	-1.1	1.2	1.5	-1.4
AA323261 lipase, hepatic	1.13857+	1.08101+	2.3	-1.16185+	1.08991+	-1.06459+	1.52232+	-1.63699+	1.1171+	1.19795+	-1.11181+	-1.1209+
AA047988 RIKEN cDNA 2410041F14 gene	-1.2	-1.059+	2.3	-1.1	-1.25687+	1.10388+	-1.11183+	-1.52779+	-1.12343+	-1.3	-1.3	-1.10113+
AA929863 ESTs_Weakly_similar_to_T46271_hypothetical_protein_DKFZp5 64P1283.1 [H.sapiens]	1.1	-1.1	2.3	1.0	-1.0	1.8834~	-1.3	1.0	-1.1	-1.1	-1.2	-1.2
AA244388 retinoic acid early_transcript_gamma	-1.1	-1.05534+	2.2	1.1	-1.2	-1.00289+	1.21671+	-1.0	1.1	-1.2	1.1	1.1
AA771355 ficolin A	1.1	-1.6	2.2	1.3	1.2	1.0	-1.1	-1.1	1.2	1.1	-1.1	-1.1
W99034 ESTs	-1.2	1.3	2.2	1.5	1.3	1.6315~	1.0	-2.0	-1.4	-1.3	-2.0	1.0
AA822106 ESTs_Weakly_similar_to_C08A_HUMAN_COMPLEMENT_CO MPONENT_C8_ALPHA_CHAIN_PRECURSOR [H.sapiens]	2.7	-1.7	2.2	-1.0	1.1	2.00788~	-1.6	-20.2	-1.5	-1.3	-1.4	-2.7
AA117310 flavin containing monooxygenase_1	1.0	-1.9	2.2	-1.7	-1.4	-1.20807~	-1.2	1.0	-1.1	1.3	-1.4	-1.3
AA789916 hydroxysteroid_11-beta dehydrogenase_1	1.7	1.0	2.2	-1.1	-1.3	-1.28848~	1.0	-1.1	1.2	-1.1	-1.4	-1.1

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AA108182 cytochrome P450, 2c29	1.0	-1.1	2.2	1.0	1.7	1.13279+~	-1.4	-1.7	-1.2	1.1	-1.0	-1.1
AI597312 hydroxysteroid dehydrogenase-1, delta<5>-3-beta	1.2	-1.5	2.2	-1.2	1.3	1.51336~	1.0	-2.55267+**	-1.2	1.2	-1.5	1.1
AA261489 hypothetical protein, i54	1.2	1.1	2.2	1.3	1.1	1.04783~	-1.1	-1.2	1.0	1.1	-1.0	-1.1
W65070 ESTs	-1.2	1.4	2.1	1.7	1.8	1.8	1.1	-2.6	-1.4	-1.4	-2.3	-1.1
W36474 metallothionein_2	-1.2	-2.2	2.1	1.2	1.9	1.8	1.1	-1.6	-1.1	1.6	-1.9	1.0
AI386062 carbonic anhydrase 3	1.1	-1.3	2.1	-1.5	1.1	2.4	-1.7	-2.1	-1.3	-1.2	-1.6	-1.5
AI509048 ATP-binding cassette, sub-family A (ABC1), member 8	-1.03366+	-1.25698+	2.1	-1.07194+	1.36706+	1.0851+~	-1.15781+	1.4	1.3	1.0	1.36594+	1.4
AA674392 ESTs_Moderately similar to A23772 LINE-1 hypothetical protein - mouse [M.musculus]	-1.2	-1.5	2.1	1.3	-1.3	2.0	-1.0	-1.3	-1.3	-1.3	1.2	-1.1
AA260931 peroxisomal biogenesis factor 11a	1.3	1.3586+	2.1	1.4	1.4	-1.02852~	1.16677+	1.5	1.1	1.7	1.2	1.5
AA822480 ESTs_Weakly similar to retinal short-chain dehydrogenase/reductase retSDR1 [M.musculus]	1.7	1.6	2.1	1.1	-1.2	2.00303~	-1.5	-2.1	1.2	-1.2	1.0	-1.7
AA108741 RIKEN cDNA 0610025119 gene	1.1	1.0	2.1	-1.3	1.3	1.0	1.2	1.2	1.2	1.1	1.1	1.0
AA572640 RIKEN cDNA 1700124F02 gene	-1.10123+	-1.00385+	2.1	-1.2	1.2	1.18494+~	-1.9	-1.9	-1.3	-1.0	-1.2	-1.2
AA712088 3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-1.1	-1.6	2.0	-1.3	-1.5	-2.18283+~	-1.1	-1.3	-1.0	1.3	-1.2	1.0
AA272831 betaine-homocysteine methyltransferase	1.3	-1.3	2.0	-1.0	1.1	-1.62438~	1.1	-4.7	1.3	-1.3	1.2	-1.1
AI386058 serum albumin variant	2.9	-1.7	2.0	1.1	-1.1	1.68338~	-1.3	-23.1	-1.4	-1.5	-1.3	-2.9
W18483 thioether S-methyltransferase	1.0	-1.5	2.0	-1.3	-1.6	-1.6	-1.9	-1.0	-1.7	1.2	-1.0	-1.2
AA867621 S-phase kinase-associated protein 2 (p45)	-1.8	-1.2	2.0	1.5	1.2	2.74767+~	-1.79102+	-2.2	-1.8	-1.4	-1.9	-1.3
AI893740 glycine N-methyltransferase	1.1	1.2	2.0	1.1	1.3	1.37381~	-1.0	-1.4	-1.1	1.0	1.2	1.4
AA420359 DNA segment, Chr 6, ERATO Doi 109, expressed	1.1	1.1	2.0	-1.5	-1.3	-1.1	1.7	1.1	1.3	1.0	1.1	-1.1
AA116636 RIKEN cDNA 1110013A05 gene	-1.5	-1.0	2.0	1.4	1.2	2.19407~	-1.2	-1.6	-1.3	-1.3	-1.8	1.1
AA511089 glutathione S-transferase, theta 2	1.4	1.2	2.0	-1.1	-1.1	1.0	-1.4	-1.3	1.2	1.0	1.0	1.1
AA024217 Public domain EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AI325330 cytochrome P450, 2b13, phenobarbital inducible, type c	1.4	-1.1	2.0	1.0	2.8	2.82816+~	1.0	1.1	1.2	-1.2	1.1	1.4
AA415264 glutamate oxaloacetate transaminase 1, soluble	1.3	1.1	2.0	-1.1	1.5	1.0	1.1	1.0	1.2	1.4	1.4	1.5
AA237607 pyruvate kinase liver and red blood cell	-1.4	-1.2	1.9	-1.2	1.5	1.3	-2.3	-1.2	1.2	-1.1	1.0	1.1
AA822117 UDP-glucuronosyltransferase 1 family, member 1	-1.0	-1.4	1.9	-1.4	1.1	1.5	-1.3	-1.2	1.2	1.1	-1.2	-1.1
W77429 selenium binding protein 1	1.0	-1.4	1.9	-1.4	1.1	-1.8	-1.4	-1.2	-1.0	1.1	-1.1	1.1
MINE KINASE [H.sapiens]	1.4	-1.0	1.9	-1.1	1.2	1.10904~	-1.3	-1.8	1.1	1.2	1.2	-1.1
AI892274 amine N-sulfotransferase	-1.0	-1.2	1.9	-1.4	-1.8	1.82011+~	-1.0	-1.4	-1.1	-1.2	-1.4	1.2
AA087863 RIKEN cDNA 2310057J18 gene	-1.2	1.2	1.9	-1.1	1.2	-1.58765~	1.5	2.9	1.6	1.1	-1.4	-1.8
AA437705 RIKEN cDNA 2410012F02 gene	-1.2	-1.0	1.9	-1.1	-1.4	1.19407~	-1.4	-1.4	-1.2	-1.1	-1.2	-1.0
AI551358 urate oxidase	1.51631+	-1.05014+	1.9	1.088+	1.10047+	-1.60003+~	1.3	-2.5088+	1.02179+	-1.2	1.3	1.0
AA822002 cytochrome P450, 2c40	1.3	-1.2	1.9	1.3	1.4	1.4	1.1	-3.9	-1.1	-1.2	-1.3	-1.2
AA674491 RIKEN cDNA 1110007F05 gene	1.3	1.14853+	1.9	-1.3	1.4	-1.15618+~	1.03774+	1.1	1.1	-1.0	-1.1	-1.2

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AA656694 cytochrome P450_2b9_phenobarbital_inducible_type_a	-1.1	-1.4	1.9	1.3	2.6	3.8	-1.3	1.1	1.3	1.2	1.1	1.2	1.2
AA545691 thymidine kinase 1	1.2	-1.2	1.9	-1.2	-1.1	1.24271~	-2.2	-1.1	1.3	1.0	-1.1	1.1	1.1
AA545691 thymidine kinase 1	-1.2	1.0	1.9	1.3	1.1	2.00841~	-1.11126+	-1.1	-1.1	1.1	-1.1	-1.2	-1.2
AA545691 thymidine kinase 1	1.2	-1.01604+	1.9	1.2	1.2	-1.23474~	-1.14543+	-1.45171+	-1.2	-1.0	1.1	1.1	1.8
AA260296 esterase 31	1.1	-1.01893+	1.9	1.0	1.2	-2.4132+~	1.23402+	-1.1	1.2	1.2	-1.1	1.1	1.1
AI120986 platelet factor 4	-1.0	1.0	1.9	1.8	1.4	1.73151~	1.1	-1.2	1.5	1.0	1.2	1.5	1.5
AI328554 aldo-keo reductase family 1, member C1	1.2	-1.7	-1.9	1.1	1.2	1.23314~	-1.7	1.5	-1.1	-1.4	1.5	1.5	1.5
AA061729 keratin complex 1, acidic, gene 13	-1.4	-1.6	-1.9	-1.5	1.0	-1.2	-2.3	1.1	-1.1	-1.3	-1.2	-1.2	-1.2
AA028346 keratin complex 1, acidic, gene 19	-1.4	-1.1	-1.9	-1.2	1.1	-1.45209~	1.3	-1.0	-1.2	-1.2	-1.2	-1.1	-1.1
AA008331_RIKEN_cDNA_2900055D14_gene	1.1	-1.81116+	-1.9	-1.6	-1.4	-1.16436~	-1.50546+	-1.0	-1.1	-1.2	-1.1	-1.1	-1.1
AI390445 ESTs	-1.6	-1.9	-1.9	-2.2	-1.0	-1.1	-1.2	-1.4	-1.6	-1.6	-1.6	-1.6	-1.6
AA674794 Mus musculus mosg protein (Mosg) gene, complete cds	-1.1	-1.3	-1.9	-1.5	-1.0	1.0	-1.4	-1.1	1.3	-1.3	-1.3	-1.5	-1.5
W53604 procollagen, type VI, alpha 2	-1.1	1.0	-1.9	1.6	1.3	-1.0562+~	-1.0	1.2	-1.0	1.1	1.1	1.4	1.4
AA607013 ESTs	-1.5	-1.5	-1.9	-2.3	-1.3	-1.3	-1.3	-2.0	-1.6	-1.4	-1.3	-1.5	-1.5
W62007 neuron specific gene family member 2	1.0	1.4	-1.9	-1.3	1.7	-2.0	1.3	-1.0	-1.4	-1.0	-1.3	1.1	1.1
AA794055 cysteine rich protein	-1.2	-1.0	-1.9	1.4	1.3	-1.34248+~	-1.0	1.2	-1.1	-1.1	1.0	-1.1	-1.1
AI593151 heparan sulfate 2-O-sulfotransferase 1	-1.3	-1.5	-1.9	-1.7	-1.1	-1.47898+~	1.21892+	-1.0	-1.4	-1.1	-1.3	-1.0	-1.0
AA273820 schlafen_1	1.7	19.5	-1.9	1.2	4.4	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1	1.1
AA619407 pancreatitis-associated protein	-1.3	1.1	-1.9	-1.4	1.3	-1.81998+~	1.5	-1.0	-1.0	-1.0	-1.0	-1.1	-1.1
AA867162_RIKEN_cDNA_4933400E14_gene	-1.5	-1.4	-2.0	-1.8	-1.1	1.0225+~	1.37023+	-1.3	-1.2	-1.2	-1.3	-1.5	-1.5
AI591831 ESTs	-1.3	-1.3	-2.0	-1.6	-1.2	-1.25542+~	-1.0	-1.1	-1.2	-1.4	-1.2	-1.1	-1.1
AI592552 phorbol-12-myristate-13-acetate-induced protein 1	1.3	-1.4	-2.0	1.4	-1.7	-3.0	-3.1	-1.3	1.2	1.3	1.4	-1.7	-1.7
AA871285 Public domain EST	1.3	-1.2	-2.0	2.1	-1.0	1.1	1.3	-1.2	1.9	1.4	1.8	1.9	1.9
AA445667_RIKEN_cDNA_4632401C08_gene	1.2	-1.2	-2.0	-1.0	1.2	5.49956+~	1.1	1.1	1.3	1.1	-1.1	-1.3	-1.3
AA591215 fatty acid binding protein 5, epidermal	-1.4	-1.0	-2.0	-1.7	1.1	-2.0	1.2	-1.2	-1.1	-1.2	-1.1	-1.2	-1.2
AI594243 CD8beta opposite strand	-1.0	-1.3	-2.0	1.2	1.4	1.16404~	1.1	1.0	-1.0	1.1	1.0	-1.6	-1.6
W69253 insulin-like growth factor binding protein 5	-1.2	-1.2	-2.1	-1.1	1.0	1.07343~	-1.0	-1.0	-1.1	-1.1	-1.1	-1.1	-1.1
AA412831 Mus musculus, clone MGC:6804, mRNA, complete cds	1.3	1.5	-2.1	-1.5	-1.7	-1.4	-1.4	-1.2	1.4	1.2	1.1	-1.3	-1.3
AA728855_RIKEN_cDNA_3230402M22_gene	-1.6	1.5	-2.1	-1.9	1.7	-2.7	1.5	-1.1	-1.2	-1.3	-1.2	-1.2	-1.2
AI048040 claudin 4	-1.4	1.1	-2.1	-1.8	1.3	-3.0	1.2	-1.2	-1.1	-1.3	1.0	-1.2	-1.2
AI428626 ESTs	-1.4	1.7	-2.3	-2.0	2.0	-2.4	1.5	-1.0	-1.3	-1.3	-1.1	-1.1	-1.1
AA684403 ESTs	1.1	1.5	-2.4	-2.2	-2.4	-1.6	1.0	-1.3	1.2	-1.1	-1.1	-1.2	-1.2
AA450922 heat shock 70kD protein 5 (glucose-regulated protein, 78kD)													

TABLE 2

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LIVER

pancreas	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
Description	PL- 4B_BDEnor	PL- 2B_BDEnor	PL- 6B_BDEnor	PL- 9B_BDEnor	PL- 3B_BDEnor	PL- 5B_BDEnor	PL- 1B_BDEnor	PL- 7B_BDEnor	PL- 9B_BDEnor	PL- 10B_BDEnor	PL- 11B_BDEnor	PL- 12B_BDEnor
AA619407 pancreatitis-associated protein	1.7	18.5	-1.9	1.2	4.4	2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1
AA062401 TATA box binding protein (TBP)-associated factor, RNA polymerase II, 3' 150kD	1.2	3.4	1.1	-1.5	-1.8	1.4	1.4	-1.4	1.1	1.1	-1.6	1.2
AA210481 clusterin	1.1	3.0	1.2	-2.0	-1.8	-1.4	1.3	-1.1	1.1	1.4	-1.2	1.2
AA437717 ESTs. Moderately similar to T34531 hypothetical protein DKFZps24P1215.1 (H.sapiens)	-1.2	2.4	1.2	1.1	1.4	-1.3	1.1	-1.2	-1.3	1.1	-1.1	1.1
AA790398 ribonuclease 1, pancreatic	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AA575501 ESTs	-1.4	2.2	1.0	-1.3	1.2	-2.4	1.3	-1.6	-1.5	-1.2	-1.3	-1.1
AA661061 ESTs	-1.1	2.2	-1.1	1.1	1.1	-1.6	1.3	-1.4	-1.3	1.0	-1.2	-1.1
AI597421 ESTs	1.4	2.1	1.0	1.4	1.2	-1.0	1.0	1.5	1.3	1.4	1.3	1.2
AA600634 signal sequence receptor, delta	1.4	2.0	1.1	-1.2	-1.0	-1.2	-1.1	-1.2	1.1	1.1	-1.1	1.1
AA458425 Swi/SNF-related matrix associated, actin dependent, regulator of chromatin, subfamily a-like 1	1.1	2.0	-1.2	1.9	1.4	1.09081+	1.4	1.5	1.3	1.3	1.3	1.6
AA571665 ESTs. Moderately similar to J38863_E1B_10K/Bcl-2-interacting protein Nip1 (H.sapiens)	1.4	2.0	1.0	1.3	1.2	-1.0	1.1	1.4	1.4	1.2	1.4	1.4
AA223023 nascent helix loop helix 1	1.4	2.0	1.0	1.3	1.2	-1.1	1.2	1.3	1.2	1.3	1.4	1.3
AA062401 TATA box binding protein (TBP)-associated factor, RNA polymerase II, 3' 150kD	-1.0	2.0	1.1	-1.9	1.1	-1.2	1.2	1.0	1.1	1.4	1.0	-1.0
AI120332 RIKEN cDNA 1810055P16 gene	1.3	1.9	-1.2	-1.2	1.1	-1.7	1.2	-1.2	1.1	1.0	-1.2	1.0
AA489630 cyclin kinase	1.7	1.9	-1.4	3.1	2.0	1.31548+	1.3	2.3	2.0	1.6	2.2	2.1
AA763351 death-associated kinase 3	1.2	1.9	-1.2	-1.1	-1.0	-1.6	1.3	-1.1	1.0	1.1	-1.2	1.0
AA543968 RIKEN cDNA 2810418N01 gene	1.2	1.9	-1.1	-1.6	1.2	-1.1	1.1	-1.2	-1.0	-1.1	-1.2	-1.2
AI549624 RIKEN cDNA 0610041E09 gene	1.6	1.9	-1.3	3.6	1.8	-1.01549+	1.1	2.2	2.1	1.6	2.5	2.3
AA162226 Public domain EST	1.4	1.9	1.0	1.5	1.2	1.1	1.2	1.4	1.5	1.2	1.4	1.3
AI643201 Mus musculus TOB3 mRNA, complete cds	1.3	1.9	1.1	2.1	1.5	1.20006+	1.25034+	1.7	1.4	1.5	1.5	1.4
AI597097 Public domain EST	1.3	1.9	-1.1	-1.0	-1.6	1.2	1.2	-1.0	1.2	-1.9	1.0	-1.3
AA607983 zinc finger protein 101	1.23774+	1.9	-1.38204+	2.4	1.8	1.1254+	1.85166+	1.432+	1.5	1.2	1.4	1.7
AA667785 potassium voltage-gated channel, Isk-related subfamily, member 1	-1.8	-1.9	-1.3	-2.2	-1.2	-1.0	-1.3	-1.4	-1.5	-1.2	-1.4	-1.5
AI152562 proliferin	1.7	-1.9	1.0	-1.2	-1.3	-1.24501+	-1.2	-1.2	-1.1	-1.4	-1.1	1.2
AA547393 ESTs	1.0	-1.9	-1.3	1.1	-1.5	1.2	1.13657*	1.3	-1.1	-1.2	1.2	-1.1
AA435278 caldesmon 1	-1.0	-1.9	-1.2	-1.3	-1.3	1.0767+	-1.8	-1.3	-1.6	1.0	1.1	-1.4
AA795319 myosin light chain, phosphorylatable, cardiac ventricles	-1.1	-1.9	-1.2	-1.4	-1.3	1.73331+	-3.0	-1.8	-1.3	1.1	1.1	1.0
AA674784 Mus musculus msg protein (Mosp), complete cds	-1.6	-1.9	-1.9	-2.2	-1.0	-1.1	-1.2	-1.4	-1.6	-1.6	-1.6	-1.6
AA546660 calpain 10	1.1	-1.9	1.4	-1.2	1.0	-1.15046+	1.1	1.0	-1.1	-1.2	-1.1	-1.0
AI606520 ESTs	1.1	-1.9	-1.1	-1.1	-1.7	1.1	1.0	1.2	-1.1	-1.2	1.1	-1.1
AI604245 protocadherin 7	-1.8	-1.9	-1.5	-1.8	-1.0	-1.46876+	-1.1	-1.2	-1.4	-1.2	-1.3	-1.5

TABLE 2

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PANCREAS

AA672330 ESTs	-1.4	-1.9	-1.1	-1.3	-1.8	1.0	-1.1	-1.1	-1.3	-1.1	-1.3	-1.1	-1.0
AA008228 peroxisomal fatty-acylated protein	-1.4	-1.9	-1.3	-2.1	1.0	-1.1	-1.2	-1.2	-1.4	-1.0	-1.4	-1.1	-1.2
W36635 carbonyl reductase 2	1.2	-1.9	-1.4	1.4	1.0	1.3	-2.3	-1.1	1.0	1.2	1.5	1.1	
AI596899 ESTs	-1.5	-1.9	-1.5	-1.6	-1.3	-1.43833~	-1.03626~	-1.1	-1.6	-1.4	-1.2	1.1	
AI117310 flavin containing monooxygenase 1	1.0	-1.9	-2.2	-1.7	-1.4	-1.20807~	-1.2	1.0	-1.1	1.3	-1.4	-1.3	
AA822027 ATPase, Cu++ transporting, beta polypeptide	1.2	-1.9	1.2	-1.4	-1.0	1.17594~	-1.2	-21.9	-1.5	-1.5	-1.8	-1.7	
AA789551 ESTs, Weakly similar to J49441 Mouse 19.5 mRNA, complete cds - mouse [Musculus]	-1.1	-1.9	-1.3	1.0	1.2	-1.2	-1.3	1.1	-1.1	1.1	1.2	-1.0	
AI551573 ESTs	-1.5	-1.9	-1.4	-1.6	-1.4	-1.48844~	-1.7	-1.5	-1.7	-1.3	-1.4	-1.2	
AA684426 ESTs	1.0	-1.9	-1.2	1.1	-1.6	1.0	1.2	1.1	-1.1	-1.3	1.2	-1.1	
AA026578 keratin complex 2, basic, gene 4	1.2	-1.9	-1.3	-1.0	-1.0	1.44671~	-2.1	1.6	1.4	-1.1	1.5	1.3	
W18822 growth arrest and DNA-damage-inducible 45 gamma	1.2	-2.0	-1.3	-1.1	1.0	1.52923~	-1.3	-1.7	1.3	-1.1	-1.3	1.4	
AI325332 transglutaminase 3, E polypeptide	-2.0	-2.0	-1.4	-2.3	-1.2	-1.3	-1.2	-1.2	-1.7	-1.4	-1.5	-1.7	
AA727521 Mus_musculus_11_kDa_secreted_protein_precursor_mRNA, complete cds	1.1	-2.0	-1.4	-1.7	1.5	2.4	-1.6	1.2	1.1	1.1	1.5	1.2	
AA220024 trophoblast specific protein	1.5	-2.0	-1.2	1.5	1.1	-1.0	-2.2	-1.2	1.4	1.1	1.2	2.3	
AA089188 uromodulin	-1.2	-2.0	-1.0	1.1	-1.3	1.0	-4.0	-1.4	-1.7	1.1	-1.2	-1.4	
AA623704 Public domain EST	1.2	-2.0	-1.0	-1.0	-1.7	1.2	-1.0	1.3	-1.0	-1.2	1.2	-1.1	
AA726162 keratin complex 1, acidic, gene 16	1.1	-2.0	1.2	-1.1	-1.0	1.3	-1.5	-1.2	1.3	-1.2	-1.1	-1.1	
AI551662 fos-like antigen 2	-2.1	-2.0	-1.4	-2.2	-1.2	-1.1	-1.3	-1.4	-1.4	-1.4	-1.4	-1.5	
W83106 ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	-1.5	-2.0	-1.7	-1.8	-1.2	-1.44607~	1.0	-1.2	-1.6	-1.3	-1.3	-1.3	
AI481911 Mus musculus, clone MGC:6727, mRNA, complete cds	-1.1	-2.0	-1.8	1.0	-1.8	-2.3	-1.5	-2.4	-1.4	-1.4	-1.4	-1.4	
AA794176 ESTs, Moderately similar to SPA-1 like protein p1294 (R.norvegicus)	-1.0	-2.0	-1.2	-1.2	-2.0	1.2	1.2	1.3	-1.3	-1.3	1.1	-1.1	
AA693177 ESTs	1.4	-2.0	1.0	1.1	-1.8	1.2	1.3	1.3	1.0	-1.3	1.4	-1.1	
AA770808 pericentriolar material 1	-1.9	-2.1	-1.6	-2.3	-1.1	-1.2	-1.0	-1.5	-1.6	-1.5	-1.6	-1.6	
AA727627 ankyrin 1, erythroid	-1.8	-2.1	-1.6	-2.5	-1.3	-1.2	-1.4	-1.4	-1.6	-1.6	-1.4	-1.7	
AA717019 ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-1.2	-2.1	-1.1	-1.5	-1.3	1.2	-2.8	-1.4	-1.8	-1.2	1.1	-1.1	
AA684191 CDC-like kinase	1.5	-2.1	-1.3	-1.1	-2.0	-1.4	-1.3	1.6	1.4	-2.1	1.4	1.2	
W54403 ATPase, Cu++ transporting, beta polypeptide	1.2	-2.1	1.1	-1.0	1.2	1.3	-2.9	-7.9	1.1	-1.1	-1.1	1.2	
AA245952 cyclin-dependent kinase-like 2 (CDC2-related kinase)	-1.1	-2.1	-1.7	-1.8	-1.2	-1.38223~	-1.2	1.1	-1.0	-1.3	-1.1	1.1	
AI385457 retinol binding protein 2, cellular	-2.0	-2.1	-1.6	-1.9	1.5	1.0	-1.3	-1.9	-1.6	-1.9	-1.5	-1.7	
AA733740 ESTs	-2.0	-2.2	-1.6	-2.9	-1.3	-1.3	-1.2	-1.6	-1.7	-1.8	-1.7	-1.8	
AA138265 RIKEN cDNA 2010309G21 gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	1.1	-1.3	-1.0	-1.0	-2.4	
AA152636 integrin alpha 4	1.2	-2.2	-1.3	1.1	-2.2	1.1	-1.0	1.3	-1.3	-1.4	1.2	-1.0	
W36474 metallothionein 2	-1.2	-2.2	-2.1	1.2	1.9	-1.3	1.1	-1.6	-1.1	-1.5	-1.9	1.0	
AA414790 leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-2.0	-1.7	-1.6	-1.8	
AI664286 tumor necrosis factor receptor superfamily, member 9	1.3	-2.3	-1.1	-1.3	-1.3	1.2	-2.7	-1.3	-1.1	-1.2	1.1	-1.7	

TABLE 2

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PCT/US02/41825

AA822105 major urinary protein 1	-1.1	-2.4	-28.7649*	-7.8	-1.1	1.43224~	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2
AA821997 myoglobin	-1.0	-2.5	1.0	1.1	1.0	-1.2	-1.8	-1.7	-4.3	-2.2	-1.1	-1.7
AA822257 myosin light chain, alkali, fast skeletal muscle	1.4	-2.5	-1.2	-1.1	-1.1	1.37858*	-1.3	1.0	-1.6	-1.4	-1.2	-1.6
AA600571 intracisternal A particles	1.9	-3.1	-1.1	1.1	-1.4	2.08495*	-1.2	1.4	1.1	-1.7	1.5	1.3
AA444538 ESTs, Weakly similar to_MDP1_MOUSE_MICROSOMAL_DIPE	-2.1	-3.9	1.2	-1.4	-1.1	-1.19866+~	1.6	1.0	1.3	-1.3	-1.3	1.3
PTIDASE PRECURSOR (M.musculus)	-1.2	-5.8	1.1	-1.8	1.1	-1.0	-1.0	-1.1	1.5	-1.3	-1.1	-1.1
W34262 heat shock protein, 25 kDa	-1.4	-10.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1
AI390138_RIKEN cDNA_3930401B19 gene												

PANCREAS

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TABLE 2

Description	spleen		panc	liv	stom	int	col	br	lung	blad	kidn	p/ut	mam
	PL_4B_BDEnor	PL_4B_BDEnor	PL_2B_BDEnor	PL_6B_BDEnor	PL_8B_BDEnor	PL_3B_BDEnor	PL_5B_BDEnor	PL_1B_BDEnor	PL_7B_BDEnor	PL_9B_BDEnor	PL_10B_BDEnor	PL_11B_BDEnor	PL_12B_BDEnor
AA821984 amylase 2, pancreatic	3.1		1.1	-1.2	-2.8	-32.0	-4.0	2.3	-1.2	4.4	-1.1	-1.1	-1.2
AA386058 serum albumin variant	2.9		-1.7	2.0	1.1	-1.1	1.68248~	-1.3	-23.1	-1.4	-1.5	-1.3	-2.9
AA822106 ESTs, Weakly similar to CORA_HUMAN_COMPLEMEN T COMPONENT C3 ALPHA_CHAIN_PRECURSOR [H.sapiens]	2.7		-1.7	2.2	-1.0	1.1	2.00798~	-1.8	-20.2	-1.5	-1.3	-1.4	-2.7
AA237793 rat regenerating fibroblast-derived mouse myoblasts	2.5		1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA982254 RIKEN cDNA 2210010C04, gene	2.3		1.6	-1.3	-2.0	-8.5	-1.3	1.6	-1.5	-2.0	-1.4	-1.1	-1.1
AA675084 elastase 2	2.3		1.4	-1.2	-2.7	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA674409 pancreatic lipase related protein 1	2.0		1.7	-1.4	-1.7	-6.9	-1.0	1.2	1.0	-1.1	-1.1	1.6	1.3
AA222208 surfactant associated protein C	2.0		-1.7	-1.3	1.4	1.2	1.23582~	-1.6	-1.1	-1.2	-1.4	1.3	1.7
AA445731 heat shock protein cognate 70, testis	1.9		1.1	1.0	-1.2	-1.1	-1.3	-1.8	3.8	-1.0	1.1	-1.2	1.1
AA717025 Mus musculus, 10 day old male pancreas, cDNA_RIKEN_full- length enriched library, clone:1810009A17, full insert sequence	1.9		-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1	-1.4
AI510069 ESTs	1.9		1.5	1.5	1.5	1.3	-1.0161~	1.2	1.4	1.0	-1.3	-1.0	-1.3
W53916 RIKEN cDNA 3300001P10, gene	1.9		1.5	1.0	1.1	1.3	-1.69676~	-1.2	1.1	1.2	1.0	1.1	1.1
AA238294 sema domain, immunoglobulin domain, (Ig), transmembrane do main (TM) and short cytoplasmic domain, (semaphorin) 4G	-1.9		-1.6	1.1	-1.7	-1.4	-1.3	-1.2	-1.4	-1.5	-1.1	1.0	1.0
AA437577 ESTs	-1.9		-1.8	-1.5	-2.2	-1.2	-1.47043~	-1.53147+	-1.5	-1.8	-1.5	-1.4	-1.5
AA426902 ESTs	-1.9		-1.3	-1.4	-2.3	1.0	-1.4	-1.1	-1.3	-1.6	-1.5	-1.3	-1.4
AA770808 pericentriolar material 1	-1.9		-2.1	-1.6	-2.3	-1.1	-1.2	-1.0	-1.5	-1.6	-1.5	-1.6	-1.6
AA684320 activin receptor interacting protein 1	-1.9		1.4	1.3	1.3	1.5	2.80454~	1.0	-2.7	-1.4	-1.1	-1.9	-1.3
AA871914 defensin related cryptidin 16	-1.9		-1.3	-1.1	1.6	1.7	2.2	1.1	-1.2	1.2	-1.1	1.1	-1.0
AA546625 ESTs, Weakly similar to SP62_MOUSE_SPLICEOSOME ASSO CIATED PROTEIN 62 [M.musculus]	-1.9		-1.6	-1.4	-2.2	-1.2	-1.4	1.2	-1.2	-1.7	-1.7	-1.4	-1.6
AI464778 ESTs	-1.9		-1.6	-1.6	-2.7	-1.1	-1.5	-1.0	-1.6	-1.7	-1.6	-1.5	-1.6
AA922098 apolipoprotein A-I	-1.9		-1.5	1.1	-2.4	2.4	2.4	-1.9	-8.0	-1.2	-2.1	-2.5	-1.6
AI325332 transglutaminase 3, E polypeptide	-2.0		-2.0	-1.4	-2.3	-1.2	-1.3	-1.2	-1.2	-1.7	-1.4	-1.5	-1.7
AA922368 inhibitor of DNA binding 4	-2.0		1.3	1.2	1.5	1.4	2.50804~	1.1	-2.1	-1.1	-1.5	-1.6	-1.2
AA793740 ESTs	-2.0		-2.2	-1.6	-2.9	-1.3	-1.3	-1.2	-1.6	-1.7	-1.8	-1.7	-1.8
AA881492 ESTs	-2.0		1.3	1.1	-1.2	1.1	1.1	1.0	-2.4	-1.5	-1.5	-1.7	-1.1
AI608086 nunt related transcription factor 3	-2.0		1.1	1.2	1.4	1.4	1.68234~	-1.75763+	-2.0	-1.6	-1.3	-1.9	-1.0
AI121690 RIKEN cDNA 1300007C21, gene	-2.0		-1.7	-1.4	-1.4	-1.4	-1.9	-1.2	-1.1	-1.7	-1.5	1.1	1.2
AI365457 retinol binding protein 2, cellular	-2.0		-2.1	-1.6	-1.9	1.5	1.9	-1.3	-1.9	-1.6	-1.9	-1.5	-1.7
AA265025 S100 calcium-binding protein A9 (calgranulin B)	-2.1		-1.3	-1.2	1.1	-1.1	-3.10848~	-1.3	1.0	1.1	-1.1	1.1	-1.6

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TABLE 2



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AI551682_fos-like antigen 2	-2.1	-2.0	-1.4	-2.2	-1.2	-1.1	-1.3	-1.4	-1.4	-1.4	-1.4	-1.5
AA414790_leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-2.0	-1.7	-1.6	-1.8
AA014727_tumor-suppressing subchromosomal transferable fragment 3	-2.1	1.1	1.8	-1.2	1.1	2.05236~	-1.8	-3.0	-2.1	-1.8	-2.9	-1.0
AA546645_cell division cycle 2 homolog (S. pombe)-like 2	-2.1	-1.1	1.3	1.4	1.1	2.3	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA444538_ESTs_Weakly similar to MDP1_MOUSE_MICROSOMAL_DIPEP TIDASE_PRECURSOR [M.musculus]	-2.1	-3.9	1.2	-1.4	-1.1	-1.1986+~	1.8	1.0	1.3	-1.3	-1.3	1.3
AA608466_ESTs	-2.2	-1.2	1.4	1.1	-1.2	1.17951+~	1.1	1.0	-1.3	-1.2	-1.1	-1.1
AI386257_calbindin-D9K	-2.2	-1.3	1.2	1.5	-53.5	-4.1	1.0	-1.2	-1.1	-1.2	-1.2	1.4
AA087193_lipocalin_2	-2.2	-1.7	-1.8	-1.3	-1.2	-1.0	-1.4	-1.1	1.2	-2.02682*	-1.6	1.1
AA034678_rhotekin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4
AA414653_ESTs_Weakly similar to KIAA0542_protein [H.sapiens]	-2.4	-1.13914+	-1.5	1.1	-1.2	1.28167+~	1.07853+	-1.27379+	-1.3	-1.1	-1.29631+	-1.1
AA771226_ESTs_Weakly similar to zinc finger protein 95 [M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.7115~	-2.0	-3.3	-2.2	-1.4	-2.4	-1.4
AA982151_proteinase 3	-2.4	1.1	1.2	-1.1	1.1	1.44236+~	-1.37705+	-1.4	-1.2	-1.2	-1.1	1.1
AA176045_forkhead box C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.6	-2.5	-1.1
AA024217_Public domain EST	-2.5	1.5	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AI428661_ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.6	-2.6	-2.1	-1.7	-2.2	-1.5
AA874101_tumor-associated calcium signal transducer 2	-2.6	-1.1	1.5	1.3	1.2	0.531~	-1.7	-2.1	-1.5	-1.5	-2.4	-1.2
AA474336_synaptonemal complex protein 3	-2.8	1.2	2.6	1.4	1.5	2.74133~	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA031015_myeloperoxidase	-2.9	-1.1	1.0	-1.1	1.5	1.05319~	-1.3	1.0	-1.3	-1.3	1.0	1.1
AA189286_ESTs	-3.2	1.4	1.5	1.5	1.3	1.7	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
AA060282_neutrophilic granule protein	-4.0	1.39257+	1.2	-1.0	1.26109+	-1.34714+~	1.71277+	1.5	1.2	-1.1	1.0	-1.4

TABLE 2

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[illegible]

TABLE 3

155	AA656394	RIKEN cDNA 111002515 gene	intestine	1	1.3	-1.2	2.6	-3.4	-1.3	-1.4	-4.1	-2.9	1.2	-2.3	-1.5	-2.1	-1.7	-1.9	-1.6	-1.6	-1.4	-1.2	-1	16256	381004	0		
192	AA547242	undifferentiated embryonic cell transcription factor 1	stomach	1	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.2	740	335593	3		
20	AA656712	myosin heavy polypeptide 1_skeletal muscle adult	colon	1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	177	439	937025	0		
202	AA756672	thyroid hormone responsive SPOT14 homolog (Rattus)	liver	1	-1.0	-1.2	-1.1	-2.2	-1.4	-1.1	-4.9	-5	-13	-11	-4.3	-8.8	-6.3	-3.8	-4.8	-5	-4.5	-4.1	34773	344307	0			
196	AI1789976	fatty acid Coenzyme A ligase, long chain 2	liver	1	-1.7	-1.7	-1.6	-1.2	-1.4	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	5	9403	164507	0		
253	AI57496	Mus musculus mRNA complete cds, similar to L-amino acid oxidase	mammary gland	1	-3.4	-5.3	-2.5	-2	-3.7	-2.4	-2.9	2.4	-3.4	-3.1	-2.9	-2.4	-3.5	-3.6	-4.2	-2.7	-4.1	-3.7	10568	710375	0			
250	AA288467	glycosylation dependent cell adhesion molecule 1	mammary gland	1	-3.7	-3.9	-3.9	-1.3	-1.6	-1.9	-1.6	-2.0	-2.4	-2.2	-1.2	-1.1	-3.2	-2.4	-4.5	-2.1	-3.1	-3.0	60942	430113	0			
277	AA754922	stearoyl-Coenzyme A desaturase 1	placenta/uterus	1	-4.9	-4.4	-3.2	-3	-3.1	-2.5	-3.9	-3.4	-3.5	-4.7	-3.5	-5.6	-2.8	-2.3	-4*	-3.8	-2.9	-2.9	17602	211579	0			
290	AA792297	procollagen, type V, alpha 1	stomach	1	-3.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	3739	102792	0			
197	AA474336	synaptonemal complex protein 3	liver	1	-3	-1.1	1.0	1.3	5.2	1.2	1.4	1	1.5	1.1	4.6	1.8	-2.7	1.3	1.3	2.7	-1.3	2	1563	144036	0			
154	AI594147	beta-2 microglobulin	intestine	1	-1.2	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	14698	516217	0			
164	AA109873	RIKEN cDNA_0610010E05 gene	intestine	1	-2.8	-2.6	-3.4	-3.1	-2.8	-3.1	-3.3	-3.2	-3.4	-3.2	-3.4	-3.2	-3.4	-3.2	-3.4	-3.2	-3.4	-3.2	9307	13365	0			
401	AA068624	hydroxyacid oxidase (glycolate oxidase) 3	stomach	1	-1.2	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	11	13	16	1222	42183	1
151	AI323162	dipeptidase 1 (renal)	intestine	1	-3	-3.8	-1.8	-1.4	-3.9	-2	-1.8	-2.3	-3.6	-1.2	1.6	3.6	1.1	-1.3	-1.2	-1.5	1.1	-1.1	5479	28413	0			
152	W56983	peripheral myelin protein, 22 kDa	intestine	1	-1.6	-2.4	-1.6	-1.6	-1.7	-2.3	-1.2	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	12	15	3400	103788	0	
156	AA793433	glutaryl aminopeptidase	intestine	1	-2.2	-2.9	-3.4	-1.5	-1.6	-1.7	-1.2	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	13	15	3804	941298	0	
181	AA239727	ATP-binding cassette, sub-family B (MDR/TAP), member 1	intestine	1	-1.2	-1.2	-2.1	-2	-1.1	1	2.1	-3	3.5	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	5179	841833	0			
107	AI385457	retinol binding protein 2, cellular	colon	1	-3.7	-1.8	-1.7	1.3	-1.7	-1	-1.3	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	16	1236	124339	0		
129	AT530591	RIKEN cDNA_2010003F10 gene	colon	1	-3.3	-1.7	-1	1.1	-1.6	1.1	-1	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1602	727407	0			
160	AA586758	ESTs	intestine	1	-1.3	-1	-1.5	-1.2	-1.6	-1.7	-1.4	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	11	1609	185392	0		
17	AA529824	fatty acid binding protein 2, intestinal	colon; mammary gland	2	-2.2	-4.9	-4.3	-2.8	3	-1.7	2	-3.5	3	3	3	3	3	3	3	3	3	3	3107	211321	0			
19	AA869173	defensin related cryptidin 6	colon; placenta/ uterus	2	-4.4	-3.7	-4.4	-1.6	-3.1	-2.6	3	3	3	3	3	3	3	3	3	3	3	3	21576	120246	0			
136	AA871914	defensin related cryptidin 16	colon	1	-1.5	-2.9	-6.6	-5.1	-6.9	-6.1	-5.8	-9.1	-10.1	-10.1	-10.1	-10.1	-10.1	-10.1	-10.1	-10.1	-10.1	-10.1	31510	258138	0			
112	AA623172	defensin related cryptidin 6	colon	1	-2.5	-3.4	1	-1.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	-2.1	9095	187884	0			
25	AA871641	defensin related cryptidin, related sequence_2	intestine; colon	2	-3.2	-3.9	1.4	-1.8	-2.9	-3	-1.5	-2.8	1	1	1	1	1	1	1	1	1	1	2	12699	12855	0		
26	AA871838	phospholipase A2_group IIA (platelets, synovial fluid)	intestine; colon	2	-3.7	-4.3	-1.3	-1.3	-1.7	-1.5	-1.1	-1.5	1	1	1	1	1	1	1	1	1	1	4076	166488	0			
27	AA869219	intelectin	intestine; colon	2	-2.4	-2.3	-1.3	-1.2	-1.2	-1.1	-1	-1.7	1	1	1	1	1	1	1	1	1	1	1	15382	233146	0		
163	AA871410	defensin related cryptidin 5	intestine	1	-3.3	-3.6	-5.2	-4.6	-5.3	-5.3	-5.1	-4.9	1	1	1	1	1	1	1	1	1	1	1	21556	241821	0		
177	AA450725	membrane metallo endopeptidase	intestine	1	-1.7	-2.3	2	-1.2	-1.3	-1.3	-1.3	-1.1	1	1	1	1	1	1	1	1	1	1	1	2399	995035	0		

TABLE 3

167	AA162211	guanine nucleotide binding protein_alpha 1	intestine	int. col	-1.0	-1.9	-1.4	-1.4	-1.2	-1.2	1	1.4	1.1	1.2	-1	-1	-1.2	-1	-1.1	-1.2	566	1833.21	0
78	W15893	guanylate cyclase activator 2 (guanylin 2, intestinal, heurstable)	intestine	int. col	-1.3	-1.5	1.4	1.4	-1.1	1.1	1.2	-1.2	-1.1	-1.1	-1.2	-1	-1.1	-1.2	-1	-1.5	574	1837	0
74	AA871663	defensin related cryptidin related sequence_7	intestine	int. col	-0.9	-0.2	-0.5	-0.6	-0.3	-0.4	-0.3	-0.3	-0.5	-0.4	-0.3	-0.3	-0.3	-0.3	-0.3	-0.3	1570	1539.8	0
83	AH81911	Mus musculus, clone MGC:6727, mRNA, complete cds	kidney	int. col	-1.1	1	-1.3	-0.5	-1.4	-1.5	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	2437	331.5	0
226	AA237607	pyruvate kinase liver and red blood cell	liver	int. col	-1.2	-1.2	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	1563	153.0	0
257	AA242102	villin	mammary gland	int. col	-0.9	-0.2	-0.5	-0.6	-0.3	-0.4	-0.3	-0.3	-0.5	-0.4	-0.3	-0.3	-0.3	-0.3	-0.3	-0.3	1830	1830.9	0
38	AA169407	pancreatitis-associated protein	pancreas; intestine	int. col	-0.9	-0.2	-0.5	-0.6	-0.3	-0.4	-0.3	-0.3	-0.5	-0.4	-0.3	-0.3	-0.3	-0.3	-0.3	-0.3	1774	1774.4	0
50	AA869181	defensin related cryptidin 6	stomach; colon	int. col	-0.5	-0.2	-0.5	-0.6	-0.3	-0.4	-0.3	-0.3	-0.5	-0.4	-0.3	-0.3	-0.3	-0.3	-0.3	-0.3	2010	2010.1	0
52	AA869166	defensin related cryptidin related sequence_10	stomach; intestine	int. col	-0.5	-0.2	-0.5	-0.6	-0.3	-0.4	-0.3	-0.3	-0.5	-0.4	-0.3	-0.3	-0.3	-0.3	-0.3	-0.3	1937	1937.0	0
14	AA146478	M.musculus, mRNA (Clontar) for IBA-V-D1-heavy chain	stomach; kidney	int. col	-0.9	-0.4	-0.8	-0.9	-0.7	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	1937	1937.0	0
12	AA445667	RIKEN cDNA 4632401C08, gene	stomach; bladder; mammary gland	int. col, kidn	-0.3	4	1.1	1.1	0.6	-1.2	1.3	-1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	490	1117.33	0
48	AA023491	RIKEN cDNA 1600012D06, gene	colon	int. col, p/ut	-1.2	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	403	1765.29	0
06	AA466153	ESTs	brain	int. kidn	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	363	363.5	5
280	A1614443	3'-phosphoadenosine 5'-phosphosulfate synthase 2	placenta; uterus	int. kidn	-0.7	-1.2	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	1937	1937.0	0
24	AA656694	cytochrome P450_2b9, phenobarbital inducible, type a	intestine; colon	int. kidn	-1.2	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	3359	3359.125	0
32	A1325330	cytochrome P450_2b13, phenobarbital inducible, type c	liver; intestine	int. kidn	-0.3	-0.3	-0.2	-0.2	-0.1	-0.1	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	239	239.73	1
3	AA107035	guanylate cyclase activator 2b (retina)	intestine; colon; mammary gland	int. p/ut	-0.2	-0.7	-0.7	-0.7	-0.6	-0.6	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	2093	2093.0	0
238	W17865	uridine-specific proline-rich acidic protein	mammary gland	int. p/ut	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	4516	4516.17	0
140	AA108495	deoxyribonuclease 1	colon	int. kidn	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	1048	1048.8	0
117	AA822473	DNA segment, Chr. 8, Brigham & Women's Genetics	colon	int. kidn	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	1048	1048.8	0
132	AA181090	cytochrome P450_subfamily IV_B, polypeptide 1	colon	int. kidn	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	-0.8	3247	324.5	0
141	AF386288	RIKEN cDNA 2700941D08, gene	colon	int. kidn	1.1	1.1	-1.4	-1.2	-1.3	-1.4	-1.8	-1.5	-1.3	-1.1	-2.2	-1.1	-1.6	-1.7	-1.6	-1.1	1716	1713.42	0
170	AA882450	RIKEN cDNA 1200011D11, gene	intestine	int. kidn	-1.4	-1.3	-1.1	-1.2	-1.4	-1.2	-1.2	-1.3	-1.5	-1.8	-1.3	1.6	1.5	1.5	1.5	1.5	2338	2327.5	0
180	AA110386	aminotransferase	intestine	int. kidn	-1.3	-1.1	-1.4	-1.5	-1.2	-1.4	-1.2	-1.2	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	1553	1542.08	2
287	A1614454	reduced in osteoclasts transporter	kidney; mammary gland	int. kidn	-0.1	-0.4	-1.2	-1.2	-1.5	-1.4	-1.4	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	8375	8375.08	0
189	AA162217	pro-B-cell colony-enhancing factor	kidney	int. kidn	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	4441	4441.07	0
219	AA511089	guanine S-transferase, theta 2	liver	int. kidn	-1.1	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	2431	2431.08	0
222	A1617362	low density lipoprotein receptor-related protein 2	stomach	int. kidn	-1.9	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	-2.2	2639	2639.02	2

459	AA157821	solute carrier family 22 (organic cation transporter), member 2	1	stomach	kidn	-1.8	2.5	4	-1.2	-1.8	-1.4	-1.7	-1.2	-1.8	-1.6	-1.5	-1.5	-2	4.3	-1.9	-1.3	-1.9	-1.2	-1.6	-1.2	-2.2	-1.13	470.5	0			
331	AA110551	phospholipid scramblase 2	1	stomach	kidn	-2.4	2.7	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	-1.4	-1.2	141.83	0			
165	AA415344	histone deacetylase 7	1	intestine	kidn, p/ut	-1.1	-1.3	-1.2	-2	-1.6	-1.3	-1.3	-1.1	-1.1	-1.2	-1.1	-1.1	-1.1	1.4	1.2	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	64.25	0			
254	W14224	N-myc downstream regulated 1	1	mammary gland	kidn, p/ut	3.1	3.3	2.1	2.2	-1.7	-1.8	-1.1	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	107.54	0			
30	AA674392	ESTs, Moderately similar to A23772, LINE-1 hypothetical protein - mouse [M.musculus]	2	liver; colon	liv	1.3	1.0	-1.3	-1.2	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	196.38	0			
213	AB90183	ESTs, Weakly similar to KICE HUMAN C, HOLINEETHANOLAMINE KINASE [H.sapiens]	1	liver	liv	-1.4	2	-1.5	-1.5	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	415.75	0			
207	AA272831	betaine-homocysteine methyltransferase	1	liver	liv	3.2	4.1	2.9	2.3	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	332.75	0			
205	AA572640	RIKEN cDNA 1700124F02, gene	1	liver	liv	-1.0	-1.4	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	371.65	4			
237	AD47988	RIKEN cDNA 2410041F14, gene	1	liver	liv	1.3	1.5	1.4	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	221.05	7			
211	AA106162	cytochrome P450, 2C29	1	liver	liv	-1.1	-1.2	2.1	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	157.86	0			
233	AA881013	cytochrome P450, 2C37	1	liver	liv	-1.5	2.5	3	-1.7	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	482.98	0			
230	AA55252	solute carrier family 27 (fatty acid transporter), member 5	1	liver	liv	-1.5	2.5	-1.5	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	482.98	0			
42	AD86058	serum albumin variant	2	spleen; liver	liv	1.8	5.9	2.9	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	155.97	0			
124	AA067003	glutathione S-transferase, mu_1	1	colon	liv, blad	4.5	6	2.4	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	337.15	0			
214	AA261489	hypothetical protein_154	1	liver	liv, blad	2.5	3.1	-1.3	-2	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	612.84	0			
111	AA230638	transcription factor-like protein ODA-10	1	colon	liv	-1.3	-1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	258.9	0			
195	AB80802	carbonic anhydrase 3	1	liver	liv	-1.1	-1.3	4.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	273.33	0			
209	W65070	ESTs	1	liver	liv, col	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	0		
215	W99034	ESTs	1	liver	liv, col	1.2	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	0		
22	AA066225	selenoprotein P, plasma_1	2	intestine; colon	liv, col, kidn	-2	2.3	1.1	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	-1.3	627.17	0		
220	W77429	selenium binding protein 1	1	liver	liv, col, kidn	-3.1	3.3	4	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	-2.8	1760	259.08	0	
171	AA647336	cytochrome P450, steroid inducible 3a11	1	intestine	liv, int	-4.6	6.9	3.3	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	-2.6	81.06	117.34	0		
175	AA237986	cytochrome P450, 3a25	1	intestine	liv, int	-2.1	3	-1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	2.6	2847	520.375	0	
186	AA087441	RIKEN cDNA 0610011L04, gene	1	kidney	liv, int	-1.4	1.7	1.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	477	0	
206	AA822117	UDP-glucuronosyltransferase 1 family, member 1	1	liver	blad, kidn	-1.1	-1.9	-1.3	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	-3.5	109.2	345.03	0
21	AA822098	apolipoprotein A-I	2	intestine; colon	liv, int, col	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	41.21	0

TABLE 3



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Description	ID	spl	panc	liver	stom	Intest	colon	brain	lung	Blad	Kdny	pl-ut	Breast	Remarks
AA242102 villin	MG225.GS.A-G.021AAAQ0F8												2.4	a specific marker expressed in tumors of the digestive tract, renal proximal tubules, and hepatic bile duct, PMID: 11717541
A1046562 lactate dehydrogenase 3, C chain, sperm specific	MG225.GS.A-G.0217AAR9E3												2.4	Expressed in many cancers PMID: 12438276
A1326499 epidermal growth factor	MG225.GS.A-G.0211AAR3H3									3.9			2.3	EGF, for review PMID: 12422312
AA469630 choline kinase	MG225.GS.A-G.0210AAQJF5				3.1				2.3	2.0		2.2	2.1	Elevated in breast, lung, colorectal, and prostate tumors, PMID: 12176020
W14224 N-myc downstream regulated 1	MG225.GS.A-G.0210AAR8B11												2.1	Overexpressed in skin hyperplasia, PMID: 11746822, p53 responsive gene ?, androgen dependent gene
AA270885 parvalbumin	MG225.GS.A-G.0218AAR4C9						2.0					2.3	-1.2	Marker of specific tumors, (like chromophobe renal carcinoma, PMID: 11504835) by expression on specific parental cell types, Neuroendocrine marker (PMID: 127902679)
AA760002 beta-glucuronidase structural, Beta-glucuronidase precursor	MG225.GS.A-G.021WAAP4G5										2.4	1.1169 5*	-1.1	Elevation in poor differentiation colorectal tumor, PMID: 11717961, in pancreatic cancer PMID: 10961372,
W16059 glutathione S-transferase omega 1	MG225.GS.A-G.0217AAR9C6										2.2	-1.0	1.0	upregulated in invasive human breast cancer lines, PMID: 12091914

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AI425345 17-beta dehydrogenase 9	MG225.GS.A- G.021HAAQ1C2			1.31173 3.0 +	1.0	1.41016 1.0 +-	1.5526 4+	1.106 11+	1.0531 +	1.1385 1+	1.0539- 9+	1.13526+	Expression elevated in epithelial ovarian tumors PMID: 8729977
AA027607 17-beta dehydrogenase 2	MG225.GS.A- G.021UAAR2A2			1.68774 1.3 +		1.29025 1.0 +-	1.2834 8+	1.023 53+		1.3	1.2	1.2	Inversed correlation with breast cancer progression PMID: 11731426 (type II decrease and type I increase high risk)
AA210481 clusterin	MG225.GS.A- G.021TAAQ1A1	3.0		-2.0	-1.8	-1.4	1.3	-1.1	1.1	1.4	-1.2	1.2	clusterin is a marker of anaplastic large cell lymphoma PMID: 12429802, expressed in human pancreatic cancer PMID: 12370533, breast carcinoma PMID: 10934144
AA790398 ribonuclease pancreatic	MG225.GS.A- G.021PAAQQC11	2.3		-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1	Expression elevated in pancreatic adenocarcinoma and preneoplastic lesions PMID: 11002220

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Table 4

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Prostate	Fold	Fold	Relation to cancer
AA982842 melanoma-inhibitory-activity protein, cartilage derived retinoic acid sensitive protein (Cdrap), (MIA/CD-RAP)	2.5		correlate with the progression of malignant melanoma and chondrosarcoma, PMID: 11918321
AA107401 prostate stem cell antigen, PSCA	2		overexpressed in human prostate cancers, PMID: 12172427
AI853055 Cystatin E (cystatin M)		4.7	Expressed in neoplastic epidermis PMID: 12100189
M31885 Inhibitor of DNA binding 1, DNA-binding protein inhibitor ID-1			Expression elevated in nasopharyngeal carcinoma cells. PMID: 12203366, Overexpressed in prostate cancer PMID: 11992094, overexpressed in medullary thyroid cancer PMID: 1111462
AW122874 PCNA		3.2	Well known
apolipoprotein D	3	2	Prostate tumor marker 9649289
Secretory leukoprotease inhibitor gene		7	Ovarian cancer candidate marker 11358798
glutathione peroxidase 3 (plasma)	2	2.5	Ovarian cancer candidate marker 11358798
apolipoprotein E	25	25	Ovarian cancer candidate marker 11358798
prostaglandin D2 synthase (21kD, brain)	12	14	Meningioma marker 11266526
glutamyl aminopeptidase	28	5.2	Elevated in var. cervical tumors 10838501
carbonic anhydrase VI	5.9	2.6	Target for anti-cancer treatment 11310605

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TABLE 4

SEQ ID	mouse EST description	corresponding human or mouse consensus sequence (as in Figure 5)	max. specific increase of	max. tissue expression														max. signal
				intest.	stom.	liver	spleen	panc.	kidney	bladder	colon	lung	brain	testis	ovary	uterus	ovary	
1	161	AA516927_sphingosine-phosphate lyase 1 (SGPL1), mRNA	intestine	1.3	1.4	2.0	3.1	1.4	2.1	1.6	1.9	1.2	1.1	1.6	2.2	2.4	2.1	1.6
2	47	AI552219 ESTs	stomach; bladder	1.1	1.1	1.3	1.3	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
3	252	AA080175 claudin_8	mammary gland	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
4	98	W57281 Mest-linked imprinted transcript 1	brain	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
5	94	AA967857 brain protein	brain	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
6	104	AA051041 potassium voltage-gated channel, subfamily Q, member 2	brain	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
7	122	AB373053 forkhead box D3	colon	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
8	115	AA034678 rho-kin	colon	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
9	118	AI323308 interleukin 3 receptor, alpha chain	colon	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
10	116	AA518917 slug, chicken homolog	colon	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
11	128	AA546945 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	colon	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
12	189	AA450534 glutamine synthetase pseudogene 1	kidney	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1

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13	235	AA415254_glutamate_oxaloacetate_transaminase_1_soluble	Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA cr: gi-4504066// [Human_jongleur_201102.747.C1]	liver	brain	-3.2	-4.3	-2.3	-2.5	1.4	-1.4	-1.4	-1.4	-1.1	-1.5	-1.5	-1.8	-3.1	-2.9	1.7	3.2	1.6	1.2	1.4	-1.0	-1.1	-1.7	27.37	857.95	0	
14	269	AA437717_ESTs_Moderately_similar_to_U34531_hypothetical_protein_DK5Zp434P12.1 [H sapi ens]	Homo sapiens cDNA FLJ34227 fis, clone FCBF3023098 si: gi-21749942// [Human_jongleur_201102.cl.16700.singlet]	pancreas	brain	-4.2	-3.4	-1.3	-3.9	-4.9	-2	-0.5	-5	-2.5	-2	-1.0	-3.1	-1.8	-2	-3.3	-2.6	-4.1	5	-4.9	-1.8	-2.3	2.6	132.5	0		
15	262	AA575501_ESTs	v194c08.1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:98334 5; est(identity):gi_2350127_gb_AA575501.1_AA575501	pancreas	brain	-3.8	-2.7	-1.2	-2.7	-4.4	-3.5	-1.6	-1.2	-2.9	-1.6	-2.2	1.1	-4.1	-2.5	-2.7	-3.1	-2.1	-2.2	-4.3	-1.9	-1.5	-2.4	-2.1	22.37	971.83	0
16	263	AA681081_ESTs	vol3h03.x1 Mus musculus cDNA, 3' end as: gi-4602318//clone=IMAGE:1180565 /clone_end-3' /gb=AF593270 /gi=4602318 /ug=Min.71891 /len=546 [gn UC Min#5746181]; m_jongleur(identity):gi_2663221_gb_AA681081.1_AA681081	pancreas	brain	-2.7	-2.5	-1	-2.3	-3.3	-3	-1.4	-1.5	-2.8	-3.3	-2.5	-1.9	-3.1	-2.3	-2.3	-2.2	-1.9	-4.1	-4.2	-1.8	-1.5	-2.4	-2.2	10.85	599.708	0
17	50	AA64603_RIKEN_cDNA_0710001E13_gene	orth Homo sapiens cyclic AMP-regulated phosphoprotein mRNA, complete cds si: gi-6563225// [Human_jongleur_201102.cl.5922.singlet]; h_jongleur(identity):gi_4318633_gb_AA64603.1_AA64603	stomach; brain	brain	-4.2	-1.4	1.3	1.5	1.1	1	1.9	-1.2	1.3	-1.1	-1.1	-1.1	-1.2	2.8	1.1	-4.3	1.1	-1.1	1.1	-1.3	1.2	-1.2	13.8	244.458	2	
18	28	AA231099_needin	Homo sapiens needin (mouse) (NDN), mRNA cr: gi-10800414// [Human_jongleur_201102.11950.C1]	stomach; colon	brain	-2.2	-1.2	2.1	1.5	1.4	1.2	1.3	1.5	-1.1	2.8	-1.9	1.1	2.1	1.1	-1.4	-1.1	-2.5	2	-1.2	1.4	-1.5	-1.5	121.6	140.73	0	
19	337	AA000370_RIKEN_cDNA_4933438K12_gene	Homo sapiens hypothetical gene BC008967 (BC008967), mRNA cr: gi-2430833// [Human_jongleur_201102.7844.C2]	stomach	brain	-4.9	-2.5	1.3	1	-4.7	-1.1	1.3	-1.6	-1.1	-1.7	-1.5	-2.6	-1.4	-1.7	1	-1.4	-1.9	-2	-1.2	-1.7	-1.2	-1.6	42.8	191.47	0	
20	333	AA425572_ESTs_Highly_similar_to_xygiu1 [R. norvegicus]	orth Homo sapiens fasciculation and elongation protein zeta 1 (zygin 1) (FEZ1), transcript variant 1, mRNA cr: gi-17103402// [Human_jongleur_201102.6883.C2]; h_jongleur(identity):gi_4271503_gb_AA425572.1_AA425572	stomach	brain	-4.7	-2.1	1.3	1.1	-1.4	-1.2	1.2	-1.8	-1.2	-1.3	-1.3	-1.5	-1.5	1.8	-1.1	-1.4	-1.7	-1.5	-1.1	-1.4	-1.1	1.4	161.6	102.833	1	
21	357	AA517337_WASP_family_1	Homo sapiens WAS protein family, member 1 (WASP1), mRNA cr: gi-4507912// [Human_jongleur_201102.1128.C1]	stomach	brain	-1.3	-1.4	1.7	1.6	1	1.5	1.2	1.4	1	1.1	-1.3	-1.1	-1.2	1	1.2	-1.1	-1.3	1.2	1	1.1	-1.2	1.91	546.833	1		
22	309	AA498760_syntaxin_binding_protein_1	ng45a05.s1 Homo sapiens cDNA 3' end cr: gi-2265371//clone=IMAGE:937712 /clone_end-3' /gb=AA524447 /gi=2265375 /ug=Hs.407835 /len=540 [Human_jongleur_201102.592.C2]	stomach	brain	-1.7	-1.5	1.6	1.4	1	1.4	-1.5	1.1	-1.4	1	-1.1	1.1	1	1	-1.4	-1.1	-1.7	-1.5	-1.4	-1.3	-1.5	-1.8	20.33	737.333	0	
23	305	AA588981_Mus_musculus_brain_cDNA_clone_MNCh-1820	Homo sapiens, Similar to expressed sequence A1415388, clone IMAGE:5734009; mRNA, partial cds cr: gi-22477646//cds=(0,1754) /gb=BC036812 /gi=22477646 /ug=Hs.404915 /len=3000 [Human_jongleur_201102.12931.C2]	stomach	brain, blood	-1.6	-1.7	1.5	1.4	-1.3	-1.1	-1.3	1.2	-1.3	-1.3	-1.3	-1.1	-1.4	1	1.5	-1.3	-1.6	1.2	-1.4	-1.3	-1.1	1.89	561	0		
24	155	AA656394_RIKEN_cDNA_1110025J15_gene	Homo sapiens cDNA FL110456 f6, clone NT2RP1001395 cr: gi-7022498// [Human_jongleur_201102.9088.C2]	intestine	brain, kidney	1.3	-1.2	-2.6	-3.4	-1.3	-1.4	-4.1	-5.9	1.2	-2.3	-1.5	-2.1	-1.7	-1.9	1	-1.6	-1.6	1	-1.4	-1.2	-1.1	163.6	361.04	0		

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67	215	W99034 ESTs	orth qc5h03.x1 Soares_pregnant_uterus_NB4PU Homo sapiens cDNA clone IMAGE:172005.3; est(identity):gi_1428963_gb_W99034.1_W99034	liver	liv, col	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4	31.5	31.6	31.7	31.8	31.9	32.0	32.1	32.2	32.3	32.4	32.5	32.6	32.7	32.8	32.9	33.0	33.1	33.2	33.3	33.4	33.5	33.6	33.7	33.8	33.9	34.0	34.1	34.2	34.3	34.4	34.5	34.6	34.7	34.8	34.9	35.0	35.1	35.2	35.3	35.4	35.5	35.6	35.7	35.8	35.9	36.0	36.1	36.2	36.3	36.4	36.5	36.6	36.7	36.8	36.9	37.0	37.1	37.2	37.3	37.4	37.5	37.6	37.7	37.8	37.9	38.0	38.1	38.2	38.3	38.4	38.5	38.6	38.7	38.8	38.9	39.0	39.1	39.2	39.3	39.4	39.5	39.6	39.7	39.8	39.9	40.0	40.1	40.2	40.3	40.4	40.5	40.6	40.7	40.8	40.9	41.0	41.1	41.2	41.3	41.4	41.5	41.6	41.7	41.8	41.9	42.0	42.1	42.2	42.3	42.4	42.5	42.6	42.7	42.8	42.9	43.0	43.1	43.2	43.3	43.4	43.5	43.6	43.7	43.8	43.9	44.0	44.1	44.2	44.3	44.4	44.5	44.6	44.7	44.8	44.9	45.0	45.1	45.2	45.3	45.4	45.5	45.6	45.7	45.8	45.9	46.0	46.1	46.2	46.3	46.4	46.5	46.6	46.7	46.8	46.9	47.0	47.1	47.2	47.3	47.4	47.5	47.6	47.7	47.8	47.9	48.0	48.1	48.2	48.3	48.4	48.5	48.6	48.7	48.8	48.9	49.0	49.1	49.2	49.3	49.4	49.5	49.6	49.7	49.8	49.9	50.0	50.1	50.2	50.3	50.4	50.5	50.6	50.7	50.8	50.9	51.0	51.1	51.2	51.3	51.4	51.5	51.6	51.7	51.8	51.9	52.0	52.1	52.2	52.3	52.4	52.5	52.6	52.7	52.8	52.9	53.0	53.1	53.2	53.3	53.4	53.5	53.6	53.7	53.8	53.9	54.0	54.1	54.2	54.3	54.4	54.5	54.6	54.7	54.8	54.9	55.0	55.1	55.2	55.3	55.4	55.5	55.6	55.7	55.8	55.9	56.0	56.1	56.2	56.3	56.4	56.5	56.6	56.7	56.8	56.9	57.0	57.1	57.2	57.3	57.4	57.5	57.6	57.7	57.8	57.9	58.0	58.1	58.2	58.3	58.4	58.5	58.6	58.7	58.8	58.9	59.0	59.1	59.2	59.3	59.4	59.5	59.6	59.7	59.8	59.9	60.0	60.1	60.2	60.3	60.4	60.5	60.6	60.7	60.8	60.9	61.0	61.1	61.2	61.3	61.4	61.5	61.6	61.7	61.8	61.9	62.0	62.1	62.2	62.3	62.4	62.5	62.6	62.7	62.8	62.9	63.0	63.1	63.2	63.3	63.4	63.5	63.6	63.7	63.8	63.9	64.0	64.1	64.2	64.3	64.4	64.5	64.6	64.7	64.8	64.9	65.0	65.1	65.2	65.3	65.4	65.5	65.6	65.7	65.8	65.9	66.0	66.1	66.2	66.3	66.4	66.5	66.6	66.7	66.8	66.9	67.0	67.1	67.2	67.3	67.4	67.5	67.6	67.7	67.8	67.9	68.0	68.1	68.2	68.3	68.4	68.5	68.6	68.7	68.8	68.9	69.0	69.1	69.2	69.3	69.4	69.5	69.6	69.7	69.8	69.9	70.0	70.1	70.2	70.3	70.4	70.5	70.6	70.7	70.8	70.9	71.0	71.1	71.2	71.3	71.4	71.5	71.6	71.7	71.8	71.9	72.0	72.1	72.2	72.3	72.4	72.5	72.6	72.7	72.8	72.9	73.0	73.1	73.2	73.3	73.4	73.5	73.6	73.7	73.8	73.9	74.0	74.1	74.2	74.3	74.4	74.5	74.6	74.7	74.8	74.9	75.0	75.1	75.2	75.3	75.4	75.5	75.6	75.7	75.8	75.9	76.0	76.1	76.2	76.3	76.4	76.5	76.6	76.7	76.8	76.9	77.0	77.1	77.2	77.3	77.4	77.5	77.6	77.7	77.8	77.9	78.0	78.1	78.2	78.3	78.4	78.5	78.6	78.7	78.8	78.9	79.0	79.1	79.2	79.3	79.4	79.5	79.6	79.7	79.8	79.9	80.0	80.1	80.2	80.3	80.4	80.5	80.6	80.7	80.8	80.9	81.0	81.1	81.2	81.3	81.4	81.5	81.6	81.7	81.8	81.9	82.0	82.1	82.2	82.3	82.4	82.5	82.6	82.7	82.8	82.9	83.0	83.1	83.2	83.3	83.4	83.5	83.6	83.7	83.8	83.9	84.0	84.1	84.2	84.3	84.4	84.5	84.6	84.7	84.8	84.9	85.0	85.1	85.2	85.3	85.4	85.5	85.6	85.7	85.8	85.9	86.0	86.1	86.2	86.3	86.4	86.5	86.6	86.7	86.8	86.9	87.0	87.1	87.2	87.3	87.4	87.5	87.6	87.7	87.8	87.9	88.0	88.1	88.2	88.3	88.4	88.5	88.6	88.7	88.8	88.9	89.0	89.1	89.2	89.3	89.4	89.5	89.6	89.7	89.8	89.9	90.0	90.1	90.2	90.3	90.4	90.5	90.6	90.7	90.8	90.9	91.0	91.1	91.2	91.3	91.4	91.5	91.6	91.7	91.8	91.9	92.0	92.1	92.2	92.3	92.4	92.5	92.6	92.7	92.8	92.9	93.0	93.1	93.2	93.3	93.4	93.5	93.6	93.7	93.8	93.9	94.0	94.1	94.2	94.3	94.4	94.5	94.6	94.7	94.8	94.9	95.0	95.1	95.2	95.3	95.4	95.5	95.6	95.7	95.8	95.9	96.0	96.1	96.2	96.3	96.4	96.5	96.6	96.7	96.8	96.9	97.0	97.1	97.2	97.3	97.4	97.5	97.6	97.7	97.8	97.9	98.0	98.1	98.2	98.3	98.4	98.5	98.6	98.7	98.8	98.9	99.0	99.1	99.2	99.3	99.4	99.5	99.6	99.7	99.8	99.9	100.0	100.1	100.2	100.3	100.4	100.5	100.6	100.7	100.8	100.9	101.0	101.1	101.2	101.3	101.4	101.5	101.6	101.7	101.8	101.9	102.0	102.1	102.2	102.3	102.4	102.5	102.6	102.7	102.8	102.9	103.0	103.1	103.2	103.3	103.4	103.5	103.6	103.7	103.8	103.9	104.0	104.1	104.2	104.3	104.4	104.5	104.6	104.7	104.8	104.9	105.0	105.1	105.2	105.3	105.4	105.5	105.6	105.7	105.8	105.9	106.0	106.1	106.2	106.3	106.4	106.5	106.6	106.7	106.8	106.9	107.0	107.1	107.2	107.3	107.4	107.5	107.6	107.7	107.8	107.9	108.0	108.1	108.2	108.3	108.4	108.5	108.6	108.7	108.8	108.9	109.0	109.1	109.2	109.3	109.4	109.5	109.6	109.7	109.8	109.9	110.0	110.1	110.2	110.3	110.4	110.5	110.6	110.7	110.8	110.9	111.0	111.1	111.2	111.3	111.4	111.5	111.6	111.7	111.8	111.9	112.0	112.1	112.2	112.3	112.4	112.5	112.6	112.7	112.8	112.9	113.0	113.1	113.2	113.3	113.4	113.5	113.6	113.7	113.8	113.9	114.0	114.1	114.2	114.3	114.4	114.5	114.6	114.7	114.8	114.9	115.0	115.1	115.2	115.3	115.4	115.5	115.6	115.7	115.8	115.9	116.0	116.1	116.2	116.3	116.4	116.5	116.6	116.7	116.8	116.9	117.0	117.1	117.2	117.3	117.4	117.5	117.6	117.7	117.8	117.9	118.0	118.1	118.2	118.3	118.4	118.5	118.6	118.7	118.8	118.9	119.0	119.1	119.2	119.3	119.4	119.5	119.6	119.7	119.8	119.9	120.0	120.1	120.2	120.3	120.4	120.5	120.6	120.7	120.8	120.9	121.0	121.1	121.2	121.3	121.4	121.5	121.6	121.7	121.8	121.9	122.0	122.1	122.2	122.3	122.4	122.5	122.6	122.7	122.8	122.9	123.0	123.1	123.2	123.3	123.4	123.5	123.6	123.7	123.8	123.9	124.0	124.1	124.2	124.3	124.4	124.5	124.6	124.7	124.8	124.9	125.0	125.1	125.2	125.3	125.4	125.5	125.6	125.7	125.8	125.9	126.0	126.1	126.2	126.3	126.4	126.5	126.6	126.7	126.8	126.9	127.0	127.1	127.2	127.3	127.4	127.5	127.6	127.7	127.8	127.9	128.0	128.1	128.2	128.3	128.4	128.5	128.6	128.7	128.8	128.9	129.0	129.1	129.2	129.3	129.4	129.5	129.6	129.7	129.8	129.9	130.0	130.1	130.2	130.3	130.4	130.5	130.6	130.7	130.8	130.9	131.0	131.1	131.2	131.3	131.4	131.5	131.6	131.7	131.8	131.9	132.0	132.1	132.2	132.3	132.4	132.5	132.6	132.7	132.8	132.9
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90	146	AA727521_Mus_musculus_11_kDa_secreted_prot ein_precursor_mRNA_complete_cds	Mus musculus 11 kDa secreted protein precursor, mRNA, complete cds cr: gi-8926323// /cds=(23,361)/gb=AF727844/gf=8926323 /ug=Mm.71887/len=524 [Mouse_jongleur_201102.2852.C1]; m_jongleur(identity):gi_2745228_gb_AA727521, l_AA727521	colon	none	-12	-13	-178	-4	-2.4	-5.5	-3.7	-6.8	-5.3	-4	-5.5	-15	-7.1	-8.7	-12	-7.4	-5.2	-5.6	-9.2	-20	-6	-9.3	-4.9	-8.3	2750	106079	0
91	192	AA762401_EST3	EB513945 RIKEN full-length enriched, 10 days lactation, adult female mammary gland Mus musculus cDNA clone D730048K19; est(identity):gi_2812148_gb_AA762401.1_AA76 2401	kidney	none	-1.6	-1.1	-1.2	-1.1	-1.2	-1	-1	-1.1	-1.2	-1.2	-1.1	-1.5	-1.4	-1.7	-1.1	-1.4	-1.3	-1.3	-1.2	-1.2	-1.2	-1.4	-1.4	-1.4	1255	329312	8
92	221	AA244388_refinoic_acid_early_transcript_gamma	Mus musculus refinoic acid early transcript 1, a pla (Raet 3), mRNA cr: gi-6679616// [Mouse_jongleur_201102.2973.C1]; m_jongleur(identity):gi_1875322_gb_AA244388, l_AA244388	liver	none	1.6	1.8	-1.1	-1	1.2	-1.4	-1.2	1	1.2	-1.1	-1.1	1.2	1.2	1.1	-1.1	1.3	1.2	-1.2	1	1.2	1	1.1	-1	1.1	131	37175	3
93	234	AA260931_peroxisomal_biogenesis_factor_11a	Mus musculus peroxisomal biogenesis factor 11a (Pex11a), mRNA cr: gi-675033// [Mouse_jongleur_201102.1926.C1]; m_jongleur(identity):gi_1897427_gb_AA260931, l_AA260931	liver	none	-1.8	-2.3	-1	-1.4	1.2	1.2	-1.5	-2	1.5	1.1	-1.3	-1.2	-1.2	-1.8	-1.5	-1.8	-1.7	-1.8	1.4	-1.6	-2	1.8	-1.2	1.2	1032	237042	9
94	231	AI509048_ATP-binding_cassette_sub- family_A_(ABC1)_member_8	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 8b (Abca8b), mRNA cr: gi- 23956075// [Mouse_jongleur_201102.9242.C5]; m_jongleur(identity):gi_4407953_gb_AI509048, l_AI509048	liver	none	-1.5	-1.4	-1.4	-1.1	1.2	1.4	-1.4	-1.3	-1.2	-1.7	-1.1	-1.2	1.3	1.1	-1.2	-1.1	1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	323	156125	10
95	224	AA068359_EST3_Weakly_similar_to_A57369_an ilfin - fruit fly [D.melanogaster]	Homo sapiens anilin, actin binding protein (scraps homolog, Drosophila) (ANLN), Mra zm73a01.s1 Homo sapiens cDNA 3' end as: gi- 1578801// clone=IMAGE531240/clone_end=3' /gb=AA071438/gf=1578801/ug=Hs.394289 /len=521 Weakly similar to preprocalikrein (AA 24 to 238) [Homo sapiens] [H.sapiens] [en]UGHS/S481014	liver	none	1.4	1.5	-1.2	-1.2	1	-2.1	1	-1.5	-1	-1.1	1.3	-1.1	-1.3	1.6	1	-1	-1.5	-1.6	-1.9	1	1.1	-1.1	-1.1	-1.1	292	229392	9
96	35	W54620_kalikrein_26	Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930412E23-undclassified transcript, full insert sequence cr: gi-12860486// /cds=UNKNOWN/gb=AK0202029/gf=12860486 /ug=Mm.45194/len=1349 [Mouse_jongleur_201102.13747.C1]; m_jongleur(identity):gi_2663256_gb_AA671177, l_AA671177	lung; bladder	none	-45	-53	-1	-1.1	-1.2	-1.4	-1.1	-1.3	-1.1	-1.3	-1.8	-1.5	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	-1.6	1802	183721	0
97	259	AA671177_RIKEN_cDNA_5930412E23_gene	Mus musculus cardiac responsive adriamycin protein (Crp), mRNA cr: gi-7304832// [Mouse_jongleur_201102.4328.C1]; m_jongleur(identity):gi_2854544_gb_AA792499, l_AA792499	mammary gland	none	1.1	1.5	-1.5	-1.2	-1	-1.1	-1.3	-1.2	-1.1	-1.1	-1.3	-1.3	-1.3	1.1	-1.1	-1.2	-1.2	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	500	236292	1
98	251	AA792499_enlyrin-like_repeat_protein	Mus musculus cardiac responsive adriamycin protein (Crp), mRNA cr: gi-7304832// [Mouse_jongleur_201102.4328.C1]; m_jongleur(identity):gi_2854544_gb_AA792499, l_AA792499	mammary gland	none	-5.5	-4.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	700	276375	0

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120	45	AA155097_ESTs	Homo sapiens hypothetical protein FLJ10563 (FLJ10563), mRNA cr: gi-8922518// [Human_jongleur_201102.3657.C1]	stomach; bladder	panc	12	-1.1	12	1.2	1.2	1.1	-1	1.3	1.1	-1	1.2	1.2*	-1.4	1.4	1	1.3	-4.5	1.5	1.2	1.4	-1.3	1.4	-1.2	2208	102.83	0	
121	11	AA155231_Public_domain_EST	orth qc96g8.x1 Homo sapiens cDNA, 3' end as: gi-3743449// /clone=IMAGE:1722110 /clone_end=3' /gb=AA192240 /gi=3743449 /acc-fis:147175 /len=410 [gnlUGIhds124018]; h_jongleur(identity):gi_1724900_gb_AA155231.1_AA155231	stomach; bladder; placenta/uteru	panc	4	-1.3	12	1.3	-1	1	1.7	1.2	1.5	-1.1	1.3	1.3	-4.4	1.1*	-1.2	1.3	-4.6	1.3	-1.1	1.3	-1.5	1.3	-1.3	2234	120.83	0	
122	54	AA518686_ESTs	orth Homo sapiens KIAA1576 protein (KIAA1576), mRNA cr: gi-24308256// [Human_jongleur_201102.7803.C1]; F_jongleur(identity):gi_2259229_gb_AA518686.1_AA518686	stomach; brain	panc	1	-1.2	12	1.3	1.1	1.4	1	1.6	1	1	1.5	1.3	-1.1	2.4*	1.3	1.3	-1.1	1.2	-1	1.2	-1.2	1.3	-1.3	2815	113.38	0	
123	52	AA604587_ESTs	orth Homo sapiens similar to intermediate filament-like protein MGC-2625 isoform 2; HOM4-TES-103 tumor anti-gen-like; similar to CGI5021 gene product (LOC126917), mRNA cr: gi-22041886// [Human_jongleur_201102.4338.C3]; h_jongleur(identity):gi_4613754_gb_AA604587.1_AA604587	stomach; brain	panc	-1.1	-1.3	12	1.3	1.1	1.4	1	1.2	1.3	-1.1	1.3	-4.2	-1.1*	1.2	1.7	1.1*	1.3	-4.2	1.1	-1.2	1.4	-1.1	1.4	-1.2	377.52	1	
124	51	AA412921_RIKEN_cDNA_492151420_gene	orth Homo sapiens cullin 5 (CUL5), mRNA cr: gi-4503166// [Human_jongleur_201102.833.C1]; F_jongleur(identity):gi_2071477_gb_AA412921.1_AA412921	stomach; brain	panc	1.4	-1	12	1.3	1.1	1.4	1	1.8	-1.1	1.5	1.1	1.1	1.3	-4.3	2.4*	1.1	1.2	-4.3	1.3	1.6	-4	1.6*	1	798	166.488	0	
125	14	AA073925_ESTs	crth AGENCOURT_7941852 NIH MGC_67 Homo sapiens cDNA clone IMAGE:6172385 5'; esq(identity):gi_1595672_gb_AA073925.1_AA073925	stomach; intestine; lung	panc	1	-1.2	14	1.2	1.1	1.2	1.4	1.1	1.2	-1	1.1	1.4	-4.2	1	-1.1	1.6	-4.2	1.1	-1.1	1.3	-1.4	1.3	-1.4	3117	107.94	0	
126	65	AA412879_RIKEN_cDNA_C330006J08_gene	Homo sapiens general transcription factor IIF, polypeptide 2 (beta subunit, 34kD) (GTF2E2), mRNA cr: gi-4504194// [Human_jongleur_201102.311.C1]	stomach; lung	panc	1.4	-1.1	12	1.2	1.1	1.4	1.1	1.2	1.1	1.4	1.1	1.2	1.3	-4.3	1.3*	1	1.1	-4.4	1.2	1.1	1.5	-1.2	1.6*	-1.1	232	706.003	0
127	4	AA481982_EST	v20h04.x1 Mus musculus cDNA, 3' end as: gi-4375208// /clone=IMAGE:904375 /clone_end=3' /gb=AA481982 /gi=4375208 /acc=Mm.33142 /ent=253 [gnlUGMm#5442316]; m_jongleur(identity):gi_4375208_gb_AA481982.1_AA481982	stomach; lung; bladder; placenta/uteru; mammary gland	panc	1.2	-1.2	12	1.2	1.1	1.1	1	1.2	1.3*	-1.1	1.3	1.2*	1.4*	-1.6	1.6	-1.1	1.4*	-4.3	1.3	1.6	-4.5*	1.6*	-1.2	571	605.542	1	
128	7	AA623175_ESTs	Mus musculus SKY-box containing gene 11 (Sox11), mRNA cr: gi-6678064// [Mouse_jongleur_201102.2327.C1]; m_jongleur(identity):gi_252705.1_gb_AA623175.1_AA623175	stomach; lung; bladder; placenta/uteru	panc	1.1	-1.4	12	1.2	1.1	1.1	1	1.3	1.3*	-1.2	1.3	-1.5	-1.2*	1.2	-2	1.2	-1.2	1.1*	-4.9	1.4	-1.2	1.6*	-1.6	-1.3	1037	453.75	1

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129	68	AA210488_ESTs	mo86f04.x1 Mus musculus cDNA, 3' end as: gi-4282215// clone=TMAGE:560479/ clone_end=3'/ gb=A1448385/ gi=4282215/ ug=Mm.30681/ len=277 [gnlUC]Mm#S431182]; m_jongleur(identity):gi_1807735_gb_AA210488_1_AA210488	stomach; mammary gland	punc	1	-4.6	1.3	1.1	1.2	-4.2	1.3	-1.1	-4.4*	-1.6	1	-1.1	1.1	-4.5	1.2	-1.2	1.2	-4.5	1.1	-4.4	1006	769292	1		
130	67	AA617112_ESTs	viz2a05.r1 Mus musculus cDNA, 5' end as: gi-2504317// clone=TMAGE:904496/ clone_end=5'/ gb=AA617112/ gi=2504317/ ug=Mm.31089/ len=352 [gnlUC]Mm#S246802]; m_jongleur(identity):gi_2504317_gb_AA617112_1_AA617112	stomach; mammary gland	punc	1	-4.3	1.3	1.1	1.2	-4.3	1.3	-1.1	-4.1	-1.4	-1.2	1.1	-1.2	1.3	-1.1	1.3	1	1.4	-4.3	1.4	-4.3	1571	408167	1	
131	15	AA623060_RIKEN cDNA_2410124.17_gene	orth Homo sapiens hypothetical protein MGC17347 (MGC17347), mRNA cr: gi-19923876// [Human_jongleur_201102.4895.C1]; m_jongleur(identity):gi_2516936_gb_AA623060_1_AA623060	stomach; placenta/mammary gland	punc	1.3	-4.2	1.3	1.1	1.1	-4.2	1.4*	1	-1.2	1.1	1.2*	-1.4	1.2	1.2	1.4	1.5	1	1.5	-4.3	1.4*	-1.2	1002	853475	1	
132	335	AI604684_RIKEN cDNA_4631422C13_gene	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631422C13:homolog to CDNA FLJ10352 FIS, CLONE NT2RM2001152, full insert sequence cr: gi-12352440// cds=(332,2401)/ gb=AK014527/ gi=12852440/ ug=Mm.30857/ len=2692 [Mouse_jongleur_201102.12200.C1]; m_jongleur(identity):gi_4613851_gb_AI604684_1_AI604684	stomach	punc	1.1	-4.1	1.2	1.1	1.2	1.1	1.5	-1.1	-1.1*	1.2	-4.2	1.5	1	1.3	-1.1	1.3	1.2	1	1.2	-1	1401	104873	1		
133	354	AA510659_ESTs	orth Homo sapiens cDNA: FLJ22823 fis, clone KAlA3974 cr: gi-10439347// gb=AK026476/ gi=10439347/ ug=Hs.398258/ len=1902 [Human_jongleur_201102.11450.C5]; m_jongleur(identity):gi_2248513_gb_AA510659_1_AA510659	stomach	punc	1.1	-4.1	1.1	1.2	1.3	1	1.4	1.2	1.2	1.3*	1.4*	-1.1	1.5	1	1.3	-1.1	1.5	1.1	1.3	-1.1	1.3	1	2074	942403	1
134	355	AA023720_ESTs	mih78b12.r1 Mus musculus cDNA, 5' end as: gi-1487635// clone=TMAGE:457055/ clone_end=5'/ gb=AA023720/ gi=1487635/ ug=Mm.23708/ len=357 [gnlUC]Mm#S56679]; m_jongleur(identity):gi_1487635_gb_AA023720_1_AA023720	stomach	punc	1.1	-1.1	1.2	1.1	1.2	1.1	-1.1	1.4	1.2	-1	-1.1*	1.2	-4.2	1.1	1.3	-1	1.5	4.1*	1.3	-1.2	1.4	1.1	1378	531483	1
135	365	AA450452_RIKEN cDNA_8430430L24_gene	Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430430L24:homolog to HYPOTHETICAL 46.9 KDA PROTEIN, full insert sequence cr: gi-12838160// cds=(63,1325)/ gb=AK018452/ gi=12838160/ ug=Mm.182246/ len=2151 [Mouse_jongleur_201102.17388.C1]; m_jongleur(identity):gi_2164122_gb_AA450452_1_AA450452	stomach	punc	1.1	-1.1	1.2	1.1	1.2	1.1	-1.1	1.5	-1	-1.1*	1.1	-1.2	-1.1	1.3	-4.3	1.1	-1	1.2	-1.2	1.2	-1.1	1346	106117	1	

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[illegible]

148	388	AA269742	RIKEN_cDNA_1110065A22_gene	Homo sapiens similar to Gliadin (LOC222404), mRNA; gi=20473752// [gi20473752 ref XM_169005.1]	stomach	panc	1.1	-4	1.1	1.3	1.3	1.2	1.4	1.1	-1.1	-1.1	1.3	1.1	1.4	1.3	1.1	1.5	1.3	1.3	1.1	1.4	-1	1732	566,458	1		
149	403	AA220774	ESTs	orth nt70b01.x5 Homo sapiens cDNA, 3' end as: gi=5053451// clone=IMAGE925225 /clone_end=3' /gb=AI732338 /gi=5053451 /ug=Hs.105821 /len=558 [gnlUGM#S1425572]; h_jongleur (strong homology); gi_1838594_gb_AA220774.1_AA220774	stomach	panc	1	-12	1.1	1.3	1.3	1.1	-1	1.4	1.1	-1.1	-1	1.2	-1.2	1	1.2	-1.3	1.4	1	1.2	-1.3	1.2	-1.2	2321	800,458	0	
150	390	AI587986	ESTs	vm50h11.y1 Mus musculus cDNA, 5' end as: gi=4597033// clone=IMAGE1001733 /clone_end=5' /gb=AI587986 /gi=4597033 /ug=Mm.31187 /len=330 [gnlUGM#S464186]; m_jongleur (identity); gi_4597033_gb_AI587986	stomach	panc	1.1	1	1.5	1.3	1.3	1.1	1	1.5	1.1	1.2	-1.1	-1.1	1.4	1.1	1.3	-1	1.1	1.3	1.2	-1.1	1.3	-1.2	1377	501,208	2	
151	380	AI596550	leukemia/lymphoma related factor	Mus musculus (leukemia/lymphoma related factor (Lrf), mRNA; cr: gi=6754571// [Mouse_jongleur_201102.3863.C1]; m_jongleur (identity); gi_4605598_gb_AI596550.1	stomach	panc	1.1	-11	1.1	1.3	1.3	1.1	1	1.6	1.1	1.1	1.2	-1.1	1.5	1.1	1.5	-1	1.3	1.1	1.2	-1.2	1.2	-1.2	1407	1082,13	1	
152	424	AA412912	ESTs	BB404618 Mus musculus cDNA, 3' end cr: gi=9224014// clone=C330037B05 /clone_end=3' /gb=BB404618 /gi=9224014 /ug=Mm.230612 /len=313 [Mouse_jongleur_201102.22092.C1]; m_jongleur (identity); gi_2071468_gb_AA412912	stomach	panc	1	-12	1.1	1.3	1.3	1.1	1	1.5	1.1	1.1	1.2	-1.1	1.5	1.1	1.5	-1	1.3	1.1	1.2	-1.1	1.4	-1.2	1969	605,438	1	
153	140	AA824475	ESTs	Homo sapiens similar to RNA polymerase I transcription factor RRN3 (LOC94431), mRNA; gi=22067165// [Human_jongleur_201102.cl.56.single]	stomach	panc	-1.1	1.1	1.3	1.3	1.1	1	1.5	1.1	1.2	1.1	1.6	-1.4	1	1.5	1.1	1.5	1.1	1.2	1.5	1.3	1	1.4	1.1	2074	623,5	2
154	415	AI604192	RIKEN_cDNA_4632433K11_gene	Homo sapiens cDNA FLJ0378 fis, clone NT2RP2004847, weakly similar to ZINC FINGER PROTEIN 135 cr: gi=2276057//  /cds=(5,976) /gb=AK074859 /gi=2276057 /ug=Hs.53996 /len=987 [Human_jongleur_201102.13667.C1]	stomach	panc	1.1	-12	1.1	1.3	1.3	1.1	1	1.5	1.1	-1.1	-1.2	-1.1	-1.1	1.2	1.1	1.2	1	1.4	1.3	1.3	-1.1	1.3	-1.2	1988	605,788	1
155	412	AA268472	RIKEN_cDNA_2410003C20_gene	BB667377 Mus musculus cDNA, 3' end as: gi=16398826// clone=C730006115 /clone_end=3' /gb=BB667377 /gi=16398826 /ug=Mm.105955 /len=706 [gnlUGM#S2255490]; m_jongleur (identity); gi_1906243_gb_AA268472	stomach	panc	1	-1	1.1	1.3	1.3	1.1	1	1.5	1.1	1.2	1.4	1.1	-1.1	1.2	1.3	1.2	1.3	1.3	1.2	-1.1	1.2	-1.2	2018	815,607	1	
156	382	AI464600	ESTs	Human phospholipase D mRNA, complete cds; v770b06.x1 Mus musculus cDNA, 3' end cr: gi=4613514// clone=IMAGE1227803 /clone_end=3' /gb=AI604347 /gi=4613514 /ug=Mm.32372 /len=421 [Mouse_jongleur_201102.12391.C1]; m_jongleur (identity); gi_2729354_gb_AA717080	stomach	panc	1.1	-1.1	1.1	1.3	1.3	1.1	1	1.5	1.1	1.1	1.2	1.4	-1	1.6	1.2	1.4	1.2	1.6	1.2	1.2	-1.1	1.4	-1	1069	618,458	1
157	314	AA717080	ESTs		stomach	panc	1.1	1	1.3	1.3	1.3	1.1	1	1.6	1.1	1.1	1.2	-1.1	1.5	1.1	1.5	-1	1.3	1.1	1.2	1.1	1.3	-1.2	1275	582,333	1	

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186	351	AA210560_Mus_musculus_Similar_to_RIKEN_cDNA_150004IN16_gene_clone_MGC:120666_Mus_musculus_Similar_to_RIKEN_cDNA_150004IN16_gene_clone_MGC:120666_NA_complete cds	Mus musculus RIKEN cDNA 150004IN16 gene (150004IN16RIK), mRNA cr: gi-13383883// [Mouse_jongleur_201102.167.C4]; [m_jongleur(identity):gi_1307816_gb_AA210560.1_AA210560]	stomach	panc	1.1	-1	-2.5	-2.5	-4	1	1.1	-1.2	1.3	1	-1.2	1.1	1.1*	-4.5	1.4	1	1.1	-1.3	1.4	1	1.3	-1.3	1.2	-1	1036	-443.62	2
187	371	AI607675_Mus_musculus_clone_MGC:78651_Mus_musculus_clone_MGC:78651_NA_complete cds	Mus musculus ring finger protein 26 (Rnf26), mRNA cr: gi-24415389// [Mouse_jongleur_201102.9751.C1]; [m_jongleur(identity):gi_4616842_gb_AI607675.1_AI607675]	stomach	panc	1.2	-1.1*	-2.5	-2.5	1.3	1.2	1.3	-1.1	-1.2*	1.2	1.2	-1.2	1.1	1.3	-1.1	1.4	1.2	1.4	-1.1	1.4	-1.1	1.4	1	1769	815.98	0	
188	394	AA265096_ESTs	602390534F1_Mus musculus cDNA, 5' end cr: gi-13053550//_clone-IMAGE:4502337/_clone_end=5'/_gb=BG793664/_gb=13053550/_gb=Mm.23322/_len=1175 [Mouse_jongleur_201102.11055.C1]; [m_jongleur(identity):gi_1901374_gb_AA265096.1_AA265096]	stomach	panc	-1	-1.2	-2.1	-2.1	1.1	1	1.9	-1	1.6	1.2	-1	1.1*	1.3	-1.2	1.2	1.1	1.2	-1.1	1.5	1.2	1.3	-1.2	1.3	-1.1	12.23	365.708	1
189	404	AA727914_ESTs	BB083334_Mus musculus cDNA, 3' end as: gi-16260742//_clone-9330181N11/_clone_end=3/_gb=BB083334/_gi=16260742/_gb=Mm.45351/_len=673 [jmlUCjMm#S1125630]; [m_jongleur(identity):gi_2745621_gb_AA727914.1_AA727914]	stomach	panc	1.3	-1.2	-2.1	-2.1	1.1	1.3	-2	-1	1.4	-1.1	1.1	1.3*	1.4	-1.3	1.1	*	1.5	-4.2	1.5	1.2	1.4	-1.1	1.5	-1.1	1015	501.417	1
190	423	AA204045_Public domain EST	orth AGENCOURT_8877739 Lupski_sciatic_nerve_Homo sapiens cDNA clone IMAGE:6198680 5'; est(identity):gi_1800681_gb_AA204045.1_AA204045	stomach	panc	1.4	-1.3	-2.2	-2.2	1.1	1.1	1.3	-1.1	1.3	-1	1	1.2	1.1*	-1.4	1.2	1.3	1.2	-4.4	1.4	1	1.2	-1.3	1.3	-1.3	90.788	0	
191	435	AA623587_ESTs	orth d121ad8.w1_Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2540054 3'; est(identity):gi_2597463_gb_AA623587.1_AA623587	stomach	panc	-4.1	-1.1	-2.1	-2.1	1	1.3	-2.3	-1.1	1.6	1	-1	1.1*	1.3	-1.2	1.1	-4.1	1.3	-1.2	1.3	1.1	1.4	-1.1	1.4	-1.2	1649	319.958	1
192	410	AA473386_ESTs	vd64f01.r1_Kaowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:805369 5'; est(identity):gi_2201613_gb_AA473386.1_AA473386	stomach	panc	-1	-1.2	-2.2	-2.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.1*	1.3	-1.1	1.2	1.1	1.5	1.1	1.2	-1.1	1.3	-1.2	1.3	-1.2	2194	774.87	1
193	318	AA259871_hypothetical_protein_MNCb-4414	Homo sapiens mRNA for YEA4 protein (YEA4 gene) cr: gi-20387030// [Human_jongleur_201102.27073.C1]	stomach	panc	-1	1	1	1	1.2	1.2	1.2	1.2	1.2	1	-1.1	-4*	1.3	-1.1	1.3	1.2	1.5	1.1	1.4	1.4	1.3	1.1	1.4	1.1	1649	279	1
194	425	AA474374_RIKEN_cDNA_5730408C10_gene	Homo sapiens DKFZP566H073 protein (DKFZP566H073), mRNA cr: gi-14149701// [Human_jongleur_201102.3235.C1]	stomach	panc	1.1	-2.2	-2.2	-2.2	1.1	1.2	1.2	1.2	1.2	1.2	1.2	1.1*	1.3	-1.1	1.3	1	1.1	-4.2	1.2	1.5	1	1.6	1	1138	144.697	0	
195	427	AA607267_Public domain EST	orth Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA cr: gi-14141162// (Human_jongleur_201102.5470.C3); [h_jongleur(identity):gi_2456160_gb_AA607267.1_AA607267]	stomach	panc	1	-1.4	-2.4	-2.4	1.1	1.1	1.4	-1.3	1.5	-1	1.1	1.1*	1.3	-1.4	1.8	-4.2	1.4	-1.3	1.4	-1.1	1.3	-1.3	1.4	-1.1	102.125	1	

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196	369	AA469648_growth_factor_crv1_(S_cerevisiae)-like (augmenter of liver_regeneration)	stomach	panc	4.1	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4	31.5	31.6	31.7	31.8	31.9	32.0	32.1	32.2	32.3	32.4	32.5	32.6	32.7	32.8	32.9	33.0	33.1	33.2	33.3	33.4	33.5	33.6	33.7	33.8	33.9	34.0	34.1	34.2	34.3	34.4	34.5	34.6	34.7	34.8	34.9	35.0	35.1	35.2	35.3	35.4	35.5	35.6	35.7	35.8	35.9	36.0	36.1	36.2	36.3	36.4	36.5	36.6	36.7	36.8	36.9	37.0	37.1	37.2	37.3	37.4	37.5	37.6	37.7	37.8	37.9	38.0	38.1	38.2	38.3	38.4	38.5	38.6	38.7	38.8	38.9	39.0	39.1	39.2	39.3	39.4	39.5	39.6	39.7	39.8	39.9	40.0	40.1	40.2	40.3	40.4	40.5	40.6	40.7	40.8	40.9	41.0	41.1	41.2	41.3	41.4	41.5	41.6	41.7	41.8	41.9	42.0	42.1	42.2	42.3	42.4	42.5	42.6	42.7	42.8	42.9	43.0	43.1	43.2	43.3	43.4	43.5	43.6	43.7	43.8	43.9	44.0	44.1	44.2	44.3	44.4	44.5	44.6	44.7	44.8	44.9	45.0	45.1	45.2	45.3	45.4	45.5	45.6	45.7	45.8	45.9	46.0	46.1	46.2	46.3	46.4	46.5	46.6	46.7	46.8	46.9	47.0	47.1	47.2	47.3	47.4	47.5	47.6	47.7	47.8	47.9	48.0	48.1	48.2	48.3	48.4	48.5	48.6	48.7	48.8	48.9	49.0	49.1	49.2	49.3	49.4	49.5	49.6	49.7	49.8	49.9	50.0	50.1	50.2	50.3	50.4	50.5	50.6	50.7	50.8	50.9	51.0	51.1	51.2	51.3	51.4	51.5	51.6	51.7	51.8	51.9	52.0	52.1	52.2	52.3	52.4	52.5	52.6	52.7	52.8	52.9	53.0	53.1	53.2	53.3	53.4	53.5	53.6	53.7	53.8	53.9	54.0	54.1	54.2	54.3	54.4	54.5	54.6	54.7	54.8	54.9	55.0	55.1	55.2	55.3	55.4	55.5	55.6	55.7	55.8	55.9	56.0	56.1	56.2	56.3	56.4	56.5	56.6	56.7	56.8	56.9	57.0	57.1	57.2	57.3	57.4	57.5	57.6	57.7	57.8	57.9	58.0	58.1	58.2	58.3	58.4	58.5	58.6	58.7	58.8	58.9	59.0	59.1	59.2	59.3	59.4	59.5	59.6	59.7	59.8	59.9	60.0	60.1	60.2	60.3	60.4	60.5	60.6	60.7	60.8	60.9	61.0	61.1	61.2	61.3	61.4	61.5	61.6	61.7	61.8	61.9	62.0	62.1	62.2	62.3	62.4	62.5	62.6	62.7	62.8	62.9	63.0	63.1	63.2	63.3	63.4	63.5	63.6	63.7	63.8	63.9	64.0	64.1	64.2	64.3	64.4	64.5	64.6	64.7	64.8	64.9	65.0	65.1	65.2	65.3	65.4	65.5	65.6	65.7	65.8	65.9	66.0	66.1	66.2	66.3	66.4	66.5	66.6	66.7	66.8	66.9	67.0	67.1	67.2	67.3	67.4	67.5	67.6	67.7	67.8	67.9	68.0	68.1	68.2	68.3	68.4	68.5	68.6	68.7	68.8	68.9	69.0	69.1	69.2	69.3	69.4	69.5	69.6	69.7	69.8	69.9	70.0	70.1	70.2	70.3	70.4	70.5	70.6	70.7	70.8	70.9	71.0	71.1	71.2	71.3	71.4	71.5	71.6	71.7	71.8	71.9	72.0	72.1	72.2	72.3	72.4	72.5	72.6	72.7	72.8	72.9	73.0	73.1	73.2	73.3	73.4	73.5	73.6	73.7	73.8	73.9	74.0	74.1	74.2	74.3	74.4	74.5	74.6	74.7	74.8	74.9	75.0	75.1	75.2	75.3	75.4	75.5	75.6	75.7	75.8	75.9	76.0	76.1	76.2	76.3	76.4	76.5	76.6	76.7	76.8	76.9	77.0	77.1	77.2	77.3	77.4	77.5	77.6	77.7	77.8	77.9	78.0	78.1	78.2	78.3	78.4	78.5	78.6	78.7	78.8	78.9	79.0	79.1	79.2	79.3	79.4	79.5	79.6	79.7	79.8	79.9	80.0	80.1	80.2	80.3	80.4	80.5	80.6	80.7	80.8	80.9	81.0	81.1	81.2	81.3	81.4	81.5	81.6	81.7	81.8	81.9	82.0	82.1	82.2	82.3	82.4	82.5	82.6	82.7	82.8	82.9	83.0	83.1	83.2	83.3	83.4	83.5	83.6	83.7	83.8	83.9	84.0	84.1	84.2	84.3	84.4	84.5	84.6	84.7	84.8	84.9	85.0	85.1	85.2	85.3	85.4	85.5	85.6	85.7	85.8	85.9	86.0	86.1	86.2	86.3	86.4	86.5	86.6	86.7	86.8	86.9	87.0	87.1	87.2	87.3	87.4	87.5	87.6	87.7	87.8	87.9	88.0	88.1	88.2	88.3	88.4	88.5	88.6	88.7	88.8	88.9	89.0	89.1	89.2	89.3	89.4	89.5	89.6	89.7	89.8	89.9	90.0	90.1	90.2	90.3	90.4	90.5	90.6	90.7	90.8	90.9	91.0	91.1	91.2	91.3	91.4	91.5	91.6	91.7	91.8	91.9	92.0	92.1	92.2	92.3	92.4	92.5	92.6	92.7	92.8	92.9	93.0	93.1	93.2	93.3	93.4	93.5	93.6	93.7	93.8	93.9	94.0	94.1	94.2	94.3	94.4	94.5	94.6	94.7	94.8	94.9	95.0	95.1	95.2	95.3	95.4	95.5	95.6	95.7	95.8	95.9	96.0	96.1	96.2	96.3	96.4	96.5	96.6	96.7	96.8	96.9	97.0	97.1	97.2	97.3	97.4	97.5	97.6	97.7	97.8	97.9	98.0	98.1	98.2	98.3	98.4	98.5	98.6	98.7	98.8	98.9	99.0	99.1	99.2	99.3	99.4	99.5	99.6	99.7	99.8	99.9	100.0	100.1	100.2	100.3	100.4	100.5	100.6	100.7	100.8	100.9	101.0	101.1	101.2	101.3	101.4	101.5	101.6	101.7	101.8	101.9	102.0	102.1	102.2	102.3	102.4	102.5	102.6	102.7	102.8	102.9	103.0	103.1	103.2	103.3	103.4	103.5	103.6	103.7	103.8	103.9	104.0	104.1	104.2	104.3	104.4	104.5	104.6	104.7	104.8	104.9	105.0	105.1	105.2	105.3	105.4	105.5	105.6	105.7	105.8	105.9	106.0	106.1	106.2	106.3	106.4	106.5	106.6	106.7	106.8	106.9	107.0	107.1	107.2	107.3	107.4	107.5	107.6	107.7	107.8	107.9	108.0	108.1	108.2	108.3	108.4	108.5	108.6	108.7	108.8	108.9	109.0	109.1	109.2	109.3	109.4	109.5	109.6	109.7	109.8	109.9	110.0	110.1	110.2	110.3	110.4	110.5	110.6	110.7	110.8	110.9	111.0	111.1	111.2	111.3	111.4	111.5	111.6	111.7	111.8	111.9	112.0	112.1	112.2	112.3	112.4	112.5	112.6	112.7	112.8	112.9	113.0	113.1	113.2	113.3	113.4	113.5	113.6	113.7	113.8	113.9	114.0	114.1	114.2	114.3	114.4	114.5	114.6	114.7	114.8	114.9	115.0	115.1	115.2	115.3	115.4	115.5	115.6	115.7	115.8	115.9	116.0	116.1	116.2	116.3	116.4	116.5	116.6	116.7	116.8	116.9	117.0	117.1	117.2	117.3	117.4	117.5	117.6	117.7	117.8	117.9	118.0	118.1	118.2	118.3	118.4	118.5	118.6	118.7	118.8	118.9	119.0	119.1	119.2	119.3	119.4	119.5	119.6	119.7	119.8	119.9	120.0	120.1	120.2	120.3	120.4	120.5	120.6	120.7	120.8	120.9	121.0	121.1	121.2	121.3	121.4	121.5	121.6	121.7	121.8	121.9	122.0	122.1	122.2	122.3	122.4	122.5	122.6	122.7	122.8	122.9	123.0	123.1	123.2	123.3	123.4	123.5	123.6	123.7	123.8	123.9	124.0	124.1	124.2	124.3	124.4	124.5	124.6	124.7	124.8	124.9	125.0	125.1	125.2	125.3	125.4	125.5	125.6	125.7	125.8	125.9	126.0	126.1	126.2	126.3	126.4	126.5	126.6	126.7	126.8	126.9	127.0	127.1	127.2	127.3	127.4	127.5	127.6	127.7	127.8	127.9	128.0	128.1	128.2	128.3	128.4	128.5	128.6	128.7	128.8	128.9	129.0	129.1	129.2	129.3	129.4	129.5	129.6	129.7	129.8	129.9	130.0	130.1	130.2	130.3	130.4	130.5	130.6	130.7	130.8	130.9	131.0	131.1	131.2	131.3	131.4	131.5	131.6	131.7	131.8	131.9	132.0	132.1	132.2	132.3	132.4	132.5	132.6	132.7	132.8	132.9	133.0	133.1	133.2	133.3	133.4	133.5	133.6	133.7	133.8	133.9	134.0	134.1	134.2	134.3	134.4	134.5	134.6	134.7	134.8	134.9	135.0	135.1	135.2	135.3	135.4	135.5	135.6	135.7	135
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204	194	AA822480_ESTs_Weakly similar to retinal short-chain dehydrogenase/reductase retSDR1 [Musculus]	Mus musculus. Similar to hydroxysteroid 17-beta dehydrogenase 11, clone MGC330360 IMAGE:513242, mRNA, complete cds cr: gi-18043883// /cds=(49,963) /gb=BC019427 /gi=18043883 /up=Mm.27300 /cct=1719 [Mouse_jongleur_201102.11619.C1]; m_jongleur(identity)/gi_2892348_gb_AA822480.1_AA822480	liver	panc, liv, int	1.8	2.1	2.2	1.5	4.4	1.1	1.2	1.6	1.4	1.5	2.1	1.5	2.5	1.7	2.2	2.6	2.3	2.2	2.3	2.8	4.6*	5869	925,917	0	
205	76	AA619838_ESTs	AY375328 Mus musculus cDNA, 3' end cr: gi-15412285// /clone=9130023H10 /clone_end=3' /gb=AV375328 /gi=15412285 /up=Mm.27632 /len=641 [Mouse_jongleur_201102.8131.C1]; m_jongleur(identity)/gi_2523714_gb_AA619838.1_AA619838	bladder	panc, liv, stom, col, brain, blad	0.1*	1.1*	1.4*	2.4	1.3*	2.1	2.1	1.2*	1.4*	2.8	3.6*	1.1*	1.2*	1.7*	1.6	1.8	1.4	1.3	1.4	1.1	1.5	2483	315,417	12 *	
206	48	AA002994_ESTs_Moderately similar to No sin flarities to any reported proteins [H sapiens]	Homo sapiens cDNA FLJ34661 fls, clone KIDNE2018989, weakly similar to Homo sapiens mRNA for KARP 1-binding protein 2 (KAB2) si: gi-21750471// [Human_jongleur_201102.61.16099.single]	stomach; brain	panc, stom	1.3	4.3	1.4*	1.7*	1.1	1.2	1.4	1.6	1.4	1.2*	1.2	1.1	2.3*	1.3	1.5	1.7	1.3	1.4	1.1	1.1	1012	714,833	1		
207	87	AA200457_ESTs	ACENECOURT_10389813 Mus musculus cDNA, 5' end as: gi-24032685// /clone=IMAGE:6594852 /clone_end=5' /gb=BU847976 /gi=24032685 /up=Mm.39474 /len=809 [gnlUGM/musS2807038]; m_jongleur(strong homology)/gi_1796661_gb_AA200457.1_AA200457	brain	panc, stom	1.2	1.2	2.1	1.4	1.7*	1.7*	1.8	1.6	1.3	1.1	1.1*	1.4	1.4	2.1	1.3	1.4*	1.6	1.1	1.4	1.1*	1.2	4476	103,339	1	
208	92	AA929596_peptidyl arginine deiminase, type II	Mus musculus peptidyl arginine deiminase, type II (Pdi2), mRNA; mus rs_dna(identity)/gi_3078943_gb_AA929596.1_AA929596	brain	panc, stom, plut	1.3	1.1	2.1	1.3	1.1	1.6	1.4	1.3	1.2	1.3	1.4*	1.1	2.1	1.2	1.3	1.3	1.3	1.2	1.1*	1.2	4.1	3893	64,458	1	
209	336	AA571416_RIKEN cDNA [190004M2]_gene	Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:190004M21; hypothetical protein, full insert sequence cr: gi-12835692// /cds=(1165,1500) /gb=AK004486 /gi=12835692 /up=Mm.22521 /len=1512 [Mouse_jongleur_201102.10923.C1]; m_jongleur(identity)/gi_2346345_gb_AA571416.1_AA571416	stomach	panc?	1	1.1	1.5	1.1	1.2	1.4	1.1	1.5	1.1	1.1	1.3	1.1	1.3	1.4	1.4	1.1	1.1	1.2	1.3	1.1	1.3	4	2393	804	0
210	442	AA823452_ESTs	vp40b1.1.1 Mus musculus cDNA, 5' end as: gi-2893320// /clone=IMAGE:1079133 /clone_end=5' /gb=AA823452 /gi=2893320 /up=Mm.23332 /len=219 [gnlUGM/musS295539]; m_jongleur(identity)/gi_2893320_gb_AA823452.1_AA823452	stomach	panc?	1.3	1.4	1.4	1.6	1.1	1.1	1.1	1.3	1.1	1.2*	1.2*	1.1	1.6	1.1	1.2	1.1	1.4	1.2	1.5	1.4*	4*	990	230,708	10	
211	356	AA683789_siruin_1 (silent mating type information regulation 2, homolog 1 (S. cerevisiae))	orth Homo sapiens cDNA FLJ90324 fls, clone NT2RP2001817, highly similar to Homo sapiens siruin type 1 (SIRT1) mRNA si: gi-22760489// [Human_jongleur_201102.4.652 (1.single)]; m_jongleur(identity)/gi_2670375_gb_AA683789.1_AA683789	stomach	panc?	1.1	1	1.3	1.1	1.2	1.1	1.3	1.1	1.1	1.1	1.2	1.6	1.1	1.2	1.1	1.3	1	1.3	1	1.3*	1	1990	48,25	1	

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212	384	AI549661	RIKEN cDNA_2410044K02_gene	yes61002.yl Beddington mouse embryonic region Mus musculus cDNA clone IMAGE:826275; esi(identity):gi_4482024_gb_AI549661.1_AI549661	stomach	panc?	-4.1	-1.9	2.4	1.5	-1.1	1.2	1.4	-4.2	1.3	-4.2	-1.1	1.7	1.1	-1.4	1.1	-1.2	1.2	-1.3	1.1	-1.1	1.2	-1.3	1.2	-1.2	23.97	68.93	1	
213	406	AI549643	RIKEN cDNA_1300017N15_gene	Homo sapiens nuclear transcription factor, X-box binding 1 (NFX1), transcript variant 1, mRNA cr: gi_22212923.1 [Human_jongleur_201102.12184.C2]	stomach	panc?	1.2	-1.1	2.4	1.6	1	1.1	1.7	-1.3	1.4	-1	-1.1	-1.2	1.4	-1.4	1.3	-1.1	1.3	-1.3	1.3	-1.1	1.3	-1.3	1.3	-1.2	22.14	80.75	0	
214	396	AI587825	RIKEN cDNA_0710001D07_gene	Mus musculus adult male brain cDNA, RIKEN full-length enriched library, clone0710001D07:unclonifiable transcript, full insert sequence cr: gi_12833293.1/ cds=UNKNOWN/gb=AK002941/gi=12833293 /ug=Mm.45160/len=1133 [Mouse_jongleur_201102.13739.C1]; m_jongleur(identity):gi_4596872_gb_AI587825.1	stomach	panc?	-1.2	-1.4	2.4	1.6	-1.3	1.1	1.8	-1.5	1.2	-1.2	-1.3	-1.1	-1.1	-1.4	1.3	-1.1	1.3	-1.3	1.3	-1.1	1.3	-1.3	1.3	-1.2	22.14	80.75	0	
215	179	AA013726	cathpsin_J	Human cathepsin L gene, complete cds cr: gi: 809233.1 [Human_jongleur_201102.11345.C6]	intestine	pl/at	-3.3	-3.1	-2.7	-1.6	-1.5	1.1	-1.7	-1.2	-1.2	-1.2	-1.1	-1.0	-1.5	-1.0	-1.4	-1.0	-2.4	-2.7	2.4	-1.2	-1.5	-2.0	1.1	2.0	1.1	0		
216	255	AA220024	trophoblast specific protein	Mus musculus trophoblast specific protein alpha (Tbpa), mRNA cr: gi_6678404.1 [Mouse_jongleur_201102.3553.C2]; m_jongleur(identity):gi_1834142_gb_AA220024.1	transitory gland	pl/at	-1.6	-2.3	-1.4	-2.7	-1.1	-1.7	-1.2	-0.8	-0.4	-1.0	-0.2	-0.5	-1.2	-0.1	-0.4	-0.5	-1.1	-1.3	-1.4	-1.5	-1.6	-1.7	-1.8	-1.9	-2.0	3.0	0.3	0
217	81	AA106071	hemoglobin_beta adult major chain	[Human messenger RNA for beta-globin	brain	sp1	5.1	10.7	-5.4	-4.7	-1.1	-5.7	-4.6	-0.8	-0.4	-1.0	-0.2	-0.5	-1.2	-0.1	-0.4	-0.5	-1.1	-1.3	-1.4	-1.5	-1.6	-1.7	-1.8	-1.9	-2.0	3.0	0.3	0
218	82	AA060763	hemoglobin_beta adult major chain	[Human messenger RNA for beta-globin	brain	sp1	5.1	10.7	-5.4	-4.7	-1.1	-5.7	-4.6	-0.8	-0.4	-1.0	-0.2	-0.5	-1.2	-0.1	-0.4	-0.5	-1.1	-1.3	-1.4	-1.5	-1.6	-1.7	-1.8	-1.9	-2.0	3.0	0.3	0
219	83	W15809	hemoglobin_beta adult major chain	[Human messenger RNA for beta-globin	brain	sp1	5.1	10.7	-5.4	-4.7	-1.1	-5.7	-4.6	-0.8	-0.4	-1.0	-0.2	-0.5	-1.2	-0.1	-0.4	-0.5	-1.1	-1.3	-1.4	-1.5	-1.6	-1.7	-1.8	-1.9	-2.0	3.0	0.3	0
220	85	AI529513	ESTs, Moderately similar to F76L_MOUSE_6PF-2-K/FRU-2.6-PZASE LIVER ISOZYME [M.musculus]	Moderately similar to F261_MOUSE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase; Fructose-2,6-bisphosphatase] [M.musculus] as: gi_15714162.1/603360763F1 Mus musculus cDNA, 5' end /clone=IMAGE:5368118 /clone_end=5' /gb=B1737149 /gi=15714162 /ug=Mm.132391 /len=896. [jmlUG/Mm#S2184367]; m_jongleur(identity):gi_4443648_gb_AI529513.1	brain	sp1	4.4	2.7	-2.5	-2.8	-1.5	-1.9	-1.2	-2.7	-2.8	-1.4	-1.2	-1.8	1.2	-1.1	-2.4	-2.5	-2.6	-2.7	-2.8	-2.9	-3.0	-3.1	-3.2	-3.3	-3.4	-3.5	1.0	0
221	96	AI605734	sepin_3	Homo sapiens sepin 3 (SEPT3), transcript variant A, mRNA cr: gi_22035517.1 [Human_jongleur_201102.12125.C2]	brain	sp1	1.1	2.7	-2.5	-2.8	-1.5	-1.9	-1.2	-2.7	-2.8	-1.4	-1.2	-1.8	1.2	-1.1	-2.4	-2.5	-2.6	-2.7	-2.8	-2.9	-3.0	-3.1	-3.2	-3.3	-3.4	-3.5	1.0	0
222	97	AA289586	protein kinase C_beta	Homo sapiens mRNA; cDNA DKFZp76110720 (from clone DKFZp76110720) /gb=AL833252 /gi=21733885 /ug=Hs.349845 /len=3602. Highly similar to KPC1_HUMAN Protein kinase C, beta-type (PKC-beta-1) [H.sapiens] cr: gi=21733885.1 Homo sapiens mRNA; cDNA DKFZp76110720 (from clone DKFZp76110720) /gb=AL833252 /gi=21733885 /ug=Hs.349845 /len=3602. [Human_jongleur_201102.20069.C1]	brain	sp1	1.1	2.7	-2.5	-2.8	-1.5	-1.9	-1.2	-2.7	-2.8	-1.4	-1.2	-1.8	1.2	-1.1	-2.4	-2.5	-2.6	-2.7	-2.8	-2.9	-3.0	-3.1	-3.2	-3.3	-3.4	-3.5	1.0	0

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[illegible]

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SEQ ID NO	mouse EST description	corresponding human or mouse consensus sequence (see Fig. 5)	spl	panc	liv	stom	int	col	br	lung	blad	kidn	p/ut	PL-11B BDE <sub>Enr</sub>	PL-11B BDE <sub>Enr</sub>
	<b>Breast</b>														
290	AA107035_guanylate_cyclase_activator_2b_(retina)	orth Homo sapiens guanylate cyclase activator 2B (uroguanylin) (GUCA2B), mRNA cr: gi-6005773// [Human_jongleur_201102.1395.C1] ; h_jongleur(strong homology);gi_1657021_gb_AA107035.1_AA107035	-12	-13	1.1	-1.1	1.1	1.2	-1.5	-1.9	-1.2	1.2	-1.3	6.5	
97	AA671177_RIKEN_cDNA_5930412_E23_gene	see Table 5	-13	-16	1.1	-1.1	-1.1	1.1	1.2	-1.1	-1.0	-1.3	-1.1	5.8/2.9	
291	W17866_uterine-specific_proline-rich_acidic_protein	Mus musculus uterine-specific proline-rich acidic protein (Upa), mRNA cr: gi-6678510// [Mouse_jongleur_201102.4046.C1] ; m_jongleur(identity);gi_1292452_gb_W17866.1_W17866	-14	-17	-1.2	-1.4	-1.2	1.1	-2.5	-1.0	-1.3	-1.3	-1.5	1.9	
292	AA242201_serine_protease_inhibitor_Kazal_type_3	Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), mRNA cr: gi-4507178// [Human_jongleur_201102.8585.C1]	1.5	1.8	-1.4	1.1	2.5	-1.0	-1.8	1.2	-9.2	-1.0	1.0	2.5	
293	AA242102_villin	Homo sapiens villin 1 (VIL1), mRNA cr: gi-6005943// [Human_jongleur_201102.1802.C1]	1.1	-1.4	-1.4	1.3	1.3	1.3	-1.6	-1.3	1.6	1.2	1.3	2.1	
294	A1046562_lactate_dehydrogenase_3_C_chain_sperm_specific	orth 7p07c08.x1 Homo sapiens cDNA 3' end as: gi-11448929// /clone=IMAGE:3644943 /clone_end=3' /gb=BF436690 /len=548 Weakly similar to DEHULC L-lactate dehydrogenase (EC 1.1.1.27) chain X - human [H.sapiens] [gnlUC]Hs#S2910008]; h_jongleur(identity);gi_3294849_gb_A1046562.1_A1046562	1.2	-1.6	-1.3	1.5	1.3	1.3	-2.2	-1.0	-1.1	-1.0	1.3	2.1	
	<b>placenta/uterus</b>														

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80	W36921_dermilune_cell_and_parotid_protein	see Table 5	-1.1	-1.2	-1.1	-1.1	-1.4	-1.4	-1.1	-1.1	-1.4	-1.1	-1.1	-1.1
79	A1326499_epidermal_growth_factor	see Table 5	1.3	-1.4	-1.2	1.2	-1.1	-1.4	-1.1	-1.4	1.5	1.3	1.2	1.2
297	AA466852_cysteine_rich_protein_61	orth Homo sapiens cysteine-rich angiogenic inducer, 61 (CYR61), mRNA cr: gi-4504612// [Human_jongleur_201102.8413.C2] h_jongleur(identity):gi_2192992_gb_AA466852.1_AA466852	1.1	1.1	-1.1	-1.1	-1.1	-1.0	-1.1	-1.0	-1.0	1.1	1.2	1.2
298	AA612413_chitinase_acidic	Homo sapiens eosinophil chemotactic cytokine (TSA1902), mRNA cr: gi-11141866// [Human_jongleur_201102.2578.C2]	-1.1	-1.3	-1.4	-1.2	-1.1	-1.0	-1.2	-1.2	2.4	1.2	-1.0	-1.0
299	AA445731_heat_shock_protein_cognate_70_testis	orth Homo sapiens heat shock 70kDa protein 1B (HSPA1B), mRNA cr: gi-5579470// [Human_jongleur_201102.8523.C4] h_jongleur(identity):gi_2158414_gb_AA445731.1_AA445731	1.1	1.1	-1.5	-1.2	-1.1	-1.3	-1.8	-1.2	-1.0	1.1	-1.2	1.1
300	AA145895_heat_shock_protein_70_kDa_1	Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA cr: gi-5579469// [Human_jongleur_201102.8523.C2]	1.1	-1.1	-1.0	1.2	-1.8	-1.7	-1.0	1.1	1.1	-1.0	-1.1	-1.1
246	AA067863_RIKEN_cDNA_2310057118_gene	see Table 5	-1.2	1.2	1.4	-1.1	1.2	-1.5	-1.5	1.6	1.1	-1.4	-1.8	-1.8
96	W34620_kallikrein_26	see Table 5	1.2	1.1	-1.1	-1.4	-1.9	-1.2	-1.5	1.1	1.1	-1.1	-1.4	-1.4

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111	5	AA498574_kallikrein_6	see Table 5	1.4	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	1.1	1.0	1.3		
301	6	AA002910_FB1_osteosarcoma_oncogene	orth Homo sapiens cDNA FLJ40060f1s, clone TC0LN2000236, highly similar to P55-C-FOS PROTO-ONCOGENE PROTEIN si: gi-21757114// [Human_jongleur_201102.cl.1192.single]; h_jongleur(identity):gi_1446351_gb_AA002910.1_AA002910	-1.0	-1.3	-1.4	-1.3	-1.1	-2.2844	1.3	1.0	-1.1	-1.0		
302	7	AA433639_heat_shock_protein_cognate_70_testis	Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA cr: gi-5579469// [Human_jongleur_201102.8523.C2]	1.7	1.1	-1.1	1.3	1.2	1.6	-1.5	1.2	1.4	1.5		
		brain		spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
218	1	AA066763_hemoglobin_beta_adult_major_chain	see Table 5	1.3	-1.2	1.4	-4.0	1.1	-4.2	1.1	-1.1	-1.3	1.5	-1.8	-2.0
219	2	W15809_hemoglobin_beta_adult_major_chain	see Table 5	1.5	-1.3	1.2	-2.9	1.3	-3.7	1.4	-1.2	-1.0	1.6	-1.7	-1.6
303	3	W14953_kinesin-associated_protein_3	orth Homo sapiens kinesin-associated protein 3 (KIFAP3), mRNA cr: gi-18105053// [Human_jongleur_201102.11853.C1]; h_jongleur(identity):gi_1537349_gb_W14953.1_W14953	-1.0	-1.0	1.4	-3.2	-1.2	-3.932	1.4	-1.2	-1.2	1.3	-1.5	-1.5
217	4	AA106071_hemoglobin_beta_adult_major_chain	see Table 5	1.3	-1.4	1.2	-3.0	-1.1	-4.3	1.3	1.1	-1.3	1.6	-1.7	-2.0
250	5	A1614738_RIKEN_cDNA_261030111_5_gene	see Table 5	1.3	1.6864	1.1	1.4	1.5	1.2409	1.3	1.4	1.5	1.5	1.5	1.6

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308	7	AA571365_Mus_musculus_MRP56_mRNA_for_mitochondrial_ribosomal_protein_S6_partial_cds	Homo sapiens mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA cr: gi-16554615// [Human_jongleur_201102.8885.C2]	-1.2	-1.1	-1.3	-1.3	-1.3	-2.2	-1.9	-1.2	-1.0	-1.4	-1.3
309	8	AA822473_DNA_segment_Chromosome_8_Bigham_Women's_Genetics_1320_expressed	Homo sapiens D-lactate dehydrogenase (LDHD), mRNA cr: gi-23821028// [Human_jongleur_201102.8179.C1]	-1.0	-1.6	-1.5	-1.0	-1.1	-1.7	-1.7	-1.2	-1.2	-1.2	-1.3
235	9	AA062408_ESTs_Moderately_similar_to_protease_inhibitor_hp131_subunit [H.sapiens]	see Table 5	-1.3	-1.2	-1.1	-1.3	-1.3	-2.0	-1.7	-1.3	-1.2	-1.5	-1.1
239	10	AA871395_Mus_musculus_Similar_to_ectonucleotide_pyrophosphatase/phosphodiesterase_3_clone IMAGE:3495326_mRNA_partial_cds	see Table 5	-1.1	-2.0	-1.3	-1.1	-1.3	-1.3	-1.92074	-1.0	-1.1	-1.0	-1.2
10	11	AA518917_slug_chicken_homolog	see Table 5	-1.6	-2.0	-1.1	-1.2	-1.1	-1.8	-1.0	-1.4	-1.2	-1.8	-1.3
310	12	AA619789_methylenetetrahydrofolate_dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA cr: gi-1369989// [Human_jongleur_201102.3990.C6]	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA cr: gi-1369989// [Human_jongleur_201102.3990.C6]	-1.1	-1.2	-1.4	-1.1	-1.1	-1.7	-1.8	-1.3	-1.1	-1.3	-1.1
36	13	AA529824_fatty_acid_binding_protein_n_2_intestinal	see Table 5	-1.5	-1.5	-1.7	-1.7	-1.1	-1.0	-1.3	-1.4	-1.1	-1.3	-1.1

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34	14	AI550591_RIKEN_cDNA_2010003F 10_gene	see Table 5	1.4	1.1	-4.8	-1.5	1.2	1.2	-1.2	-1.6	-1.3	-1.5	-1.2	-1.1
37	15	AA869173_defensin_related_cryptdin 6	see Table 5	1.2	1.1	-4.2	-1.5	1.4	-1.3	1.5	1.1	1.0	1.0	1.2	1.5
39	16	AA623172_defensin_related_cryptdin 6	see Table 5	-1.0	1.1	-1.1	1.1	1.4	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.5
311	17	AI893944_forkhead_box_G1 1	orth Homo sapiens. Similar to Forkhead-like transcription factor BF 1, clone MGC:33583 IMAGE:4823883, mRNA, complete cds si: gi:23241914// [Human_jongleur_201102.cl.11482. single]. h_jongleur(identity):gi_5599846_gb _AI893944.1_AI893944	-1.7	-1.0	1.7	1.5	1.5	1.1	-1.7	-1.5	-1.1	-1.6	-1.1	-1.1
236	18	AA619953_ESTs_Weakly_similar_to T25027_hypothetical_protein_T20D 3.5_	see Table 5	-1.0	1.2	1.4	1.3	-1.0	-1.5	-1.4	-1.3	-1.2	-1.5	-1.0	-1.0
8	19	AA034678_rhotekin	see Table 5	-2.3	1.0	1.2	-1.0	1.2	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4	-1.4
90	20	AA727521_Mus_musculus_11_kDa_s ecreted_protein_precursor_mRNA_c omplete_cds	see Table 5	1.1	-2.0	-1.4	1.1	1.5	-1.6	1.2	1.1	1.1	1.5	1.2	1.2
71	21	AA822098_apolipoprotein_A-I intestine	see Table 5	-1.9	1.5	1.1	-2.4	1.4	-1.9	-9.0	-1.2	2.1	-2.5	-1.6	-1.6
48	1	AA619407_pancreatitis- associated_protein	see Table 5	1.2	1.0	-1.9	1.2	1.4	-2.4	-1.3	1.0	-1.2	1.3	1.1	1.1

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312	2	AA237986_cytochrome_P450_3a25	Homo sapiens cytochrome P450 variant 3A7 (CYP3A7) mRNA, complete cds si: gi-12082808// [Human_jongleur_201102.c190.sing let]	1.5	-1.2	1.3	-1.1	-1.1	1.2	1.1	1.1	1.2	1.2	-2.2	-1.1	-1.1	1.0	1.1	1.3
31	3	W56983_peripheral_myelin_protein_22_kDa	see Table 5	1.5	1.0390+	1.4	1.1	1.1	1.1	1.1	1.1	1.2	1.2	1.1	1.2	1.1	1.1	1.2	-1.2
290	4	AA107035_guanylate_cyclase_activator_2b (retina)	see Table 5	-1.2	-1.3	1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.2	-1.2	-1.9	-1.5	-1.3	-1.3	-1.3	1.5
53	5	AA110886_aminionless	see Table 5	-1.1	1.06399+	1.1	1.2	1.2	1.2	1.2	1.1	1.1	1.1	1.0	-1.2	-1.1	-1.1	1.5	1.5
314	6	AA109873_RIKEN_cDNA_0610010 F05_gene	Homo sapiens hypothetical protein FLJ10830 (FLJ10830), mRNA cr: gi-8922698// [Human_jongleur_201102.3671.C21]	-1.1	-1.1	1.1	-1.0	-1.0	1.3	1.3	1.3	1.3	1.3	1.0	1.0	1.1	-1.1	1.0	1.0
315	7	A1323162_dipeptidase_1 (renal)	Homo sapiens dipeptidase 1 (renal) (DPEP1), mRNA cr: gi-4758189// [Human_jongleur_201102.8623.C11]	1.3	-1.3	-1.4	1.3	1.3	1.3	1.3	1.3	1.3	1.3	-1.3	-1.5	-1.3	1.0	1.0	-1.3
41	8	AA871838_phospholipase_A2_group_IIA (platelets_synovial_fluid)	see Table 5	-1.1	-1.0	-1.2	1.0	1.0	1.0	1.0	1.0	1.0	1.0	-1.3	-1.9	-1.3	1.3	1.3	1.3
24	9	AA656394_RIKEN_cDNA_1110025J15_gene	see Table 5	1.4	1.3	1.1	-1.4	-1.4	1.4	1.4	1.4	1.4	1.4	-1.1	-1.1	-1.1	-1.2	-1.2	-1.2
304	10	AA656694_cytochrome_P450_2b9_phenobarbital_inducible_type_a	see above	-1.1	-1.4	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.1	-1.3	-1.3	1.1	1.2	1.2
46	11	W15890_guanylate_cyclase_activator_2_intestinal_heatsstable	see Table 5	1.0	1.0	-1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2	-1.1	-1.5	-1.1	-1.0	1.1	1.4

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317	12	A132330_cytochrome_P450_2b13_12 phenobarbital_inducible_type_c	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6 (CYP2B6), mRNA cr: gi-20522261// [Human_jongleur_201102.5324.C1]	1.4	-1.1	1.4	1.0	1.1	1.2	-1.2	1.1	1.4
292	13	AA242201_serine_protease_inhibitor_Kazal_type_3	see Table 5	1.5	1.8	1.4	1.1	1.2	-1.0	-1.0	1.0	1.5
1	14	AA516927_sphingosine_phosphate_lyase_1	see Table 5	1.1	1.1	1.4	1.2	1.3	-1.0	1.3	1.0	-1.0
319	15	AA638765_metallothionein_1	Homo sapiens metallothionein 2 pseudogene 1 (processed) (MT2P1) on chromosome 4	1.0	1.1	1.4	1.2	1.2	-1.3	1.5	-1.9	-1.2
71	16	AA822098_apolipoprotein_A-I	see Table 5	-1.9	-1.5	1.1	-2.4	-2.4	-1.2	-2.1	-2.5	-1.6
295	1	AI549624_RIKEN_cDNA_0610041E09_gene	see above	1.4	1.0	-1.3	1.0	1.1	-1.1	1.6	1.5	1.5
130	2	AA617112_ESTs	see Table 5	1.4	1.4	-1.2	1.3	1.4	1.9	1.3	1.4	1.3
123	3	AI604587_ESTs	see Table 5	1.2	1.3	-1.1	1.3	1.5	1.8	1.3	1.5	1.9
321	4	AA544433_dihydroorotate_dehydrogenase	Homo sapiens dihydroorotate dehydrogenase (DHODH), nuclear gene encoding mitochondrial protein, mRNA cr: gi-16753222// [Human_jongleur_201102.3057.C1]	1.2	1.5	1.0	1.2	1.4	1.1	1.4	1.0	1.7

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324	15	AA146478_M.musculus_mRNA_(3C 10) for IgA V-D-J-heavy chain	Mus musculus, clone MGC.6342 IMAGE:3488305, mRNA, complete cds cr: gi-12805256// [Mouse_jongleur_201102.2422.CBI 8]; m_jongleur(identity):gi_1715876_gb AA146478.L_AA146478	-1.3	1.0	-1.6	-2.0	-2.4	-1.1	-1.4	-1.4	1.5	2.0	1.1	1.1	1.6
325	16	AA158775_protein_tyrosine_phosphatase_receptor-type_M	orth Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA cr: gi-18860903// [Human_jongleur_201102.4361.C1] ; h_jongleur(identity):gi_3691957_gb AA158775.L_AA158775	1.023671	1.1	-1.25924	1.1	1.02178~	1.2	1.3	1.3	1.0	1.1	1.1	1.1	1.3
206	17	AA002994_ESTs_Moderately_similar_to_No_similarities_to_any_reported_proteins [H.sapiens]	see Table 5	1.1	1.0	-1.3	-1.1	-1.26031~	-1.4	1.0	1.0	-1.3	1.2	-1.2	-1.2	-1.0
189	18	AA727914_ESTs	see Table 5	1.6	1.2	-1.1	1.5	-1.12394~	1.7	1.4	1.4	1.8	1.3	1.6	1.6	1.5
101	19	AA588976_ESTs	see Table 5	1.1	1.4	-1.5	1.8	1.17861~	2.1	1.8	1.8	1.9	1.4	1.9	1.9	2.1
199	20	AA162023_ESTs	see Table 5	1.3	1.5	-1.1	1.1	1.33992~	1.3	1.7	1.7	1.8	1.2	1.7	1.8	1.8
125	21	AA073925_ESTs	see Table 5	1.3	1.6	-1.4	2.0	-1.27677~	1.1	1.7	1.7	1.9	1.2	1.7	1.9	1.9
326	22	AA608457_DNA_polymerase_epsilon	gi5453925refNM_006231.1 Homo sapiens polymerase (DNA directed), epsilon (POLE), mRNA	1.1	1.2	-1.4	2.3	1.12103~	-1.9	1.6	1.6	1.4	1.3	1.6	1.6	1.3
165	23	AI551677_ESTs	see Table 5	1.2	1.3	-1.3	1.4	1.00395~	1.0	1.3	1.3	1.5	1.5	1.3	1.3	1.3

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273	24	AA624604_Public_domain_EST	see Table 5	-1.09414~	1.8	-1.1	2.3	2.1	1.4	1.3	1.5	1.1	1.3	1.4
249	25	AI447967_ESTs	see Table 5	1.1	1.7	1.04557+	2.3	1.8	-1.08065~	1.4	1.3	1.5	1.3	1.4
107	26	AA116829_RIKEN_cDNA_2610018 G03_gene	see Table 5	1.1	1.8	-1.5	1.5	1.8	1.2778~	1.5	1.5	1.3	1.5	1.5
129	27	AA210488_ESTs	see Table 5	1.7	1.8	-1.1	2.1	1.5	1.2483~	1.2	1.4	1.4	1.4	1.4
191	28	AA623587_ESTs	see Table 5	1.1	1.3	-1.3	2.4	1.5	-1.10185~	1.2	1.6	1.2	1.5	1.5
131	29	AA623060_RIKEN_cDNA_2410124 L17_gene	see Table 5	1.5	1.5	1.1	2.4	1.8	-1.3	1.8	1.4	1.4	1.4	1.4
281	30	AI551943_ESTs_Weakly_similar_to JC2378_acetyl-CoA_C- acetyltransferase [Hsapiens]	see Table 5	1.2	1.1	-1.4	2.4	1.3	1.05496~	1.4	1.4	1.3	1.3	1.4
267	31	AA470284_serine/threonine_kinase_5	see Table 5	1.1	1.9	-1.3	2.4	1.3	1.3	1.5	1.4	1.2	1.2	1.3
126	32	AA412879_RIKEN_cDNA_C330006J 08_gene	see Table 5	1.8	1.8	-1.0	2.4	1.2	-1.3	1.1	1.4	1.5	1.5	1.5
106	33	AA607983_zinc_finger_protein_101	see Table 5	1.3779+	1.5	-1.32014+	2.4	1.5	1.1254~	1.4	1.4	1.3	1.4	1.4
250	34	AI614738_RIKEN_cDNA_261030111 5_gene	see Table 5	1.3	1.08619	1.1	2.4	1.5	1.2409~	1.5	1.4	1.5	1.5	1.5

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64	AA881013_cytochrome_p430_2c37	see Table 5	1.0	-4.1	2.8	1.1	1.6	1.5	-1.2	-2.6	1.0	1.1	-1.1	1.5
329	AI507919_alcohol_dehydrogenase_1, complex	Human mRNA for liver alcohol dehydrogenase (EC 1.1.1.1) gamma 2 subunit from ADH3 locus sr: gi-28403111 [Human_jongleur_201102.cl2404.sif.nglet]	1.2	-4.2	2.5	1.4	-4.2	1.3	-1.0	-1.4	1.1	1.1	-1.3	-1.3
65	AI52452_solute_carrier_family_27_(fatty_acid_transporter), member_5	see Table 5	1.2	1.3	2.6	1.0	1.0	-1.0036-	-1.7	-1.7	1.1	1.0	1.3	1.2
330	AA474336_synaptonemal_complex_protein_3	orth Homo sapiens synaptonemal complex protein 3 (SYCP3), mRNA cr: gi-2423357911 [Human_jongleur_201102.4259.C3] ; h_jongleur(strong homology)gi_2202563_gb_AA474336.1_AA474336	-2.8	1.2	2.6	1.4	1.5	2.74113-	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
331	AA237317_solute_carrier_family_2_(facilitated_glucose_transporter), member_2	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2), mRNA cr: gi-455785011 [Human_jongleur_201102.11033.C1]	1.0	1.21261+	2.7	1.1	1.4	1.71211-	2.06124+	1.30389+	1.35560+	1.0	1.33801+	1.39713+
319	AA638765_metallothionein_1	see above	1.0	1.1	2.7	1.2	1.4	1.6	1.2	-1.6	-1.3	1.5	-1.9	-1.2
56	AA162217_pre-B-cell_colony-enhancing_factor	see Table 5	1.2	-4.2	2.7	1.0	1.1	1.0	1.0	1.0	-4.1	1.0	1.0	1.0
245	AA274023_apoptosis_inhibitory_6	see Table 5	1.30984+	1.01923+	2.7	1.0003+	1.01434+	-1.52171-	-1.07118+	1.01954+	1.07526+	1.15311+	1.35964+	1.34636+

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243	14	AA543982_interleukin_1_receptor_ty pc_1	see Table 5	-1.00156+	-1.72344+	2.4	1.14256+	-1.0782+	-1.37095~	1.46047+	1.30476~	1.0216+	1.0616+	1.1	-1.09458+
333	15	AA245848_hydroxysteroid_dehydrog enase-3_delta<S>-3-beta	Homo sapiens hydroxy-delta-5- steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2), mRNA	1.5	-1.3	2.4	-1.2	1.2	-1.53338-	-1.5	-1.3	1.2	1.2	-4.1	1.2
76	16	AA760070_Mus_musculus_iracygly cerol_hydrolase_mRNA_complete_cd	see Table 5	1.2	-1.4	2.4	1.1	1.1	1.4	-1.1	1.2	-1.5	1.1	-4.1	-1.3
334	17	AA027607_hydroxysteroid_17- beta_dehydrogenase_2	Homo sapiens hydroxysteroid (17- beta) dehydrogenase 2 (HSD17B2), mRNA cr. gi-4504502// [Human_jongleur_201102.518.C1]	1.3	-1.3066+	2.4	1.3	1.48714+	-1.29025~	-1.28348+	-1.03351+	1.3	1.3	-4.2	1.2
28	18	A1789976_fatty_acid_Coenzyme_A_li gase_long_chain_2	see Table 5	1.0	-1.4	2.4	1.0	-1.0	-1.2	-1.6	-1.2	-1.1	1.2	1.5	-1.4
48	1	AA619407_pancreatitis- associated_protein	see Table 5	1.7	1.3	1.9	1.2	4.4	2.4	-1.1	-1.5	1.0	-1.2	1.3	1.1
335	2	AA062401_TATA_box_binding_prot ein_(TBP)- associated_factor_RNA_polymerase_ II_S_150kD	orth Homo sapiens, Similar to TATA box binding protein (TBP)- associated factor, RNA polymerase II, S, 150kD, clone IMAGE:3636799, mRNA cr. gi- 15559581// [Human_jongleur_201102.11703.C2 ]; h_jongleur(identity)gi_1556203_gb AA062401.1 AA062401	1.2	1.4	1.1	-1.5	-1.8	1.4	1.4	-1.4	1.1	1.1	-1.6	1.2
226	3	AA210481_clusterin	see Table 5	1.1	1.0	1.2	-2.0	-1.8	-1.4	1.3	-1.1	1.1	1.4	-1.2	1.2

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		AA437717_ESTs_Moderately_similar_to_T34531_hypothetical_protein_D_KFZp434P1215.1 [H.sapiens]	see Table 5	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pl/ut	mam
14	4	splecu		-1.2	-2.4	-1.2	1.1	1.4	-1.3	1.1	-1.2	-1.3	1.1	-1.1	1.1
116	1	AA821884_amyase_2_pancreatic	see Table 5												
336	2	AI386058_serum_albumin_variant	Homo sapiens albumin (ALB), mRNA cr: gi-8392890// [Human_jongleur_201102.252.C13]	1.1	1.1	-1.2	-2.8	-32.0	-4.0		-1.2	-4.4	-1.1	-1.1	-1.2
248	3	AA822106_ESTs_Weakly_similar_to_CO8A_HUMAN_COMPLEMENT_COMPONENT_C8_ALPHA_CHAIN_PRECURSOR [H.sapiens]	see Table 5	1.9	-1.7	2.7	1.1	-1.1	-1.3	-1.3	-33.1	-1.4	-1.5	-1.9	-2.9
337	4	AA237793_rat_regenerating_islet-derived_mouse_homolog_1	Homo sapiens regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein) (REG1A), mRNA cr: gi-4506470// [Human_jongleur_201102.658.C1]	2.5	-1.7	2.2	-1.0	1.1	-2.6779	-1.8	-20.2	-1.5	-1.3	-1.4	-1.2

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### Claims

1. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 5; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
2. The method of claim 1 wherein the sample is taken from a bodily fluid.
3. The method of claim 2 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.
4. The method of claim 1 wherein the level of the polypeptide is determined by a method selected from the group consisting of immunohistochemistry, western blotting, ELISA, antibody microarray hybridization and targeted molecular imaging.
5. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 6; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
6. The method of claim 5 wherein the sample is a tissue sample.
7. The method of claim 6 wherein the tissue is selected from the group of tissue consisting of brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta and uterus.
8. The method of claim 5 wherein the level of the polypeptide is determined by a method selected from the group consisting of immunohistochemistry, western blotting, ELISA and targeted molecular imaging.

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9. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide-encoding polynucleotide, wherein a higher level of the polynucleotide compared to the level of the polynucleotide in a subject free of cancer is indicative of cancer, and wherein the polynucleotide is selected from the group consisting of:
  - a) the polynucleotides listed in Table 6;
  - b) polynucleotides having sequences that differ from the polynucleotides in (a), without changing the polypeptide encoded thereby; and
  - c) polynucleotides which are at least 70% homologous to the polynucleotides of (a).
10. The method of claim 9 wherein the sample is a tissue sample.
11. The method of claim 10 wherein the tissue is selected from the group of tissue consisting of brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta and uterus.
12. The method of claim 9 wherein the sample is a is taken from a bodily fluid.
13. The method of claim 12 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.
14. The method of claim 9 wherein the level of the polynucleotide is determined by a method selected from: RT-PCR analysis, in-situ hybridization, polynucleotide microarray and Northern blotting.
15. A method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of said polypeptide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 5 and Table 6; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
16. The method of claim 15 wherein the sample is taken from a bodily fluid.
17. The method of claim 16 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.

18. The method of claim 15 wherein the level of the polypeptide is determined by a method selected from the group consisting of Western blotting, ELISA and targeted molecular imaging.
19. A method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject before treatment, and comparing it with the level of said polynucleotide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of:
  - a) the polynucleotides listed in Table 6;
  - b) polynucleotides having sequences that differ from the polynucleotides in a), without changing the polypeptide encoded thereby; and
  - c) polynucleotides which are at least 70% homologous to the polynucleotides of a).
20. The method of claim 19 wherein said sample is blood or bone marrow cells.
21. The method of claim 19 wherein the level of the polynucleotide is determined by RT-PCR analysis.
22. The method of claim 15 or 19 wherein the treatment is administration of a chemotherapeutic drug.
23. The method of claim 15 or 19 wherein the treatment is radiotherapy.
24. The method of any one of claims 1, 5 or 9 wherein a change in the level of the polynucleotide or polypeptide as compared with the normal level is indicative of an abnormality in a tumor suppressor gene or a biological pathway in which a tumor suppressor gene is involved.
25. The method of claim 24 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
26. The method of any one of claims 1, 5 or 9 wherein a change in the level of the polynucleotide or polypeptide as compared with the normal level is indicative of the effectiveness of a drug that modulates the activity of a tumor suppressor gene.
27. The method of claim 26 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
28. A method of identifying a diagnostic marker for a cancer comprising:

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- a) obtaining a first cell from a first cell type of said cancer, said cell comprising a defective tumor suppressor expression;
  - b) obtaining a second cell of the first cell type, wherein said second cell comprises a wild-type tumor suppressor expression;
  - c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and
  - d) selecting at least one gene of step c) as a diagnostic marker for the cancer.
29. The method of claim 28 further comprising:
- a) obtaining a first cell from a second cell type of said cancer, said cell comprising a defective tumor suppressor expression;
  - b) obtaining a second cell of the second cell type, wherein said second cell comprises a wild-type tumor suppressor expression;
  - c) identifying genes having an increased level of expression in the first cell of the second cell type as compared to the second cell of the second cell type;
  - d) comparing the genes having an increased expression in the first cell type with the genes having an increased expression in the second cell type;
  - e) identifying genes having an increased expression in the first cell type but not in the second cell type; and
  - f) selecting at least one gene of step (e) as a diagnostic marker of a cancer of the first cell type.
30. The method of claim 28 or 29 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
31. The method of claim 28 wherein the identification of step c) is performed using a microarray.
32. The method of claim 29 wherein the identification of step e) is performed using a microarray.
33. The method of claim 29 wherein the identification of step c) and e) are both performed using a microarray.
34. A method for screening for compounds that modulate the activity of a tumor suppressor gene comprising:
- a) obtaining a cell comprising a defective tumor suppressor expression;
  - b) measuring the level of expression of a marker of Table 5 or 6 in the cell;
  - c) contacting the cell with a test compound; and
  - d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after said contacting step as compared to the level of expression before said contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.



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35. The method of claim 34 wherein the change in the level of expression in step c) is a reduction in the level of expression.
36. Use of compounds identified according to the method of claim 35 in the treatment of cancer or as anti-cancer drugs.

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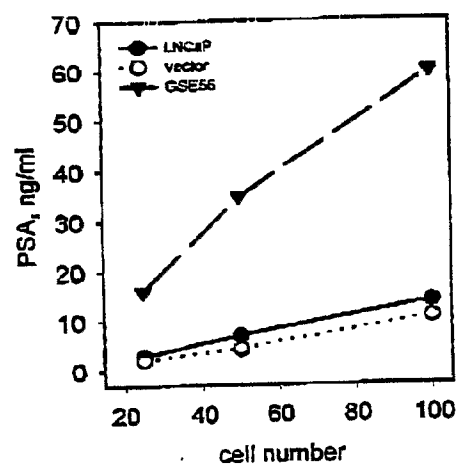
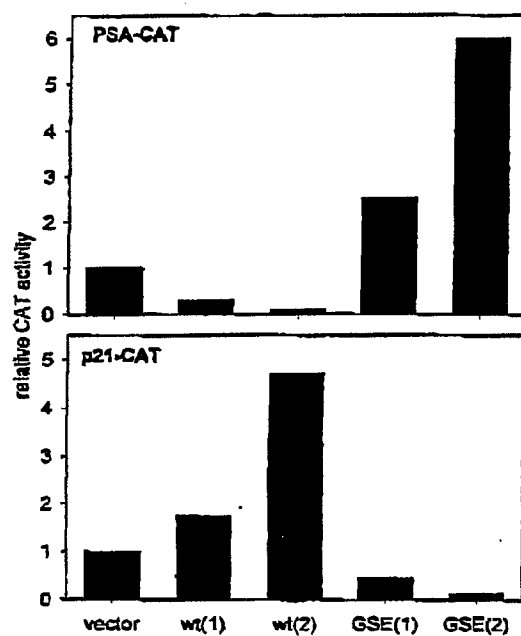


FIGURE 1

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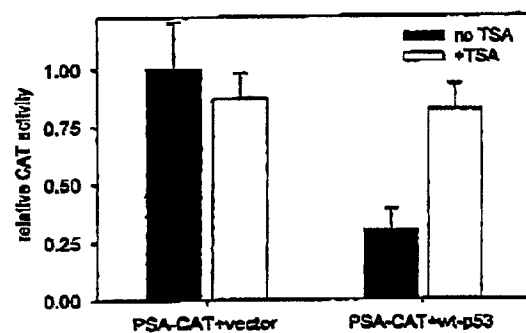
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**FIGURE 2**

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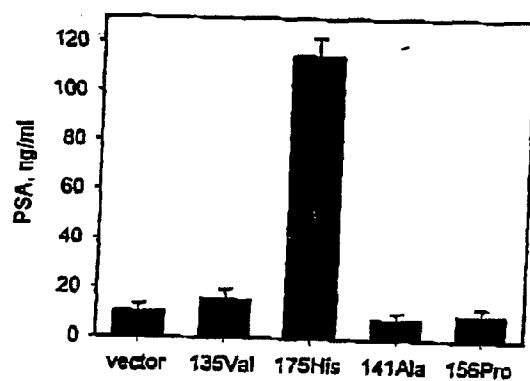
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**FIGURE 3**

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**FIGURE 4**

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**Figure 5**

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65 AGCCTGTGCCCTGGGTCTCGAGGGTCATGGCTGTGCTTGGTCACTGCTGTCTGACTG
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>H\_1.0.0\_22120 Homo sapiens, glutamate-ammonia ligase (glutamine synthase), clone MGC:20322  
IMAGE:4137547, mRNA, complete cds cr: gi-15080156/// [Human\_jongleur\_201102.10208.C8] [SEQ ID NO:  
12]

5 GGCATGAGGCGAGAGTGGGAGAAGAGCGGAGCGTGTGAGCAGTACTGCGGCCTCTCTCC  
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15 GCCCATTACCGGGCTGCTGTATGCTGGAGTCAAGATTGCGGGACTAATGCCGAGGTC  
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50 CTCAATTGTAACAACTGTGTAAGTGCCTCAAGCAGCACTTATAAATCAGCCTAACATAA  
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>H\_1.0.0\_3492 Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase  
1) (GOT1), mRNA cr: gi-4504066/// [Human\_jongleur\_201102.747.C1] [SEQ ID NO: 13]

55 GGCACGAGGGAATCTCTTGATTCCTAGTCTCTCGATATGGCACCTCCGTCAGTCTTTGC  
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65 CTTGCGCATCTGGAACCTGGAGAGAGATGCTGGGCCATTGCTATTTTGTGTCTGAAGG  
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CAAGCAGGTTGAGTATCTGGTCAATGAAAAGCACATCTACCTGCTGCCAAGTGGTCGAAT  
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5 AGGACTGAAAGCTGCTCTGGTGAAGCAGCCTCTGTTTAAACCGGCCCCACATGAAGAGAA  
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15 >H\_1.0.0\_58926 Homo sapiens cDNA FLJ34227 fis, clone FCBF3025098 si: gi-21749942///  
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70 >M\_1.0.0\_53089 vu13h03.x1 Mus musculus cDNA, 3' end as: gi-4602318/// /clone=IMAGE:1180565  
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5 GCAGAGGATAGCCTTGAATTGTGAATGCTTTGAGCCCAATACCCCAAGGTCCAACCTAG  
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NN  
10 NNNNNN

>H\_1.0.0\_48153 Homo sapiens cyclic AMP-regulated phosphoprotein mRNA, complete cds si: gi-6563225///

[Human\_jongleur\_201102.c1.5922.single] [SEQ ID NO: 17]  
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30 TNN

>H\_1.0.0\_25158 Homo sapiens necdin homolog (mouse) (NDN), mRNA cr: gi-10800414///

[Human\_jongleur\_201102.11950.C1] [SEQ ID NO: 18]  
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[Human\_jongleur\_201102.7844.C2] [SEQ ID NO: 19]  
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25 TGTCCCTGGCCGTGGGCTTCATTCTGGGCGAGCGCGCCCGGAGCGAGGGTCTCAGGG  
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>H\_1.0.0\_5504 Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA cr: gi-  
7669505/// [Human\_jongleur\_201102.1642.C5] [SEQ ID NO: 26]  
30 ATGAGTTCTGACTCTGAGATGGCCATTTTGGGGAGGCTGCTCCTTTCCCTCCGAAAGTCT  
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35 GCTGTGCTGTACAACCTCAAAGAGCGCTACGAGCCTGGATGATCTACACCTACTCAGGC  
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45 ATTGAATGCTCTGATCACCAACCCATACGATTATGCTTTCGTGATCAAGGGGAG  
ATCAGAGTCCCGAGCATGTGATGACCAAGAAGAGTTGATGGCTACAGATAGTGCCATTGAA  
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50 GCCCTCTGCTACCTAGGGTCAAGGTGCGCAATGAGTATGTACCAAAGGTCAAACCTGTG  
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65 GGTGTGCTGGAAGGCATCCGCATCTGCAGGAAGGCTTCCCAAGCAGAACTCTTATGCA  
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70 GCAAGAGTGGAGTACAGAAAATGGTGGAAAGAGAGTCCATCTTCTGCATCCAGTAC  
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AAACCCCTCCTCAAAGTGCAGAGACAGAGAAGGAGATGGCCAACATGAAGGAAGAATTT  
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5 GCCAAAATCAAGAGGTGACTGAGAGAGCTGAGGATGAGGAAGAGATCAATGCTGAGCTG  
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30 CTGCAGGATGCTGAGGAACATGTAGAAGCTGTGAATGCCAAATGTGCTTCCCTTGAGAA  
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40 ATGCAGAGCACACTGGATGCTGAGATCAGGAGCAGGAATGATGCCATTAGGCTCAAGAAG  
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45 CACACCCAGAACACCAAGCCTGATCAACACCAAGAAGAAGCTGGAGACAGACATTTCCAA  
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CCATTTTGTACTTATGACTTTTGGAGATAAAAAATTTATCTGCCA  
>H\_1.0.0\_10487 Homo sapiens thyroid hormone responsive (SPOT14 homolog, rat) (THRSP), mRNA cr: gi-  
4507496/// [Human\_jongleur\_201102.3891.C1] [SEQ ID NO: 27]  
60 AACATGCAGGTGCTAACCAAGCGTTACCCCAAGAACTGCCTGCTGACCGTCATGGACCG  
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CTTCACCATGCTCAAGGCCATCTGTGTGGATGTGGACCATGGGCTGCTGCCGCGGGAGGA  
65 GTGGCAGGCCAAGGTGGCAGGCAGCGAAGAGAAATGGAACCCGACAGACAGAGGAAGTCCA  
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GGAAATGACGGGACAAGTTTGGTAGACCTTGGACACTAGGGAAGATCCCTTCACATGATA  
GAAGACAGACTCTTTGATGAGGTGCGCGGAGCAGTTCACTAGCCAATGATGAGAGCAGAA  
AGGCCTAGACCTGCAGCCAGAAGTGAAGGCGGCTCAGTTCTCCGGGATGCTTCTCTACCT  
70 CCGTGAACCAATCTCTGGATTCCAGTCACTGGCTCACCTTTAGAAATGTCTGTTGCTATT  
CACTGCTCCCTCGCTCTCTTAAACAGCTTGGGGAGGTGACCAGTGGTTCAAGAGGAGT

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AGACAATTACCTGTCCAGTGTGGTATGGTAGGAAGAGTGTAGGTGTTGGCACGTGACCAA  
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5 TGATTTTTTTTTCTCCCCCTCTCCCCAATGTATTGTCTCTGGCCCTTGCTTTTACCCCT  
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CACTGATGAGATCAACAACAGGTGAACATAAACCTATTATTATTGACAGAACTAATAAA  
AAATCCAAAGCCTTGT  
>H\_1.0.0\_6779 Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 2 (FACL2), mRNA cr: gi-  
10 12669906/// [Human\_jongleur\_201102.2170.C2] [SEQ ID NO: 28]  
CGGGCAGTGACAGCCGGCGCGGATCGCGCTCCACGGAGGAGAATCAGCTTAGAGAACTA  
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20 TAGACCTGAGTGGGTGATTATTGAACAAGGATGCTTTGCTTATTGATGGTGATCGTTCC  
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25 AGCCAACAGAGCGGAAGCCCAAGCCTCCAGCACCTGAAGATCTTGCAAGTAAATTTGTTTAC  
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30 GGTGCTTCAACCCATCTGTCTTCCCGTGGTTCCAAGACTGCTGAACCGGATGTTTGAACG  
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35 AGGATACGGACAGACAGAGTGCACCTGCCGGGTGCTGCCTAACCATGCTGGAGACTGGAC  
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45 CACATTGCACCTGAAATTTTCTATCGACAATGGCCTTCTGACTCCAACAATGAAGGC  
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65 TTATAATGCTACCTGATTTCTATGAATGTGTTTGACAAGCCAAAATCTAGGATGTAGA  
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70 CATATATGTATCTTAAATTGACAAAAAGTCAATAATTTGTCACTTGGGGTTTTGAATG  
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ATGAAGGAAACCAAAATAAATATTTCTGCATTTTCG

&gt;M\_1.0.0\_12589 Mus musculus L-amino acid oxidase 1 (Laol), mRNA cr: gi-21914876///

[Mouse\_jongleur\_201102.7471.C1] [SEQ ID NO: 29]

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TTTAGCTTGAAGGAAATGTCTCCTGCTACAAACAATAACAAGCAAAAAG

&gt;M\_1.0.0\_25869 Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN full-length

enriched library, clone:D730050C14:glycosylation dependent cell adhesion molecule 1, full insert

sequence cr: gi-12862225/// /cds=(48,503) /gb=AK021358 /gi=12862225 /ug=Mm.219621 /len=626

[Mouse\_jongleur\_201102.19220.C1] [SEQ ID NO: 30]

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TTCAGAGAAGAGCTGATTTCCAAAGATAATGTGGTATAGAATCTACCAAGCCAGAGAAT

CAAGAGGCCAGGATGGGCTCAGGAGCGGGTCATCTCAGCTGGAAGAGACCACAAGACCC

ACCACCTCAGCTGCAACCACTCAGAGGAAAATCTGACCAAGTCAAGCCAGACAGTGGAG

GAAGAAGTGGGTAATAATGAAGGATTGTAACTGGTGAGAGACATAATCTCTGGT

GCCAGTCGTATCACGAAGTCATGAAGACAAAACACCTAACCACTAAGTCCCATGCTAGG

TGGTGCCTTCATCAGCCACATTCTGTCTATCTGACCACCACTCTCAGTCTGCCCTTTGA

TGTCTTACATTAAAGTATTGCAACCGN

&gt;M\_1.0.0\_4293 Mus musculus peripheral myelin protein, 22 kDa (Pmp22), mRNA cr: gi-6679394///

[Mouse\_jongleur\_201102.1994.C1] [SEQ ID NO: 31]

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CAGTGAGCGAATGGCTGAGTCTGTCCAGGCCACCATGATCCTGTCTGTCTATCTTACGG

TCCTGGCTCTGTTCTCTTCTCTGCCAGCTCTTCACTCTCACCAAGGCGGGCGGTTTT

ACATCACTGGATTCTTCCAAATCCTTGTGGTCTGTGCGTGATGAGTGACGCGGCATCT

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5 ACTTTACATCCTAACACTATAACCAAGCTCAGTATCTTTGTTTGTTCGTTTTCCTTT  
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15 GTTGTATTACTACAATAAAATAATCTCAAAGCCTTCGTCAGTCCACAGTTTTCTCAGC  
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AACTC  
20 >M\_1.0.0\_3000 Mus musculus ATP-binding cassette, sub-family B (MDR/TAP), member 1B (Abcb1b), mRNA  
cr: gi-6755045/// [Mouse\_jongleur 201102.1138.C3] [SEQ ID NO: 32]  
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25 GGAGAGAAGAAAGAAAGAAACCTGCTGTTGGCGTATTTGGGATGTTTCGCTATGCAGATTG  
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30 GCTCATAGTTGCTACATCCAGGTTTCACTTTGGTGCTTGGCAGCTGGAAGACAGATACA  
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35 TGGATTGTCTGCTTTGTGGGCAAAGGTATTGACTTCATTTACTAATAAGGAACTCCA  
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65 AGGGGCGATGGGCGCCAGGCTTGCTGTAGTTACCCAGAATGTAGCAAACTCGGGACAGG  
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70 ACCATACAGAAATGCGATGAAGAAAGCACAGCTGTTTGGGATCACGTTCTCTTCAACCA  
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ACAACCTCATGACTTTTGAAAAATGTTATGTTGGTATTTTCTGCTGTTGTCCTTTGGTGCCAT  
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5 GAAGCCTACTCTGTTAGAAAGGAAATGTAAAAATTAATGGAGTCCAGTTTAACTATCCAC  
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10 CATTGCAGAGAACTCGCCTATGGAGACAACAGCCGGGCGGTCTCATGAGGAGATTGT  
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15 TGAGAACGGCAAGATCAAGGAGCAGCGCACCCACAGCAGCTGCTGGCGCAGAAAGGCAT  
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>M\_1.0.0\_6080 Mus musculus retinol binding protein 2, cellular (Rbp2), mRNA cr: gi-6677686///  
[Mouse\_jongleur\_201102.2997.C1] [SEQ ID NO: 33]

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35 GTTCCTCAGATGTAAACCCACCATGAGCTTCACCTGGCCAAATCAATGCTCCTTATGTG  
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40 GCAGTTCTTTGAGCTGGGCTTATGACCTTTGACTCTATTATCTTTATATACCTGGTCCA  
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>M\_1.0.0\_10044 Mus musculus RIKEN cDNA 2010003F10 gene (2010003F10Rik), mRNA cr: gi-21312989///  
[Mouse\_jongleur\_201102.5595.C1] [SEQ ID NO: 34]

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55 GCTCCTGCCTGTTTGGAGGCCTCAGACATGTGTAAGTGTGCGCGCTGCGCTGGGG  
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65 GAGGTTTAGTCACTGAGTACCATAGGCCACCCCTAATACCTCATTCTGGAAGTCTGA  
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70 AACATAGTTATGTTCTGGAAATAAAATCTGTGCTCTCAAGG

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AC  
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[Mouse\_jongleur\_201102.3937.C10] [SEQ ID NO: 37,38,39,49]  
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15 TATTGTACACGCTCTGCTGTGCTGAACATGGAGACCACAGAGGACAAGACGACCATGAG  
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6681162///  
20 [Mouse\_jongleur\_201102.3937.C1] [SEQ ID NO: 40,47]  
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GATGAAGAGACTAAAACCTGAGGAGCAGCCAGGGGAAGAGGACCAGGCTGTGTCTGTCTCC  
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25 TGCAAAATGCAATCCAAATAAGCCTGCAATTGGCACCAAGATCCAAATAAACAGCATAA  
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CAGA  
>H\_1.0.0\_52731 Human RASF-A PLA2 gene encoding synovial phospholipase, exons 2 through 5 si: gi-  
190885///  
30 [Human\_jongleur\_201102.cl.9676.singlet] [SEQ ID NO: 41]  
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35 AGAGGTTGATGCTTTCAATCTCTGGAGGAAATACTGAGGCCGAGCCTCCATGGGTGCTTGG  
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40 GTTGTGTGTGTGTGTGTGTGTGTGTGTCATTGCTGGAGGGCACTCCTGTGTGCTCTGA  
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50 CCCCCAAGGATGCAACGGATCGGTGAGGCCACCTATCCCTCCCTACCTCCTAGACTCTG  
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60 AAAGACTCCAGTGGGAAGTAAACAAACAGATAAGGCATTAACACAGCCTGAGGCTTGAGG  
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25 CCAGTGGAGTCCATCGCTGTTTCTTCTTGGCTTTGGAGTGTGATATCAGTTATATCCA  
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>H\_1.0.0\_2865 Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class)  
(GNA11), mRNA cr: gi-4504036/// [Human\_jongleur\_201102.505.C2] [SEQ ID NO: 45]  
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45 CAAGAAGGACCTCTGGAGGACAAGATCCTGTACTCGCACCTGGTGGACTACTTCCCCGA  
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>H\_1.0.0\_25937 Homo sapiens guanylin mRNA, complete cds cr: gi-183414/// /cds=(8,355) /gb=M97496  
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65 AACCCCAAGCTAATAACAGATTCCAGAGT

>H\_1.0.0\_15482 Homo sapiens pancreatitis-associated protein (PAP), transcript variant 2, mRNA cr:  
gi-21070994/// [Human\_jongleur\_201102.6563.C1] [SEQ ID NO: 48]  
GGGAGGGTCCCTTCTCAGGAGCACAGGAACCTCAGACTCAGCAAGGGTGTCTTGGGA  
70 GGGCTCGGGATGGGAGAGTACACAGATTCAAACTCATTAGAACTGTAGAAGATGATG  
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CAAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTATCTTGGATGCTGCTT  
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>M\_1.0.0\_7660 Mus musculus 129 defensin-like gene 4C-4, complete cds cr: gi-531850///  
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>H\_1.0.0\_22580 Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA cr: gi-22095356///  
[Human\_jongleur\_201102.10520.C1] [SEQ ID NO: 52]

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10 ATGTGGACTCCTCCGGGCAAGTGCACTGTGTGTACCTCTGCTCTATGAGAGCGGCCGCA  
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>H\_1.0.0\_8885 Homo sapiens amnionless protein (AMN), mRNA cr: gi-13569914///  
[Human\_jongleur\_201102.3017.C1] [SEQ ID NO 53]

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20 >H\_1.0.0\_18445 Homo sapiens solute carrier family 22 (organic anion transporter), member 8  
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[Human\_jongleur\_201102.56.C168] [SEQ ID NO: 55]  
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>M\_1.0.0\_47876 Moderately similar to L1 repeat, Tf subfamily, member 18 [Mus musculus] [M.musculus]  
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>H\_1.0.0\_2238 Homo sapiens betaine-homocysteine methyltransferase (BHMT), mRNA cr: gi-4502406///  
[Human\_jongleur\_201102.291.C1] [SEQ ID NO: 60]  
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>H\_1.0.0\_23524 Homo sapiens cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide  
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40 ACCTCATTTCCCAAGGGCACAACCATATAACTTCCTCACTTCTGTCTACATGACAACA  
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TTAAGAAAAGTAACCTTCTCATGCTTTCTCAGCAGGAAACCGAATTTGTGTGGGAGAGG  
GCCTGGCCCGCATGGAGCTGTTTTATTCTGACCTTCATTTTACAGAACTTTAACCTGA  
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45 TCCCGCCCTTCTATCAGCTGTGCTTCATTCCTGTCTGAAGAAGCACAGATGGTCTGGCTG  
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TCTTCTGACCCGTCATCTCACATTTCCCTTCCCCCAAGATCTAGTGAACATTGAGCCCTC  
CATTAAAAAAGTTTCACTGTGCAAAATATCTGCTATTCCCCATACTCTATAATAGTTAC  
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50 AATAGGGAATTC

>H\_1.0.0\_11755 Homo sapiens solute carrier family 27 (fatty acid transporter), member 5 (SLC27A5),  
mRNA cr: gi-13325056/// [Human\_jongleur\_201102.4565.C1] [SEQ ID NO: 65]  
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55 CTGGGGCCTGGGGCAGCCAGTGTGGCCAGTGCCTGTGGCCTTGACCTGCGCTGGCTCCT  
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60 AGATGCTTTCGAGCGGCGAGCACGAGCGCAGCCTGGCAGGGCACTCTTGGTGTGGACGGG  
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GGGCTGCCCAACAGCCTGGATCAACCCGCATGGCCGGGGGATGCCCTGGCGCACTCTGT  
65 GCTGAGCTCTGGGGCCCGGGTGTGTTGGTGGAGCCAGACCTCGGGAGAGCCTGGAGGA  
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TACACCAGGGGTGGGGGCTCTGGGGGCTGCCCTGGATGCAGCGCCCTCCCAACCAAGTGCC  
TGCTGACCTGCGTCTGGGATCACATGGAGAAGCCCTGCCCTTTCATCTATACCTCGGG  
GACCACTGGCCTCCCGAAGCCAGCCATCTCACGCAATGAGCGGGTACTGCAGATGAGCAA  
70 GATGCTGTCTTATCTGGGGCCACAGCTGATGATGTGTTTACACGGTCTGCCTCTGTA  
CCAGGTGATGGGACTTGTGCTGGGATCCTCGGCTGCTTAGATCTCGGAGCCACCTGTGT

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TCTGGCCCCCAAGTTCCTACTTCTCTGCTTCTGGGATGACTGTGCGGAGCATGGCGTGAC  
AGTGATCCGTGTATGTGGGCGAGCTCCTGCGGTACTTGTGTAACTTCCCGAGCAACCAGA  
GGACCGGACACATACAGTCCGCTTGGCAATGGGCAATGGACTACGGGCTGATGTGTGGGA  
GACCTTCCAGCAGCGCTTCGGTCTATTCGGATCTGGGAAGTCTACGGCTCCACAGAAGG  
5 CAACATGGGCTTAGTCAACTATGTGGGGCGCTGCGGGGCCCTGGGCAAGATGAGCTGCCT  
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GAGGGACAATCAGGGCTTCTGCATCCCTGTAGGGCTAGGGGAGCCGGGGCTGTGCTGAC  
10 CAAGGTGGTAAGCCAGCAACCCTTCGTGGGCTACCGCGGCCCCCGAGAGCTGTGGAACG  
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15 CGCTTGGCTCCCTGCCTACGCTACCCCCCATTTTCATCCGCATCCAGGACGCCATGGAGGT  
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>M\_1.0.0.25491 AV209686 Mus musculus cDNA, 3' end cr: gi-6150394/// /clone=1700120N04 /clone\_end=3'  
/gb=AV209686 /gi=6150394 /ug=Mm.140823 /len=167 [Mouse\_jongleur\_201102.18799.C1] [SEQ ID NO: 66]  
NGAGGCCACACTTCCATTCCGGCCTTTTTCGACGGGGACTGCTTAAGGTTTGCCTTGC  
25 GCAGGACAGCAGACAGCTGGACTTCTACCACCTTTCCCGAGCCTCTGAATAAAGTGT  
TAAAT  
>gi|3743331|gb|AI192122.1|AI192122 qc95h03.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
IMAGE:1722005 3', mRNA sequence [SEQ ID NO: 67]  
TTTTTTTTTGAAAAATATAAAATTTAATAAAGGTACATCTCTTAATTACAATAATTAT  
30 TGACCAAGTAGTTTTCCTTTAAATGAACCTTTAATAATGCATAATTTACAGTCTAAAGTA  
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TATATTTATACATAAAACCCCTTTCAAACCAAGGGAGAGCTGGAGCCCTCAATATAGGG  
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35 AGGTAACAGAGGAGGTGCTGCTGGGTG  
>H\_1.0.0.6007 Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA cr: gi-4885590///  
[Human\_jongleur\_201102.1857.C1] [SEQ ID NO: 68,79]  
GGGGGTGGAGCTGCCAGAGTAAAGCAAAGAGAAAGGAAGCAGGCCCCGTTGGAAGTGGTTG  
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40 CGGGAGGAACAGAGAGCCAGGACCAAGCTCCTTATGTAAAGCAACCCAGCCTGGAGCA  
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45 CTCGATTAATAATACACATCTTAAGAAATAAGGTTTCAGAGCATATTCCTGTTTATCAAC  
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50 AAACAGTTGAAACTCCATCGCCTCATTACCATCATGAGCATCATCAATCATGGACATC  
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55 CTCCTAGGAGCTGATGCTGCCATTGTGACATCTGATATTTGAAAAACAGGGTCTGCAA  
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AGCAGCTTATACCACAGAGCCAGTGCCAGTTGACGCTGAAAGAAATCAGGCACAAAAAGT  
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CAATTTCTATTTCCAGCATTTTATAAACTACCAAAATAGTGAACCAAAAAATAGAAATTAG  
60 ATTTGTGCAAAACATGGAGAAATCTACTGAATTGGCTTCCAGATTTTAAATTTTATGTAT  
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65 TCTTTTCAATCTTCTACTTTTAACTAATAAAATAAGTGGATTTGTATTTTAAAGTCCAG  
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TTATCTTTTGTATATCTAAGACTCATCTGATTTTACTATCACACATGAATAAAGCCTT  
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AAGATATAAGGGGAAGATAATATTGTCTGTCTCTATATTGCTTAGTAAGTATTTCCATA  
70 GTCAATGATGGTTTAAATAGGTAAACCAACCCCTATAAACCTGACCTCCTTTATGGTTAAT  
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AATAAAAAACCTTAAGCTG

>H\_1.0.0\_25343 Homo sapiens selenium binding protein 1 (SELENBP1), mRNA cr: gi-16306549///  
[Human\_jongleur\_201102.12047.C1] [SEQ ID NO: 69]

5 CACCAGCACAGCAAACCCGCCGGGATCAAAGTGTACCACTCGGCAGCATGGCTACGAAAT  
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CCACTGTGGATGTTGACCCCAAGTCTCCCAAGTATTGCCAGGTATCCACCGGCTGCCCA  
TGCCCAACCTGAAGGACGAGCTGCATCACTCAGGATGGAACACCTGCAGCAGCTGCTTCG  
10 GTGATAGCACCAAGTCGCGCACCAAGCTGGTGCTGCCAGTCTCATCTCCTCTCGCATCT  
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AGGACATCCATGCCAAGTGCCTGAACTGGCCCTTCTCCACACAGCCACTGCCCTGGCCAGCG  
GGGAAGTGATGATCAGTCCCTGGGAGACGTCAAGGGCAATGGCAAAGGGGGTTTGTGC  
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15 CAGTCTCCCAATGTCTTACGAGATGGCTTCAACCCCGCTGATGTGGAGGCTGGAAGTACG  
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20 AAATGCCAGGCTGATCACCAGACATCTGCTCTCCCTGGACGACGCTTCTCTACTTTCA  
GCAACTGGCTGCATGGGACCTGAGGCAGTATGACATCTCTGACCCACAGAGACCCCGCC  
TCACAGGACAGCTCTTCTCGGAGGACGATTTAAGGGAGGCCCTGTGCAAGTGTCTG  
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GAGGCCCTCAGATGATCCAGCTCAGCCTGGATGGGAAGCGCCTCTACATCACCACGTCGC  
25 TGTACAGTGCCTGGGACAAAGCAGTTTACCTGATCTCATCAGGAAGGCTCTGTGATGC  
TGCAGGTTGATGTAGACACAGTAAAGGAGGGCTGAAGTTGAACCCCAACTTCTGGTGG  
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30 AGCATGTACACACACAGCCCAAGCTGAGACTGTGGCAATGTGTGAGTCATATACATTTACT  
GACCACTGTTGCTTGTGTCTCACTGTGCTGCTTTTCCATGAGCTCTTGGAGGCACCAAGA  
AATAAACTCGTAACCTGTCTCTC

>H\_1.0.0\_24583 Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A  
thiolase) (ACAA27), nuclear gene encoding mitochondrial protein, mRNA cr: gi-5174428///

35 [Human\_jongleur\_201102.11645.C1] [SEQ ID NO: 70]  
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40 CGCTGGGACCCCGCCAGGAGCCCAAGGAGTGTGAAAGGGCAGGGGCGTGGCTCTCG  
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TGTAAGTGTCTGCTAAGCGAACGCCCTTGGAGCTTACGGAGGCCCTCTGAAAGACTTCAC  
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45 TGAAACAGTTGACAGTGTGATTATGGCAATGTCTGACAGATTTCTCAGATGCTATATA  
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TAAAGAAGCTGAAGTTGTTTATGTGGAGGAACCGAAAGCATGAGCCAAAGCTCCCTACTG  
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50 ATGGGTATCAITTAACAGATCAGCATGTCCAGCTCCCCATGGCAATGACTGCAGAGAATCT  
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60 TGCTTTGGGTCACCACTGGGAGGATCTGGATCAAGAATTACTGCACACCTGGTTCACGA  
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65 GCATGTATCATGAATAGGAGCCCATGTAGAAAGTACATTTCTCAGATTGAACCAAGTGA  
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>H\_1.0.0\_2171 Homo sapiens apolipoprotein A-I (APOA1), mRNA cr: gi-4557320///  
[Human\_jongleur\_201102.263.C2] [SEQ ID NO: 71]

70 NGAGAGACTGCGAGAAGGAGGTCCCCACGGCCCTTCAGGATGAAAGCTGCGGTGCTGAC

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5 GCTCGGCCCTGTGACCCAGGAGTTCTGGGATAACCTGGAAAAAGGAGACAGAGGGCCTGAG  
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10 CGCAGAGCTCCAAGAGGGCGCGCGCCAGAAGCTGCACGAGCTGCAAGAGAAGCTGAGCCC  
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15 GTGAGGCGCCCGCGCCGCCCTTCCCGTGCTCAGAATAAACGTTTCCAAAGTGGG  
>H\_1.0.0\_15335 Homo sapiens L-kynurenine/alpha-aminoadipate aminotransferase (KATII), mRNA cr: gi-  
13518236/// [Human\_jongleur\_201102.6487.C1] [SEQ ID NO: 72]  
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35 AGTGAACGCAAAAGGAAATCTATGAGCTTGCAAGAAAATATGATTTCCTCATAATAGAA  
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50 GGCCCTGCATGCACCTTGGCCCTGCATGGCAGAAACAGACCCCTGTCTCTAAAAAAGAGAAA  
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>H\_1.0.0\_12049 Homo sapiens cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13  
(CYP2A13), mRNA cr: gi-19743563/// [Human\_jongleur\_201102.4706.C1] [SEQ ID NO: 73,74]  
60 ACTGCCACCATGTGGCTCAGGCTGCTTCTGGTGACCTTGTGGCTGCCTGACTGTG  
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65 TTCAGCGGCGGAGCGGACAGGCCACCTTCGACTGGCTCTCAAAGGCTATGGCGTGGCG  
TTCAGCAACGGGAGCGCGCAAGCAGCTCCGGCGCTTCTCCATCGCCACCTAAGGGGT  
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GACGCCCTCCGGGCGAGCAGCGGCCAATAATCGATCCACCTTCTCTGAGCGGCACA  
GTCTCCAATGTATCAGCTCCATTGTCTTTGGGGACCGCTTTGACTATGAGGACAAAGAG  
70 TTCCTGTCACTGTTGCGCATGATGCTGGGAAGCTTCCAGTTACGGCAACCTCCACGGGG  
CAGCTCTATGAGATGTTCTCTTCGGTGATGAAACACCTGCCAGGACCACAGCAACAGGCC



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5 ATGAAGCACCCAGAGGTGGAGGCCAAGGTCCATGAGGAGATTGACAGAGTGATCGGCCAAG  
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10 GATAAGAAGGGGAGTTTAAGAAGAGTGATGCTTTTGTGCCCTTTTCCATCGGAAAGCGG  
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15 TTGTGGGAGGGGGGGGCTAAGAAATGGGGGCAGTGGGGGAAGGAAGGGGAGAGGTGGTTA  
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TTCCTGA

>H\_1.0.0\_21557 Moderately similar to HEM1 HUMAN 5-aminolevulinic acid synthase, nonspecific,  
20 mitochondrial precursor (Delta-aminolevulinate synthase) (D cr. gi-5850819/// ws61h08.x1 Homo  
sapiens cDNA 3' end /clone=IMAGE:2501727 /clone\_end=3' /gb=AW003903 /gi=5850819 /ug=Hs.407036  
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30 TCTGCTCATTAGTTCATCACAGACTTCGTGTTTTTCAGCAGCATCTGCAACCCGCACAGG  
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35 AACACAACCAAGGCTTTGCCAAGTGTTCCAGAAATGATGTCCATTTTGGCATGACTCC  
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60 CGTCCG

>H\_1.0.0\_5587 Homo sapiens carboxylesterase 3 (brain) (CES3), mRNA cr: gi-6912297///  
[Human\_jongleur\_201102.1674.C1] [SEQ ID NO: 76]

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GCACCTGGGGATGAACACAGTCGGGGAACTGGGGTCACCTGGACCAGGTGGCTGCACTAC  
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>H\_1.0.0.19636 Homo sapiens hydroxysteroid (11-beta) dehydrogenase 1 (HSD11B1), mRNA cr: gi-  
5031764/// [Human\_jongleur\_201102.8752.C1] [SEQ ID NO: 77]  
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TG  
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70 CCGCCCGCCCCAGCCGCTGGCCAAGGCCGCGCTCGCGCAGGCGCAGTCCCGCTCCCGC  
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30 CATGATTACTCCTAAATTTGTGAAGTTTATAGTTCTATTGTCTTTAAATGTAACATCATGT  
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>M\_1.0.0\_7616 Mus musculus demilune cell and parotid protein (Dcpp), mRNA cr: gi-9910187///  
35 [Mouse\_jongleur\_201102.3917.C1] [SEQ ID NO: 80]  
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40 ACAAGGACGGTCAAGTGATGGCTCAACTGCCGGAAGGAAATGGTAGCCAGACTGTCTA  
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>M\_1.0.0\_4827 Mus musculus submaxillary gland androgen regulated protein 1 (Smr1), mRNA cr: gi-  
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50 [Mouse\_jongleur\_201102.2306.C2] [SEQ ID NO: 81]  
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60 >H\_1.0.0\_38894 Homo sapiens carbonic anhydrase VI gene, exon 6 si: gi-6652972///  
[Human\_jongleur\_201102.c1.310.singlet] [SEQ ID NO: 82]  
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TCACCAGCCTCCCTGCACTGAGAACGTCCACTGGTTTGTGCTGGCAGATTTTGTCAAGC  
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10 /clone\_end=5' /gb=AA267673 /gi=1904410./ug=Mm.24323 /len=136 [gnl|UG|Mm#S161770] [SEQ ID NO: 83]  
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15 [Human\_jongleur\_201102.942.C2] [SEQ ID NO: 84]  
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>H\_1.0.0\_14570 Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma)  
55 (SSR3), mRNA cr: gi-6005883/// [Human\_jongleur\_201102.6056.C1] [SEQ ID NO: 85]  
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AGGAAGTTAATAACTGGTTCTCTGTGTTCCAAGCACAAATATTACAACCTCTTTTGAACCG  
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5 >gi|4505154|ref|NM|002402.1| Homo sapiens mesoderm specific transcript homolog (mouse) (MEST), mRNA  
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50 >M 1.0.0\_5828 Mus musculus 11 kDa secreted protein precursor, mRNA, complete cds cr: gi-8926323///  
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>gi|16442925|gb|BB513945.2|BB513945 BB513945 RIKEN full-length enriched, 10 days lactation. adult  
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65 TTTAAATTTGTCCTGATGGTCATGCTGAAAAGTTAAAGGAAAACCAAACATTGATCTT  
TGAGCATTTTAAATTGATCATTTGAATCAGATAAATGTTTTGTTTTATTCTGCTTATAA  
CACATCATCCATAAATTGATACAAATTGGAGTTGATATAAATTGACAGAAATTTGTACGCT  
ATATTTTAAAACTGGCTGCTATGGTTGGGTAAAGTGCTCTCAACGGCTGTGTATTGAA  
GGTTTGCTGTGTTCTTCACTCTGTGGTGCTCCTGGGAAGCAGGGAAAACTGGAATGTGGA  
70 GTCTTCCCTCAGGGTGTGCTGCTGCTTTGTTTACACCACCAAGCAAGCAGCTTCC  
TTGGTCTCATATTTCCACCACAAATATTCTGCTGCCACAGGCCAGTGGAATGGATC



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ACAGGCTGAAACTTCTAAATCGAGAGCCAAATAAACCTTTCTGCTTTTAAAGTTGATT  
TGCTCTCAAGTACTTGTACAGAAACGGAGGATGAATGCAAAGATTTTATTGTAATGTAAA  
TAGCTAATGAGATT

>M\_1.0.0\_6038 Mus musculus retinoic acid early transcript 1, alpha (Raet1a), mRNA cr: gi-6679616///  
[Mouse\_jongleur\_201102.2973.C1] [SEQ ID NO: 92]

5 GCGCCGCTTGGCCGGGCGCTGTAGTCAGTTACCTGCTCCGCGGGCGAACACGTGCGGG  
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10 CTAGCAAGAAGCTCAAAGGACAGAGAAGTGTGTGCAGAGGTGAGAACTGCTGGAATC  
CCCTGGAGCAGCAGTCAAGAAAGTTGTGAGCTGCTCGATTCAGAGGCTGCAGTTCAAG  
ACACCAACTTTTTCTTTCTTCCACCTTCCCTGACACTATTGCCAATAGTCCCTGAGGGCG  
CAGCTGTTGCCACAGTCACATCTGTGAGAAGAAACCATGGCCAAGGCAGCTGACCAAG  
15 CGCCATCATTTTATGATTCAGAAGCTGTTAATTCTACTGAGCTATGGATACACCAACGGG  
CTGGATGATGCACACTCTCTTAGGTGCACTTGACCATCAAGGATCCTACCCAGCAGAT  
CCTCTCTGGTATGAAGCGAAGTCTTAGTGGATGAAATACTTATCCTCCATTTAAGTAAC  
ATAAACAAGACCATGATCTCAGGTGACCCAGGGGAGACAGCAAAAGCCATGAAGTGGG  
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ACCAAGTGGACACTCACAGACCAATGGTTACCCACATTTACAAGTCACCATGATTAT  
20 CCGCAAGCCAGGGCCAAACTCCTAGTGCCACCTGGGAATTCACATCAGTGACAGTTAC  
TTCTTCACCTTCTACACAGAGAATATGAGCTGGAGATCAGCTAATGATGAATCAGGGGT  
ATCATGAATAAATGGAAGATGATGAGGGGAATTTGTGAACAATTGAAATCTCTGATACCC  
GAATGCAGACAGAAATTTGATGAATTTAAAGTCAGTCCAAAGGAAAGCCAGATCAACC  
TCAAGGTCCCCAGTATCACCCAGCTTACATCAACTTCCCCGCTTCCACCTCCAGCCAC  
TCTACTCTTAAGAAAGGATTATCTCTGTGGGACTCATCTTCATATCTTTATTATTGCA  
25 TTTGCATTTGCGATGTGAAGAGGAAATATTATACCAAGGAGAGGCCAGAGSAGGGCATC  
GGATCCCTGGAAGTGGAGTTACAGTTGGTTTCCAATACTGGGAAGTGAATCCAGGACCT  
CTCCAAGAACAGCAAGTCTCTTTGCTACTGAGCCTTATCTCCCTCCTTAATACATTTCT  
TTAATAAGAGAATATAGTTTGAATATTATTAAACCCAGGGCAAGTCCCACAGTAAGCTTC  
ACAATAAAGTTGATTGTTTTCAGAATCAAAAAGGAAACACATTTTAAATGAGTGTCTATG  
30 GCCAGTTATCACATCGTTTGTAGCAATGTATGATGGAGGACGTCCAGGTCCGTCTAAAAA  
AATGCCAGGCAATACAGCAACATCTAAGAAACTGGTAAATTTAA

>M\_1.0.0\_4198 Mus musculus peroxisomal biogenesis factor 11a (Pex11a), mRNA cr: gi-6755033///  
[Mouse\_jongleur\_201102.1926.C1] [SEQ ID NO: 93]

35 GCGCAGCTCCAGGGGACCCACGAGGGAGCGGCGCAACGCGTGGCTGTGGGTGGGAGCC  
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GTGGTACTGAAGCTCAAGAGGCTGGAGACCACTGTGAGCACTGGCCGTAATGGTTTCA  
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40 GCGCCCGCTTATGCTGACATTAGCCAACTCAACCGCTGGTTTATTACATCTGTGAC  
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AGGTGGGCGGCTCGCCATTACTACTACTTCTCTTGTGAGCCTGGTCCGGGATCTGTAT  
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45 CTCTCTCTATTCAGTCTCTAAGCGGACATCTCCCTTGTCTCTGGACACCGTGAAGAAC  
TTCTGTGACATCCGTGATCCCTCTGAACAGCTTGGGATCTACAAGTCCAATCTCGGCGTG  
GTAGGACTTGGAGGTCTCATATCCTCTTTGGCTGGTCTCCTCACGGTAGTGTATCCTCAG  
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>M\_1.0.0\_15194 Mus musculus ATP-binding cassette, sub-family A (ABC1), member 8b (Abca8b), mRNA cr:  
gi-23956075///  
[Mouse\_jongleur\_201102.9242.C5] [SEQ ID NO: 94]

50 GGTGTTTGGCAGACCAACCCAGAGCTGAGATCATAACTCCCGCTGAGAGCAGCTTTCA  
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55 ACAAACTTGTGCTTTATTACAGAAGAACCTTCTTAAGAAATGGAGACTGAAAGGGAGTC  
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60 AGAAAAATATCAAGGAATTAACAGAAAGTCATGCAGAAATAATAAGAGTCATTTTTCTGA  
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65 CCATCCTTTTGTCCGTCAGAAGGAATTCGACTGATTTCTTTATTTTCACTGCATCAT  
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70 ATCTATGATCACTTTGGCTTTCTTAATGAGTGCTTGGTGAGGAAGTCTGCTCTCACTGG  
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ATACCTCCCTGCACCTGTGGAAATGGACTCTCAGTCTCTTTAGCCCTTTGCCTTCACACT  
AGGAATGGCCAGCTCTTACGTGTGGATTATGATTAAATTTCTAATGCACCCCTGATCC  
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GTATCTGGCCCTGATGATGTACTTCGAAAAAGTTCTGCCAAATGAATACGGACATCAGCA  
5 CTCTCCCTGTTTTTCTGAAATCTTCATTTTGGCTACAAACACGAAAGCCTGCTCATGT  
GATTCTGAAGATGGAAATAGACCCCGTTCCCTTCATCAGGTGACTCGTTTGAACCGGTGTC  
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10 ATTATCTGTTCCTACTAAAGGTTCTGTCAACATCTATAATAATACTTATCAGAAATGGC  
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15 TTTAGGAGATTTCTAGATTTTCTACTGGATGAGCCACCGCTGGCTGGATCCCTTTTC  
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30 GGAACGCCAGAACATAGCTTTGGAAAGTCGATGCTTCTGGAAACAGAGATGGTACAGATGA  
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60 GTCTGGAAGGCTGAGGTGATTGGATCCATCCAACATCTCAAAGCAAATTTGGCAAGA  
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65 AAAGTGAAGCTCCTCCACAGGAAGAGGCTTAAGCCAAAAATATCTCTCCTCTTCTCTC  
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TCTGTAGAAATGTTGAATAAACAGTTACTTTT  
70 >gi|8923831|ref|NM|018685.1| Homo sapiens anillin, actin binding protein (scraps homolog,  
Drosophila) (ANLN), mRNA [SEQ ID NO: 95]  
GCTGGAAGCCGAGAGGAGAGACAGCTGGTTGTGGGAGAGTTCCCCCGCCTCAGACTCCT

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TCAGCCATAGTTTCTCTTATCCAGGTGTTGAAATTTAAACTCTGGTGTAGATACCCGGC  
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5 GAGCTTGAGGTTACACACTGGAGCTCATCTGGGTATTATATTTGACGGGTGTAATGCT  
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>M\_1.0.0\_20499 Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library,  
clone:5930412E23:unclassifiable transcript, full insert sequence cr: gi-12860486/// /cds=UNKNOWN  
10 /gb=AK020029 /gi=12860486 /ug=Mm.45194 /len=1349 [Mouse\_jongleur\_201102.13747.C1] [SEQ ID NO: 97]  
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15 GTAGTCAGATTGGGTTTGTAGTTACAACCTTGTGACTTAATAGTTACACAAGTGTAGTCAG  
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35 GGAACTCACTCTGTAGACCAGGCTAGCCTCAAACCTCAGAAATTCACCTGCCTCTGCCTCC  
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45 CCCGCTCTGGTTCTTACTAGATGACGTATTACTCTACACCTGATGTCTAGACAGCTATCT  
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>M\_1.0.0\_8300 Mus musculus cardiac responsive adriamycin protein (Crap), mRNA cr: gi-7304882///  
[Mouse\_jongleur\_201102.4328.C1] [SEQ ID NO: 98]  
70 TCAGTCAAGAGGAGGTGAACCTGAGGATGGTCCAGAGAGGTGAGCCTGAGGTTGGTCCA  
GGGAGGTGAGTCTGAGGTTGGCCAGAGGAGGTGGAGTCTGAGGTTGGTCTTGAGGAGA

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5 TGAGCCACTGGCCCCCTGTAACAGCAGAGTGTTTATCCTCCGAGGAGGCGCTGGGCTTGAC  
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25 AGCATCCCCAACATGGTTTGAAGAGACTGTAGGTGCCCGCTGGAGCAGGAGAGTCTGT  
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30 TTCCAGACACTAGTCTGGAATGAAAATTCACCTGCCTCTGAATGGCCACTGGTGGGG  
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40 GAAATTATGACTGAACCTGTGGATGTGCCGAGGTTTCTGAAGCTGCGCTGGAGAACAA  
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45 GCATGTCTGGAGGAAACGCGAGATGTCTGAACTGTGTGCTGAACAAGGAGCCAAAATC  
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50 ACCCTCGGTGCGGACCTCAAGGTCAAGAACTGTGCTGGGAAGACCCCATGGATCTGGTG  
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55 CAAATAGGAGAGATGTCAAAGAGCTTCAAGAAAGCACTGGGTGTAGGTGTAAAT  
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60 GTGTTCTCACTTGCAAAAGCTATTCAAGGTACTTTTAAAGGCAAGGGTGTATCCCG  
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AGATTTGGTTCCGTTTGGTTGTTTACCAGATCACATGATGTGATGTCCCAAGGTGAAGG  
CAACGTGAGGAGTGCCGCATGTAGGGAGATGGAGGGAGTAGGCAATGGGGCCAGGAAAA  
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65 GTGTTGTATGATATTTTATATTTATATAAATGCAAACTAATTCTCGG  
>M\_1.0.0\_11385 Mus musculus choline kinase (Chk), mRNA cr: gi-7304958///  
[Mouse\_jongleur\_201102.6600.C1] [SEQ ID NO: 99]  
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GCATTTCCCGCGCGCGCCCGAGAGGCGGCATCCAGCGGACCTGAGTGTGGCCCTC  
70 TCGTGTCTGCGCGCCCGCGCTTCTCGGCGCTTGTCCAGCATGAAACCAAGTTCTGTC  
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GCCCCGACGCGCGCTAGGGCAGCAGCGGACGCGCAGGCGAGCTGGAGTCCAAGCAG  
CTTGTGCGCGAACCCCACTCTCGCGCTGCGCGCGCGCGCGCGCTTGTGCGCTG  
CCCCGCGCGCATCACCGCGCTAGCGGACGAACAACCGAGCCCCGAGCAGGCGCAGG  
GCCTACCTGTGGTGAAGGAATTCCTGCCCGAGCTGCGAGGCTTCCGAGGACAG  
TTCACATCAGTGTATCAGGGGTGGTCTCAGTAACATGCTGTTCCAGTGTCTCCCTGCCA

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GACTCCATAGCCAGCGTTGGCGATGAGCCTCGGAAAGTGCTCTTGCGGCTCTATGGGGCA  
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5 GCTGAGAAAATGGCCACATTCATGGTATGAAAATGCCATTCAATAAGGAACCAAAATGG  
CTTTTGGAAACAATGGAAAAATACCTGAATCAAGTACTAAGACTCAAATTCAGCAGGGAG  
GCCAGAGTTTCAGCACTGCACAAGATCCTCTCTTACAACCTGCCTCTTGAGCTCGAGAAC  
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10 ATTGACTTTGAGTACAGCAGTTTACAATTACAGGGGATTTGACATTGGAATCATTTCTGT  
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ACTGTGAAGTGGCTCAACAGGAGGAGCCTGAGTTGTGGGGTCTATGGATGGCAACAGCT  
25 GATCTGTACAGGCTACACTTGACTGTGGGTATGCAAGGTGGCAGCTGCAGCCCTCCTGTG  
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TAACTGGGTGTGCTTTATAGCTCCAGCTTCTGGGAGGAGCAGTGGAGCCAGCTCCCTCA  
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30 GGTAGATTAGAGCTGTGAAATCCATGTACATTAATACCAATGGGATAAACTTAGATTTT  
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>H\_1.0.0\_45987 Homo sapiens mutant guanine nucleotide-binding protein G(s), alpha subunit mRNA,  
complete cds si:-gi-3142636/// [Human\_jongleur\_201102.cl.4319.single] [SEQ ID NO: 100]

35 ATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT  
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AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCTCAACAGCAA  
GATCTGCTCGCTGAGAAAGTCCCTGCTGGGAATCGAAGATTGAGGACTACTTTCCAGAA  
TTTGCTCGCTACACTCTCTCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTG  
40 ACCCGGGCCAAGTACTTCATTGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGAT  
GGGCGTCACTACTGCTACCTCATTTACCTGCGCTGTGGACACTGAGAACATCCGCGCT  
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TAA

>M\_1.0.0\_53252 AV304517 Mus musculus cDNA, 3' end as: gi-16393611/// /clone=5730521N16 /clone\_end=3'  
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45 AATCCAAAAATCAAAATTGAGGGGAAAAGGGGACAGAGAGATAGCTCAATGGTTAAAGCA  
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>H\_1.0.0\_13522 Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 10 (ABCC10), mRNA  
cr: gi-21541819/// [Human\_jongleur\_201102.5425.C1] [SEQ ID NO: 102]

60 TTCTAATGATCCCATCACCAAGTAGCAACGCTAGTACCCAGGATTTTCTTCTAGTT  
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65 GTGCTCTCTGCTCTTCCCTTGTCTCCCGAGGAGTCCAGATTACATCCTACCTGCACTCC  
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70 TCCAGCCCTAGTGTGACCGTGTGTGGCATTGCAGCAGGAGGCACACTTCTGCCCCCACT  
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CTATGCACTGGGATGGGCAGCTCCTGGGGGACACGAGAACCCTGGGCTCAGGAGCCCCT  
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5 GGACATTGCCGCTCCCCCAAGACTGCAGCCAACCTACCTGGCTCGTGTCTTCAGGC  
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CTATGCTCTGGGGCTAGCCGGTGGGGCTGTGCTGGGTGCTGTGCTGCAGAATCAGTATGG  
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CCTGCAACTGGCCATCACCTCTACCTGCTGTACCAGCAGGTAGGCGTGGCCTTCGTGGG  
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20 AGTGTCTCTGGACCGGATCCAGCTTTCTCTCGACCTTCCAACCAACAACCCCGAGCCCTA  
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25 CCACAGGCTGCGTGGGCTGTGGCAGTGCAGGGGCTGCCAAGGGCTTGGGCTGGCCAC  
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35 GCAGAGCACATCTGGTCGCTGCTGCAGGAAGAAAGCAAGAGGAGGGCGCGTGGCCCT  
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45 GGCAGGCCTGCTGGGGCTCCTGGCCGTGCTGGGCTCTGGCCTGCCCTGGCTGCTGCTCT  
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60 CTTTTTGTTCAGTGGGACTGTTCCGGAAAACTGGACCCCGAGGGCTACATAAGGACAG  
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70 AGCATCCTGAGGCTTCCCAAGAACAGGCTCTGCTCTGGCCCTCTTGATCTGGAACGC  
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TCCATCTTACATTCTGTGTATTAAAAAATAATATTTCTGGTGT

>H\_1.0.0\_15053 Homo sapiens hypothetical protein FLJ10815 (FLJ10815), mRNA cr: gi-8922691///  
[Human\_jongleur\_201102.6327.C1] [SEQ ID NO: 103]

5 ATGTGATGCATGCTCAGTGTCTCCGCAGCCGGCTCGGAAAGAAATCCCCAAGCTCCAT  
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15 ATGGGTATGCTGGTTTTCATCATCAGTGGCCTTGTCACTCTGGCCTACTGCTCCCAGGCC  
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50 ACTACCCAGAGAC

>gi|4483340|gb|AI550977.1|AI550977 vj19d05.y1 Barstead mouse irradiated colon MPLRB7 Mus musculus  
cDNA clone IMAGE:922185 5', mRNA sequence [SEQ ID NO: 104]

55 AATTCGTCGACATGCAGTGGCACCAAGAAACCAAACTTGGGCTGGTGACGTGGTTCAGCA  
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CCCCAATACACAAATAAATGTAATTAGTCATA  
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[Human\_jongleur\_201102.cl.56.single] [SEQ ID NO: 105]  
60 TGGTGTTCGTCCAGAGTTTCCCCCTTGGCGGTGGTGGAGGTGGTAACCGTGATAGTAG  
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70 CTGGAACCTTCTCATCTTAATACAGAACAGAGCACGTTTAAAGTACTTCAACAAAG  
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GATGTGCCTACGCCAAAACAATTCTGTAGCAGATGTAAAGAACCTATATCCATCATCATCT  
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15 [Mouse\_jongleur\_201102.9115.C3] [SEQ ID NO: 106]  
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>H\_1.0.0\_10016 Homo sapiens hypothetical protein FLJ10563 (FLJ10563), mRNA cr: gi-8922518///  
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35 TATGTTTACATAAAAAATAAATAAAGTATTACAGCATAGCAAAACCTC  
>H\_1.0.0\_11371 Homo sapiens similar to intermediate filament-like protein MGC:2625, isoform 2; HOM-  
TES-103 tumor antigen-like; similar to CG15021 gene product (LOC126917), mRNA cr: gi-22041886///  
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>H\_1.0.0\_3667 Homo sapiens cullin 5 (CUL5), mRNA cr: gi-4503166/// [Human\_jongleur\_201102.833.C1]

[SEQ ID NO: 124]

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 70 AAAGATAGTTGATTATATGCAATCAGATGGCATTCACAAACTTAACTGGAGCATATACA  
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AAATGGTGAATATTATTAATATTGTATAATAGGAGTGGGAAGACTGCCTCCTTTTTTTGA  
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GCCGAGAGCTCGGAAGCCGAGAGCAACCTGCCCCGGGACGCGCTGGACACCGAGGAGGGA  
GAGTTTATGGCGTGACGCCGCTGGCCCTGGACGAGAGCGACCCGGACTGGTGCAAGACG  
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70 CTTTGGATACCTTGAATTCAGTGTAGTAATATTTTCAGACGTTTCCCAATAAGTGTGT  
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65 >H\_1.0.0\_38087 Homo sapiens similar to RNA polymerase I transcription factor RRN3 (LOC94431), mRNA  
si: gi-22067165/// [Human\_jongleur\_201102.c1.56.single] [SEQ ID NO: 153]  
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70 ATATGCTGCATTAGAGAAATGATTTTTCATTTCTCCCAAGAAAACTGTTGCGTTTG  
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TGTTGAAGAACAGCTGTTAGATCCAGACATAAAGGATGACCAGATCATCACTGGCTGC

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TAGAATTCGGTTCTTCTGTCTACTTGACAAAAGACTTTGAGCAACTTATCAGTATTA  
TATTGAGATTGCCCTTGGTTGAATAGAAGTCAAACAGTAGTGGAGAGTATTGGCTTTTC  
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5 ATGATGAAGATGATAATCTTCCTGCAAATTTTGACACATATCAGAGCCTTGCAAATAA  
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20 AGCTTTTGAGCGGAAACCTGAAAGAAGTTTGACAGTATCCTCAGAGTCTGAATTTGAGC  
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>H\_1.0.0\_27490 Homo sapiens cDNA FLJ90378 fis, clone NT2RP2004847, weakly similar to ZINC FINGER  
PROTEIN 135 cr: gi-22760577/// /cds=(5,976) /gb=AK074859 /gi=22760577 /ug=Hs.53996 /len=1987  
25 [Human\_jongleur\_201102.13667.Cl] [SEQ ID NO: 154]

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30 CCCCAGGAGCCAGGTTCTTTCCACTGTGCTCTGTGCCCTGCTGCCCTCCGGCTGGTTTCG  
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60 >M\_1.0.0\_56987 BB667377 Mus musculus cDNA, 3' end as: gi-16398826/// /clone=C730006J15 /clone\_end=3'  
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ACTAGAATAACCTGGGAATAGTCAAGAATATTGTCATCTGGATCCCATTTAATTTATGGA  
ATNCTTTATGGTCAAACCTCTTTAAGATGGGCTCAGGCACTAAACT  
>gi|388764|gb|L11702.1|HUMPHOSPD Human phospholipase D mRNA, complete cds [SEQ ID NO: 156]  
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5 GGTTCCACCGTGTGGCCTTTCAACACACGTAGAAATAGGACACAGAGCTCTGGAGTTTCTT  
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CAGGCTGGAATCGGTTCCTGATTGTTTTACCTTAGCATCTGCAAAGGAGGAAAATTC  
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10 CGAGAGAACTATCCCTTCCCTGGGAGAAGGACACAGAGAACTGGTAGCTTCTTGTTT  
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30 GATGTGAATGGAGACATGGAACCCGATCTGGTCATCGGCTCCCTTTTGACACAGGTGGA  
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60 ATAGAAAGCATAGTATAC  
>M\_1.0.0\_19077 vv70h06.x1 Mus musculus cDNA, 3' end cr: gi-4613514/// /clone=IMAGE:1227803  
/clone\_end=3' /gb=AI604347 /gi=4613514 /ug=Mm.32372 /len=421 [Mouse\_jongleur\_201102.12391.C1] [SEQ  
ID NO: 157]  
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65 CACAATACATAGAGACAGAAAGCATCTTGAGTAGGCAAGACCCCAAGATGCGGCAAGC  
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70 AGCGGTCAACAGGCTTGTGGCTGACAGGCTGTGGGGCTGCAGCCCTACAGGCTGATGGGG  
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GTGTCGAGTCAGCGCAGTCAGGCTGACTGGAAGTTGGCTTTTGTCTATCACACTTATCGT  
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5 GGCAGAAAACCTGACTACAAGGCGGCTTGACAGGAACGATGGCAGGCAAGGACTAGGCTCA  
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>H\_1.0.0\_30299 602849886F1 Homo sapiens cDNA 5' end cr: gi-14504763/// /clone=IMAGE:4991396  
/clone\_end=5' /gb=BI086433 /gi=14504763 /ug=Hs.169061 /len=855. Weakly similar to kinase suppressor  
15 of ras [Mus musculus] [M.musculus] [Human\_jongleur\_201102.16424.C1] [SEQ ID NO: 158]  
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25 ATTAGACTCCAAAACCCAGAAAAGGAAAGGTTGATGGGAGTGAGACCTGATGTGGATTCA  
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65 >gi|15689855|gb|BI714160.1|BI714160 ie33g03.x1 Kaestner ngn3 wt Mus musculus cDNA 3', mRNA sequence  
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70 TTATCAAGGCATGAAGCAACATCAAGAAGCATAGTAACGCACCTTGTATCTTAACAAA  
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TCAAGATAACTAATGTTCAGGAAGGAGAAAGTGACAATTCCTTAAGAAAGCACTCCCGTT  
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AAACTGTCA

>H\_1.0.0\_2912 Homo sapiens interleukin 13 (IL13), mRNA cr: gi-4504644///  
[Human\_jongleur\_201102.525.C1] [SEQ ID NO: 161]

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>M\_1.0.0\_7164 Mus musculus killer cell lectin-like receptor subfamily A, member 21 (Klra21), mRNA  
cr: gi-21361215/// [Mouse\_jongleur\_201102.3652.C9] [SEQ ID NO: 162]

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>H\_1.0.0\_14332 Homo sapiens step II splicing factor SLU7 (SLU7), mRNA cr: gi-20127500///  
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5902033/// [Human\_jongleur\_201102.3438.C1] [SEQ ID NO: 164]  
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10 CCTCACCTCTCATAACATTGATTGTTAATGAGGATGTTCAAACGTTCTTCTAATTTTGT  
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 65 GGGGGCCAGAGTAGCTGATGTAGGAGTACTGGGAGGCCAGACGGCACAGGCTCTCAAGG  
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 GACCACCAAGAGGAAGACCCACCCACGGCGGGACAGATGCGGGGTACGTTAAAGGGAG  
 70 AGCCAGAGAACTCATGGGTGAGGATGGAGTCCGAGGAGACTGCTGGGAGCCCGCTGTG  
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GGCCCTCCCCAGCAGAGCAGCCAGCAACAGTGTGTCTCTGTGGTCATAAACTCCAGGGA  
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GCAGCCAGAGAGGAGGTGTCCCTTCCTCGCCAGACAGCGCGCTTCTCTCTGGCCTT  
TCCCAGGGCCTGTGAGTGCCTCAGGAAGCAGCTGGGCCCTCTGGGAAGGCTGTGTTCAGC  
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>H\_1.0.0\_579 Homo sapiens hypothetical protein MGC26914 (MGC26914), mRNA cr: gi-21699059///  
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>H\_1.0.0\_22812 Homo sapiens hypothetical protein MGC18216 (MGC18216), mRNA cr: gi-22748948///  
[Human\_jongleur\_201102.10675.C1] [SEQ ID NO: 198]

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35 >M\_1.0.0\_18917 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library,  
clone:2900075A18;homolog to CAM-KII INHIBITORY PROTEIN, full insert sequence cr: gi-12851285///  
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AAGTATAATATAAGCCACATGTATAAATAAAATTTCTACTAGCTACC  
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40 GAGTTGGCAGCTTGGAAAGCTGAGGAGGCGAGGGTGGACCTGCTTCTTACTCTGCCCC  
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50 >M\_1.0.0\_47422 vp40b11.r1 Mus musculus cDNA, 5' end as: gi-2893320/// /clone=IMAGE:1079133  
/clone\_end=5' /gb=AA823452 /gi=2893320 /ug=Mm.25352 /len=219 [gnl|UG|Mm#S299539] [SEQ ID NO: 210]  
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TGACCATGTTTTCTGTTGAGCGGCATTCCTCCATGTGCA  
55 >H\_1.0.0\_48696 Homo sapiens cDNA FLJ90324 fis, clone NT2RP2001817, highly similar to Homo sapiens  
sirtuin type 1 (SIRT1) mRNA si: gi-22760489/// [Human\_jongleur\_201102.cl.6521.singlet] [SEQ ID NO:  
211]  
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65 TCAGGTAGTTCTCGATGTCCTAGGTGCCAGCTGATGAACCGCTTGCTATCATGAAACC  
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5 CCAGCCTTGCCAGATCATTTTGAACCAGGTATGCTATTGCGGCAGCACCTCCCGAGATGT  
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10 TCTCAGCCAATTGCTAGAACTTGGAAAGTAGTAGTCGGAACCATGCAATGGACCCCTGTGCC  
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55 >M\_1.0.0\_20492 Mus musculus adult male brain cDNA, RIKEN full-length enriched library,  
clone:0710001D07:unclassifiable transcript, full insert sequence cr: gi-12833293///cds=UNKNOWN  
/gb-AK002941 /gi=12833293 /ug=Mm.45160 /len=1133 [Mouse\_jongleur\_201102.13739.C1] [SEQ ID NO: 214]  
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70 AAGTTACTTACCTGGGTGTGGGTTTGAAGATGGAAGACTTAATTCAGCAAGAACGCA  
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TCAGAGCCACAACCTAGACTCTGGCGGTGGGGATGGAACGCGGAGGCCAGCTCTGAGCG  
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5 CTCTCATCTTCCATGTGGAACGATATCCATCAATTTAATACATCTACTTTCCG  
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50 TGGTGAAAAGAAAGATCTGAAGTGGGGCAAGGGCAAGCAAAACAGCAGGGACTTCCCA  
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55 TTTGTGAAGGCAAAATGTTAGGTGGATAAGACATAGTTCTGTGTGAAGGCATAAATAACT  
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60 AGGAGAATCTCTTCTACTTCATTTATGAGATTCTTTTTTCTACTTTTTTTTTTGGTTT  
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>gi|29445|emb|V00500.1|HSBGLX Human messenger RNA for beta-globin [SEQ ID NO: 217,218,219]  
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65 GTGGATGAAGTTGGTGGTGAAGCCCTGGGCAGGCTGCTGGTGGTCTACCTTGGACCCAG  
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70 CCTGAGAACTTCAGGCTCCTGGGCAAGTGTCTGGTCTGTGTCTGGCCCATCACTTTGGC  
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GCCCTGGCCCAAGTATCACTAAGCTCGCTTCTTGCTGTCCAATTTCTATTAAAGGTT  
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GGATTCTGC

5 >M\_1.0.0\_62347 Moderately similar to F261 MOUSE 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase  
1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-  
biphosphatase ] [M.musculus] as: gi-15714162/// 603360763F1 Mus musculus cDNA, 5' end  
/clone=IMAGE:5368118 /clone\_end=5' /gb=BI737149 /gi=15714162 /ug=Mm.132391 /len=896.  
[gnl|UG|Mm#S2184367] [SEQ ID NO: 220]

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15 TCCTTTCCACACTTACTCTCTGAGTACCCACAGATGCAGAGGTTAGATGTGGGTAGAAG  
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20 GCCAGCCTGGTGAAGTGGAGTCTCGAGTGTCTGAGCAGAGGGGCTGGCAGCAGAGCACAT  
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25 >H\_1.0.0\_25516 Homo sapiens septin 3 (SEPT3), transcript variant A, mRNA cr: gi-22035571///  
[Human\_jongleur\_201102.12125.C2] [SEQ ID NO: 221]  
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30 GAAGACCGGTTTCGACTTCAACATCATGTCGTGTTGGCCAGAGTGGACTGGGCAAAATCAAC  
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65 >H\_1.0.0\_33714 Homo sapiens mRNA; cDNA DKFZp761J0720 (from clone DKFZp761J0720) /gb=AL833252  
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(PKC-beta-1) [H.sapiens] cr: gi-21733885/// Homo sapiens mRNA; cDNA DKFZp761J0720 (from clone  
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5 ATTCTTGCCATTATTTTCAAAGTTTAATAGTTTGCAGAAATAGATACTCAAGCCAAAG  
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GCCTACTCGCCTGGAGACATGTGGAGTTCTTAGGGGTCTGCAGCCACCTCGGGGAGCTG  
GGAGATTCCCTCCAGACACTCTACATATAGGAAGGTGATGCTTCTATCTCATTTCCGCA  
CGGCTTTTCTCGCGTATTCTGTAGCGCTTCTCCGCCACTGTGTCCATAAACTTAGGG  
70 TTATCTTTAGAGACTTCTTCTGGTAACACCACTGTGATGGGTGAGAGTCAACAGCTTC  
ACCACCACCTCAGTGACACGGGANGGACCTCTGAGTCAGAGGAATGGGTGGTACAGGTG

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GAGACCCGAAGGTAAGTACTTGTCTTCGNCCTGTGTGAAGGTTAGCCAACTGGGAAACCC  
AGTTTGAACCTGGTTCGTT CAGCTTGCTCCAGCAGGGAATGAGGTGTTGAGCATCTTTCGAC  
TGGAAGAGCTGCAGCAGTTCCCTGTANTGCTCTGTNAGCCTTTCCGCACCTGGAGCGAGT  
CGTTAAGTCCCTGGGCAGGTTAGCTGG

5 >H\_1.0.0\_16024 UI-H-B11-abz-f-03-0-UI.s1 Homo sapiens cDNA 3' end cr: gi-6140309///  
/clone=IMAGE:2713493 /clone\_end=3' /gb=AW136176 /gi=6140309 /ug=Hs.370779 /len=397.Weakly similar to  
YZA1\_HUMAN HYPOTHETICAL PROTEIN [H.sapiens] [Human\_jongleur\_201102.6858.C2] [SEQ ID NO: 227]  
TGATTCCTTCAGCTGACTGCAAGAGCGTTTATTGTACACGAGTTACACTTGGCCACAAGAG  
AACAGAGCTAGTCCAGAGTGC CGGGGTTCCAGGGCAGAGGGCCAGCGGGACTGTTTGGT  
10 TGTGAGGAAGGTGGTCATTTTCCAGGTGATCTCGGCGAGGTGACGTTCCGGGTCTACTG  
AGACTTATTACCGATGGCAGCATACAGTCCGATCGCTTGTTCGGGCTTCAGCATCCCTT  
ACTTCTGCTCCTG CAGGCTTCGTGGGTGCACGGGCTGGTTTACTTGGACCTCTGCCTCAT  
CTTTCTTCTCTGCGCTTCAGCTGCGCATCTCTTCTTCCGCCACTTCGCTCTCATGGC  
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15 >H\_1.0.0\_2410 Homo sapiens death-associated protein kinase 3 (DAPK3), mRNA cr: gi-4557510///  
[Human\_jongleur\_201102.336.C1] [SEQ ID NO: 228]  
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20 GGAGTGAAGCTGCTGGAAGGCGGACCGGCGCCATGTCCACGTTTCAGGCAGGAGGACGT  
GGAGGACCATATGAGATGGGGAGGAGCTGGGCAGCGGCCAGTTTGCGATCGTGCGGAA  
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25 GGTCTCATCTCGGAGCTGGTCTCTGGCGGGGAGCTCTTTGACTTCTCGGCGGAGAGGA  
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30 GAACTATGAGCCGCTGGGCTGGAGGCGGACATGTGGAGCATCGGTGTCATCACCTATAT  
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CCTGGAACATTTCCTGGTAAGGCGATCCGGCGGCGGAACTGTCGTGGTGAGGACAGCGG  
35 CCGCAAGCCCGAGCGGCGGCGCTGAAGACCAAGCGCTCTGAAGGAGTACACCATCAAGTC  
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GGAGGAGCGGCGGCGCGAGGAGGGCTGCGCGAGCTGCAGCGCAGCGCGGCGCTCTG  
CCACGAGGACGTGGAGGCGCTGGCGGCCATCTACGAGGAGAGGAGGCTGGTACCGCGA  
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40 GGCGCTCAAGCGGCAGGCGCAGGAGGAGGCCAAGGGCGCGCTGCTGGGGACCAGCGGCT  
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45 TGCCCGAGCGCCACCGAGCTGGAGGCGGAGTGGGAGGAGCTGGAGCCAGGCCCGTAAGTTC  
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ACCTTCACCCCTGCATCGTGGTGACCTGGGACCTCCAGGCAGCGTGGCTGTGGCAC  
CGTGAGGGTTGGGACCCACCGAGGCGCAGAGGCGGCCGAATGCAGCCCTGGTTTCAGGCC  
CGGAGGAGGGTTTGCGGGTAGTTGCACGACAATTTCGGCGGGTGTGCTGTGTGCTGCC  
50 ATTAGCCAGGAGGAGGTGCTGGGACGGGAGGCTGGGATGGACGGCGGACAGGCAGTCC  
CCACGCTGTGGGTGGGCGCGGCTTGGTGGGGTCTTCCACTGTGTGCCCTTCTCGCCGA  
GGCCGCTCCCGGGGTGGGGTGCCCTGCTGCGGACTCTCCGCGAGCCCCATCGTTCG  
GCCTGTGGACGCTTAGGCAAGAGCGGCCCTCTGCAGCCAAGAGAAATAAAATACTGGCTT  
CCAGAT

55 >H\_1.0.0\_60877 Homo sapiens, KIAA0186 gene product, clone MGC:13345 IMAGE:4333095, mRNA, complete  
cds si: gi-15214811/// [Human\_jongleur\_201102.cl.20423.singlet] [SEQ ID NO: 229]  
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60 TCGCGCGCCCCAAGGGCAACTGCCTGCCTTCAACGAGGATGGACTCAGACAAGTTCTGGA  
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65 TAATAATTATAAAAGATCTCTTGCTACTTATATGAGGTCACTGGGAGGAGATGAAGGTTT  
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70 ACTCACTCTCTCCACCACTCCCTTCACTCCCTCTTTGATTTTAGAAGCTATAGACATTG  
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TTTTTTTAATGTGTACACTATTCTTCTACTCTTTTTTGGTTTTGGTTTTGTTTTGTAG  
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5 TTAATGAAAGTAAACATGGTTACATTGAATCTCTTAAATAAGCAGTCACTTGGCTGGA  
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15 CACAATTTTTTTTTCTTTTACTTCTAGAAGTGTATAATTTTAAAGCTTTTACTTTGGT  
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TGGAGCCTGGGTGATAGAGTGAACACTGTCTTGCCNNNNNNNNNNNNNNNNNNNNNN  
N  
>H\_1.0.0\_4048 Homo sapiens zootin related factor 1 (ZRF1), mRNA cr: gi-22049761///  
[Human\_jongleur\_201102.987.C3] [SEQ ID NO: 230]  
20 GTGAGACTGGCCTCCACACCACGAAAGATCCATCCCGGAAGTGCTTACTGGTCTCTCCA  
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CCGCGCCCATCATGCTGCTTCTGCCAAGCGCCGCGACGGCCGGGGCACCCGCATCACCC  
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25 CTTTTGTTAAGAGGAGAAACAGAAATGCTTCTGCTCTTTTCAGGAACTGGAGGATAAGA  
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30 ACTTCACTTGCATAACTAAAGCTTATGAAATGTTATCTGATCCAGTGAAGAGACGAGCAT  
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35 AAGCAGAATGTCGTGATGAGAGAGATCGATTGAAAAGCAGAACAGAGCAACAGAGCAC  
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40 TGGCAAAGAAGGAAAAAGATATCCAGAAAAAGCCATTAAGAAGGAAAGGCAAAACTTC  
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45 AAATAAATGAGCAAAATCAGAAAAGAGAAAGAGGAGCTGAGGCTCGTATGCGACAAGCAT  
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>H\_1.0.0\_61535 Homo sapiens cDNA FLJ36226 fis, clone THYMU2001018, moderately similar to MOBI  
PROTEIN si: gi-21752445/// [Human\_jongleur\_201102.cl.22024.singlet] [SEQ ID NO: 231]  
60 ACTTCCGCCCCCTCGCCTGCCATTGGAAGTCTGAGCCGAAGTCTGCGGCCACCGA  
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CGCGGCCAACATGAGCTTCTTGTGTTGGTAGTCGCTCTTCTAAACCTTTTAAACCAAGAA  
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TAGCTGAAAGTATAGGTTTATTAGAAAATAAATGATCTCCCTCTCTTAAGGTAATTATTT  
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TTTGACATTTTACGATTTTTTTTGAAAAAAAATGTGACAACAATATAAATAGTTGTTGT  
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AGAGCAATTTTCAAG

>H\_1.0.0\_113724 Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]  
as: gi-20365192/// UI-E-EJ1-aka-c-14-0-UI.r1 Homo sapiens cDNA 5' end /clone=UI-E-EJ1-aka-c-14-0-UI  
/clone\_end=5' /gb=BQ189641 /gi=20365192 /ug=Hs.373409 /len=566. [gnl|UG|Hs#S4404983] [SEQ ID NO:  
232]

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GGAGGAAGTCCCTAGTTTATGTCATGTGAACAGGAAATCTTGGGTGGCGAGATGGCTCAA  
CGGCTAAGAACACTTATTGCTCTTCTGAAGGCCCTGAGTTCAAATCCCAGCAATCACATG  
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>H\_1.0.0\_5968 Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,  
pigment epithelium derived factor), member 1 (SERPINF1), mRNA cr: gi-4505708///  
[Human\_jongleur\_201102.1833.Cl] [SEQ ID NO: 233]

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AGACATCCATGGTACCTATAAGGAGCTCCTTGACACGGTCACTGCCCCCAGAAGAAGCT  
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TATCCCT

>H\_1.0.0\_21590 Homo sapiens, similar to sphingosine kinase, clone MGC:40267 IMAGE:5213270, mRNA,  
complete cds cr: gi-22539642/// [Human\_jongleur\_201102.9905.C4] [SEQ ID NO: 234]

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GCGCCGCGGCTCCCAACCGCTCTGGAGCTCCGGGAGGGGACACGGCAACCTGGATGGCTG  
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 10 CTGGTGCGGTGCGAGGAGCTGGGCCGTGGGACGCTCTGGTGCTCATGTCTGGAGACGGG  
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 25 AGCGGTTGCGTGGAGCCCCCGCCAGCTGGAAGCCCCAGCAGATGCCACCGCCAGAAGAG  
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 30 CACCCACGAACCAATCCAATAAAGTGACATTCCC  
 >H\_1.0.0\_15972 Homo sapiens proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), mRNA  
 cr: gi-5803122/// [Human\_jongleur\_201102.6827.C1] [SEQ ID NO: 235]  
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>H\_1.0.0\_19679 Homo sapiens CD5 antigen-like (scavenger receptor cysteine rich family) (CD5L), mRNA  
cr: gi-5174410/// [Human\_jongleur\_201102.8776.C1] [SEQ ID NO: 245]

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55 TATCCTGAGGCTTCCACAATGTTCCCTCCTGTGAGCCAAGGAGGCAAACTGCACAAGC  
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>gi|16398196|gb|AV378849.2|AV378849 AV378849 RIKEN full-length enriched, adult male cecum Mus  
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70 NATGTGGTAAGAAATACCAGAAATGTAGATTTTGGACTTTGGATTAGTTGTTTGTGTTCC  
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CAAAGGGAATCTTTGTTCTCAAAGAAACCAAAACCCACACACTATATTAGCTATGATT  
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5 CAACTCCAGTCACTGGAATTGAGTTTACCCGAGCCATCTTGCTCGCCCATTTTAAACCC  
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10 >H\_1.0.0\_4005 Homo sapiens serine/threonine kinase 12 (STK12), mRNA cr: gi-4759177///  
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25 ACAATGTGTGGCACCCTGCACTACCTGCCCCAGAGATGATTGAGGGGCGCATGCACAA  
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30 CGGAGGGTGCTGCTCCCTCTGCTGCCCTCAATCTGTGCGCTGATGGTCCCTGTCAATCACT  
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35 mRNA, complete cds cr: gi-22713409/// [Human\_jongleur\_201102.10581.C2] [SEQ ID NO: 268]  
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C

>H\_1.0.0\_20190 Homo sapiens hypothetical protein CL25022 (CL25022), mRNA cr: gi-7661547///  
[Human\_jongleur\_201102.9081.Cl] [SEQ ID NO: 269]

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15 CAAAGCCCTTTTCAGATGCAGGATCATCAGGTTCCGATGAGTCTCATGTGGCTGCTGCACC  
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25 CTACCGACATTAGGATTCTCTGTTGATGACCTTGGATGCTGTAAAGTGATTTCGTATAG  
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30 TAAATGCAAAATGTTCAATTTATTTATTCATATCATGAATACAGTTGAACACATCCACATT  
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wolffian duct Mus musculus cDNA clone 6720465D24 3', mRNA sequence [SEQ ID NO: 270]

35 ACCAGGCCCGCCGCCATACCCCTCAAAACTTTGGGGTATACAAAAATTTATCGTTGGG  
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45 CTCAAACAGATGTATAGATTGGAGATTTTCTGTATGTATTTTATCCACCCCT  
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>H\_1.0.0\_13832 Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA cr: gi-  
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[Human\_jongleur\_201102.744.C2] [SEQ ID NO: 274]  
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35 AAGATTTATACAAAAGATTAAATACCAGGATCACACCCGAGTCAATGGGGAGAGGAA  
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45 TGCTGAATAAACCCATTGAAGAAATCATTGTACAGAAIGGAAAAGTAATTGGTGTAAAAAT  
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70 TTCTTACCACTTTCTTATTTCCCTATGTCTTTAAATTCCTTGATCTGCTCATTTCACTA  
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1

CGTCATTGTGAATTATCTCTAGA

>H.1.0.0.6694 Homo sapiens mRNA for period (Drosophila) homolog 3 hPER3, complete cds cr: gi-13160924/// [Human\_jongleur\_201102.2143.C5] [SEQ ID NO: 275]

5 NAGCAGGCGGAGTCCTGAAAGTCGAGCGAGCTCCGGGTITTTGAAAATGTTGGAGGGAAA  
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10 AACAGCAAGATCGAAACAGAGTTTCTGAAGAACTTATCATGGTTGTCCAAGAAATGAAAA  
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70 TGAATGTTAAGATTTTTTCTTCTGATTTTAAATACACGTAATCTTTTGAAGCAGACA  
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TTTTGTAGTTGAATTGTCTTCTAAAGAGATTGGATGGCCTCTAAAGAGGTATGTGTATCT  
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5 GAAATGCCACCTACAGGTGTGTACTTTTCATAATGGTTTCCATGAATGTAGTACGTTCA  
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>H 1.0.0\_9423 Homo sapiens cDNA FLJ10331 fis, clone NT2RM2000635, highly similar to Homo sapiens  
mRNA for KIAA0729 protein cr: gi-7022294/// [Human\_jongleur\_201102.3321.C2] [SEQ ID NO: 276]  
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70 GAAGCAGTGGTCTGCTAGCAGTAGTGGGCATAGTATGATCTAGCAATGAGGTTAAT  
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CAGATATTGAAGCCCTCAAAGAGGAAGATGAAGACGATGATCATGGTCATAATCCTCCCA  
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70 GTACATATGTAATTTTGAATCTTTTAAACCTGAAAAATAAATAGTCATTAAATGTTG

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 >H\_1.0.0.24134 Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA cr: gi-  
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>gi|23623688|gb|BU700918.1|BU700918 UI-M-DJ1-bty-f-10-0-UI.s1 NIH\_BMAP\_DJ1 Mus musculus cDNA clone  
UI-M-DJ1-bty-f-10-0-UI '3', mRNA sequence [SEQ ID NO: 289]  
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5 AACAGAAAGACAGCACCTTCTTGAGACAGGACACTCCAGCTTTGCTTACATGCCCCGACA  
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25 >M\_1.0.0\_7865 Mus musculus uterine-specific proline-rich acidic protein (Upa), mRNA cr: gi-6678510///  
[Mouse\_jongleur\_201102.4046.C1] [SEQ ID NO: 291]  
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>H\_1.0.0\_19196 Homo sapiens heat shock 70kDa protein 1B (HSPA1B), mRNA cr: gi-5579470///  
55 [Human\_jongleur\_201102.8523.C4] [SEQ ID NO: 299]  
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65 GCATTCTACCCCGAGGAGATCTCGTCCATGGTGTGACCAAGATGAAGGAGATCGCCGAG  
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70 GACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGGACACCCACTGGGTGGGAGGAC  
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>H\_1.0.0\_19194 Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA cr: gi-5579469//  
 [Human\_jongleur\_201102.8523.C2] [SEQ ID NO: 300,302]

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TACTGCCATCTTACGACTATTCTCTTTTAAATACACTTAACTCAGGCCATTTTTTAAG  
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>H\_1.0.0\_41040 Homo sapiens cDNA FLJ40060 fis, clone TCOLN2000236, highly similar to P55-C-FOS  
PROTO-ONCOGENE PROTEIN si: gi-21757114/// [Human\_jongleur\_201102.cl.1192.singlet] [SEQ ID NO: 301]

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>H\_1.0.0\_24972 Homo sapiens kinesin-associated protein 3 (KIFAP3), mRNA cr: gi-18105053///  
[Human\_jongleur\_201102.11853.Cl] [SEQ ID NO: 303]

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(CYP2B6), mRNA cr: gi-20522261// [Human\_jongleur\_201102.5324.Cl] [SEQ ID NO.: 304,317]  
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30 TGCACTGGTGTCTTTGGATTCCCTGATATGTTCTTCAAATCTGTGAGAATTAAATAAAC  
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>H\_1.0.0\_135942 Homo sapiens similar to data source:MGD, source key: MGI:102849,  
evidence:ISS-kallikrein B, plasma 1-putative (LOC201859), mRNA as: gi-20472737///  
[gi|20472737|ref|NM\_114391.1|] [SEQ ID NO: 305]  
35 ACAGCTATGGGGAAGATATTTGGTGTCAAAGTAATGATGATTCGAGTATGTCGGTGCA  
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40 CTTTTAAGTGTGACTGATGACGAAGGGAACAGGCTAAGTCATGAAGATATTCGAGAAGAA  
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>gi|1088447|dbj|D49387.1|HUMANPDPLB Human mRNA for NADP dependent leukotriene b4 12-  
hydroxydehydrogenase, partial cds [SEQ ID NO: 306]  
45 GGCAGTGGAACTCTCGGCTCCTGAGCTTCAGGATGGTTCGTACTAAGACATGGACCCCTG  
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>H\_1.0.0\_19867 Homo sapiens mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding  
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65 CGGCGTCTGCGCAGTGCAGCGCCTTTAAGCCCGGGCTCGCGCTCTCGGACCGTGCTTT  
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70 CGGGTATTCTTGGTGGATTTTATGCACCCACCGCAGCTGTTGAAAGCATGTTGGAGCA  
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[Human\_jongleur\_201102.8179.C1] [SEQ ID NO: 309]  
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>H\_1.0.0\_10681 Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent),  
methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA  
cr: gi-13699869///  
[Human\_jongleur\_201102.3990.C6] [SEQ ID NO: 310]  
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>H\_1.0.0\_55112 Homo sapiens, Similar to Forkhead-like transcription factor BF-1, clone MGC:33583  
IMAGE:4823883, mRNA, complete cds si: gi-23241914/// [Human\_jongleur\_201102.cl.11482.singlet] [SEQ  
ID NO: 311]

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>H\_1.0.0\_38297 Homo sapiens cytochrome P450 variant 3A7 (CYP3A7) mRNA, complete cds si: gi-  
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5 GGGTGAAGGAGACCAGCATGCCTGTGTACTGCACGTGCGCGGGAGACTTCGCCCTCACC  
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>H\_1.0.0\_12060 Homo sapiens 3-hydroxysteroid epimerase (RODH), mRNA cr: gi-19743807///  
10 [Human\_jongleur\_201102.4709.C1] [SEQ ID NO: 327]  
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25 AGCAAAGTTGGAAGAAGCCCCAAGCATATTAAGGAGACCTATGGACAGCAGTATTTTG  
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>H\_1.0.0\_43235 Human mRNA for liver alcohol dehydrogenase (EC 1.1.1.1) gamma 2 subunit from ADH3  
locus si: gi-28403/// [Human\_jongleur\_201102.cl.2404.singlet] [SEQ ID NO: 329]  
40 GATGCACTCAAGCAGAGAAGAAATCCACAAGTACTACCAGCCTCCTGGTCTGCAGAGAA  
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60 AACATACAGATGCCCTCCCTGTAGCAGTTTTCAGCCTCCTTACCCTACATGATCTGG  
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>H\_1.0.0\_11188 Homo sapiens synaptonemal complex protein 3 (SYCP3), mRNA cr: gi-24233579///  
65 [Human\_jongleur\_201102.4259.C3] [SEQ ID NO: 330]  
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70 GAGTGGATCAGAGGAAGATGTTATTGAAGGGAAGACTGCAGTCATTGAGAAACGTAGGAA  
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 >H\_1.0.0\_23435 Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2  
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>gi|4504508|ref|NM|000198.1| Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid  
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4504502/// [Human\_jongleur\_201102.518.C1] [SEQ ID NO: 334]  
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polymerase II, S, 150kD, clone IMAGE:3636799, mRNA cr: gi-15559581///  
60 [Human\_jongleur\_201102.11703.C2] [SEQ ID NO: 335]  
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60 TGTGTTGAATGTTAACTTTGTGTCTAAAGTTAATTTTAAAGATGTTGAATGTTCACTT  
ATGATTTTGAAGTACATAAACCACCTTTTATATAAG  
>H\_1.0.0\_2140 Homo sapiens albumin (ALB), mRNA cr: gi-8392890// [Human\_jongleur\_201102.252.C13]  
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65 AAGTGATTGGGAGCGCCTCGGCATCCCCATGAGTGTGCTGATGGGGGCCAATTTGCCA  
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70 GAGTTGGTGCAGTGGCACACCTGTGGTCCCAGCTACTTAAGAGGCTGAGGTGGGAGGATC  
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AATAAATATTTTTTAAAAAGAGTCCTTCCCTCAAAGCCTTGCCCCCTCTCACTTTAGGC  
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10 TAGGGCTTTACAATGGAATGGTCAATAGATGGGAAGTCAACTAGAGAGAAGAGTGGTTT  
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15 GCTTCTGTGATGGCTGGGCTTTGGCGACAACCAAGGCGGCAGTGTCCGGCTGGGTCT  
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TGGCTTTTACCT

>H\_1.0.0\_3308 Homo sapiens regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic  
thread protein) (REG1A), mRNA cr: gi-4506470/// [Human\_jongleur\_201102.658.C1] [SEQ ID NO: 337]  
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70 GTCTCAGAGCCAGGCCAAGAGCCAGACAGAGTTGCCAGGCCCGGATCAGCTGCC  
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5 TGTGAGCCTGACCTCAAGCACAGGATTCAGAAATGGAAGGATGTGCCTTGTGAAGACAA
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10 >gi|5031940|ref|NM|005596.1| Homo sapiens nuclear factor I/B (NFIB), mRNA [SEQ ID NO.:338]
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Figure 5

>gi|10190552|ref|NM|003901.1| Homo sapiens sphingosine-1-phosphate lyase 1 (SGPL1), mRNA [SEQ ID NO: 1]

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>H\_1.0.0\_131819 Homo sapiens mRNA for putative cytoplasmatic protein (ORF1-FL2i) as: gi-12214172///

[gi|12214172|emb|AJ245876.1|HSA245876] [SEQ ID NO: 2]  
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55 AGGGTTTGGCCATCACCTATGGCCTGCTGGAGGAGTGTGGCCTTAGGAYGGAGCTGGATA  
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TGTGCTCTCTCGTGTTCAGGTGGAGTAGAGACAGTAATGGGTAGAGACTTTAGGAAT  
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NN  
NN  
NN

>H\_1.0.0\_21316 Homo sapiens claudin 8 (CLDN8), mRNA cr: gi-21314655///

[Human\_jongleur\_201102.9749.C1] [SEQ ID NO: 3]  
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70 AAACCTTCTGGGAAGGACTGTGGAATGAAATGCGTGAGGCAGGCTAACATCAGGATGCAGTG  
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>M\_1.0.0\_17482 Mus musculus LB9 gene, partial sequence cr: gi-687696///  
[Mouse\_jongleur\_201102.10974.C1] [SEQ ID NO: 4]  
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65 AGCCTGTGCCCTGCTCTCGAGGCTCATGGCTTGTCCCTGGTCACTCCTGTCTGACTG
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>H\_1.0.0\_22120 Homo sapiens, glutamate-ammonia ligase (glutamine synthase), clone MGC:20322  
IMAGE:4137547, mRNA, complete cds cr: gi-15080156/// [Human\_jongleur\_201102.10208.C8] [SEQ ID NO: 12]

5 GGCATGAGGCGAGAGTGGGAGAAGAGCGGAGCGGTGTGAGCAGTACTGCGGCCTCCTCTCC  
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CAGGGTCCCATATTACTGTGGTGTGGGAGCAGACAGCCCTATGGCAGGGACATCGTGGAG  
20 GCCCATTACCGGGCTGCTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTG  
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25 AGCAAGCGGCACCACTACCAATCCGTGCTATGATCCCAAGGAGGCCCTGGACAATGCC  
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55 CTCAATTGTAACAACTGTGTAAGTCCCAAGCAGCACTTATAAATCAGCCTAACATAA  
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>H\_1.0.0\_3492 Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA cr: gi-4504066/// [Human\_jongleur\_201102.747.C1] [SEQ ID NO: 13]

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15 >H\_1.0.0\_58926 Homo sapiens cDNA FLJ34227 fis, clone FCBBF3025098 si: gi-21749942///  
[Human\_jongleur\_201102.cl.16700.single] [SEQ ID NO: 14]  
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70 >M\_1.0.0\_53089 vul3h03.x1 Mus musculus cDNA, 3' end as: gi-4602318/// /clone=IMAGE:1180565  
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10 NNN  
NNNNNN

>H\_1.0.0\_48153 Homo sapiens cyclic AMP-regulated phosphoprotein mRNA, complete cds si: gi-6563225///  
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30 TTNN  
NNNNNN

>H\_1.0.0\_25158 Homo sapiens necdin homolog (mouse) (NDN), mRNA cr: gi-10800414///  
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60 NO: 22]  
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35 >H\_1.0.0\_26649 Homo sapiens, Similar to expressed sequence AI415388, clone IMAGE:5734009, mRNA,  
partial cds cr: gi-22477646/// /cds={0,1754} /gb=BC036812 /gi=22477646 /ug=Hs.404915 /len=3000  
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>H\_1.0.0\_20198 Homo sapiens cDNA FLJ10456 fis, clone NT2RP1001395 cr: gi-7022498//  
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>H\_1.0.0\_3735 Homo sapiens undifferentiated embryonic cell transcription factor 1 (UTF1), mRNA cr:  
gi-4507858/// [Human\_jongleur\_201102.841.C1] [SEQ ID NO: 25]

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>H\_1.0.0\_5504 Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA cr: gi-  
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CTCAGCACAGAACTATTTAAGATTAAGAATGCTTATGAGGAATCTTTAGACCAACTTGAA  
ACCTTGAAACGGGAAATTAAGAATCTGCAGCAGGAGATTTCTGATCTCACTGAACAGATT  
35 GCAGAAAGGAGAAAGCGCATCCATGAACCTGGAAGAAATAAAGAAGCAAGTTGAGCAAGAA  
AAGTCTGAACCTGCAACAGCTGCTTAGAGGAGGAGAGGAGCATCTCTGAACATGAAGAGGA  
AAGATCCTGCCATCCAGCTTGAGTTGAACCAAGTCAAGTCTGAGGTTGATAGGAAAAAT  
GCTGAAAGAGATGAGGAATTGACCAGATGAAGAGAAACCATTAGAATCGTGGAGTCC  
ATGCAGAGCACACTGAGTCTGAGATCAGGAGCAGGAATGATGCCATTAGGCTCAAGAA  
40 AAGATGGAGGAGAGCTCAATGAATGGAATCCAGCTGAACCATGCCAACCGCATGGCT  
GCTGAGGCCCTGAGGAATATAGGAACACCAAGCCATCCTCAAGGATACCCAGCTCCAC  
CTAGATGATGCTCTCCGAGCCACAGAGGACCTGAAGGAACAGCTGGCTATGCTGAGCGC  
AGAGCCAACTGCTGCTCAGGCTGAGATCGAGGAACACAGGCCAGTCTGGAACAGACGAG  
AGGAGCAGGAAATCGCAGAACAGGAGCTCCTGGATGCCAGTGAACGTGTTGAGCTCTG  
45 CACACCCAGAACACCCAGCTGATCAACCAAGAAGAAGCTGGAGACAGACATTTCCCAA  
ATCCAGGGAGAGATGGAAGACATCATCCAGGAAGCCCGCAATGCAGAAGAGAGGCAAG  
AAGGCCATCACTGATGCTGCCATGATGGCTGAGGAGCTGAAGAAGAACAGGACACAGC  
GCCATCTGGAGCGGATGAAGAAGAACTTGAACAGACGGTGAAGGACCTGCAGCATCGT  
CTGGATGAGGCTGAGCAGCTGGCCCTGAAGGTTGGGAAGAAGCAGATCCAGAAACTGGAG  
50 GCCAGGGTTCGTGAACCTGAAGTGAAGTTGAAGTGAACAGAAGCGCAATGTTGAAGCT  
GTCAAGGGTCTACGCAACATGAGAGAAAAGTGAAGGAACCTCACTACCAAACTGAGGAA  
GACCGCAAGATATTCTACGCTCAGGACCTGCTGGACAAGCTGCAAGCAAGGTGAAA  
TCCTACAAGAGACAAGCTGAAGAAGCGGAGGAACAATCCAACGTCAACCTCTCCAAATTC  
CGGAGGATCCAGCAGAGCTGGAGGAGGCCGAGGAAAGGGCTGACATTGCTGAGTCCCAG  
55 GTCAACAAGCTGAGGGTGAAGAGCAGGAGGTTCAACAAAAATCATAAGTGAAGAGTAA  
TTTATCTAACTGCTGAAAGGTGACCAAGAAATGCACAAAATGTGAAAATCTTTGTCACT  
CCATTTGTACTTATGACTTTTGGAGATAAAAAATTTATCTGCCA

>H\_1.0.0\_10487 Homo sapiens thyroid hormone responsive (SPOT14 homolog, rat) (THRSP), mRNA cr: gi-4507496/// [Human\_jongleur\_201102.3891.C1] [SEQ ID NO: 27]

AACCATGCAAGTGCTAACCAAGCGTTACCCCAAGAACTGCTGCTGACCGTCATGGACCG  
60 GTATGCAGCCGAGGTGCACAACATGGAGCAGGTGGTGTATGATCCCCAGCCTTCTCGGGGA  
CGTGCAGCTGAGTGGCCCTGGGGGCCAGGCCAGGCTGAGGCCCTGATCTCAACCTA  
CTTCACCATGCTCAAGGCCATCTGTGTGGATGTGACCATTGGCTGCTGCCCGGGGAGGA  
GTGGCAGGCCAAGGTGGCAGGCAGCGAAGAGAAATGGAACCCGAGAGACAGAGGAAGTCGA  
65 GGACGAGAGTGGCTCAGGAGAGCTGGACCTGGAAGCCCAAGTTCACCTGCATTCTCCAG  
CTTCCATCATCTCTCATGCACCTCACCGAGAAAGCCAGGAGGTGACAAGGAAATACCA  
GGAAATGACGGGACAGATTGGTAGACCTTGGACACTAGGGAAGATCCCTTCACATGATA  
GAAGACAGACTTTGATGAGGTCGGCGGAGCAGTTCCTAGCCAATGATGAGAGCAGAA  
AGGCCATAGACCTGACGCCAGAAAGTGAAGCGGCTCAGTTCTCCGGGATGCTTCTCTACCT  
70 CCTGAGCACCAATTCCTGATTCCAGTCACTGGCTCACCTTTAGAAATGTCTGTGCTATT  
CACTGTCTCCCTCGCTCTCTTAACAGCTTGGGAGGTTGACCATGGTTCCAGAGGGAGT

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AGACAAATTACCTGTCCAGTGTGGTATGGTAGGAAGAGTGTAGGTGTTGGCACGTGACCAA  
AATTCACATCCCTCCCTCATGGCAGTCATTTCAGTATGTGTAATGTACAAAGTTATTTAAAC  
CATTGGAGCCTAAATCCCTCATCTATAAAATGGGGATAATATTCTACCTCCCAAGCT  
TATGAAACTAAACATGATGAATCAAAGCCCTTGGCATGTGAGGGCTATTAAATAGCC  
TGATTTTTTTTCTCCCTCTCCCAATGTATTGCTCTGGCCCTTGTCTTTTACCT  
CCAGAGCTAAGAGGTAGCAGAGTCTCTTGGGATGAGTGATTACCCCTCTTACTTGGCGAC  
CACTGATGAGATCAACAACAGGTGAACATATAAACCTATTATTATGTCAGAACTAATAAA  
AAATCCAAAGCCTTGT

>H\_1.0.0\_6779 Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 2 (FACL2), mRNA cr: gi-  
12669906/// [Human\_jongleur\_201102.2170.C2] [SEQ ID NO: 28]

CGGGCAGTGACAGCCGGCGCGGATCGCGCTCCACGGAGGAGAATCAGCTTAGAGAACTA  
TCAACACAGGACAATGCAAGCCCATGAGCTGTTCCGGTATTTCGAATGCCAGAGCTGGT  
TGACTTCCGACAGCTGCGTACTCTTCCGACCAACACGCTTATGGGCTTCGGAGCTTT  
TGCAGCACTCACCACCTTCTGGTACGCCACGAGACCCAAACCCCTGAAGCCGCCATGCGA  
CCTCTCCATGAGCAGTCACTGGAAGTGGCGGTAGTGGTGGTGCACGAAGATCCGCACTACT  
TGACAGCGACGAGCCCTTGGTGTATTCTATGATGATGTCAACAATTATACGAAGGTTT  
CCAGAGGGGAATACAGGTGTCAAATAATGGCCCTTGTTTAGGCTCTCGGAAACAGACCA  
ACCTATGAAATGGCTTTTATATAAACAGGTTGCGAATGTGCGGAGTGCAATAGGCTCAGC  
ACTGATCCAGAAGGGCTTCAAGACTGCCCCAGATCAGTTCATTGGCATCTTTTGCTCAAAA  
TAGACCTGAGTGGGTGATTATTGAACAAGGATGCTTTGCTTATTGATGGTATCGTTTCC  
ACTTTATGATACCCCTTGGAAATGAAGCCATCAGCTACATAGTCAACAAGCTGAACCTCTC  
TCTGGTTTTTTGTGACAAGCCAGAGAAGGCCAACTCTTATTAGAGGGTGTAGAAAATAA  
GTTAATACCAGGCCCTTAAATCATAGTTGTGATGGATCCCTACGGCAGTGAACCTGGTGG  
ACGAGGCCAGAGGTGTGGGGTGGAAAGTCAACAGCATGAAGGCGATGGAGGACCTGGGAAG  
AGCCAACAGACGGAAGCCCAAGCCTCCAGCACCTGAAGATCTTGAGTAATTTGTTTTCAC  
AAGTGGAACTACAGGCAACCCCAAAGGAGCAATGGTCACTACCGAAACATAGTGAGCGA  
TTGTTTCACTTTTGTGAAAGCAACAGAGAATACAGTCAATCCTTGGCCAGATGATACTTT  
GATATCTTTCTTGCTCTCGCCCATATGTTTGAAGAGTGTAGAGTGTGTAATGCTGTG  
TCATGGAGTAAAAATCGGATTTTTCGAAGGAGATATCAGGCTGCTCATGGATGACCTCAA  
GGTGCTTCAACCCACTGTCTTCCCGTGGTTCGAAGACTGCTGAACCGGATGTTTGACCG  
AATTTTCGGACAAGCAACACACCGCTGAAGCGATGGCTCTTGACTTTGCTTCCAAAGAG  
GAAAGAGCAGAGCTTCCGAGCGGCATCATCAGAAACAACAGCCTGTGGCACCAGGCTGAT  
CTTCCACAAAGTACAGTGCAGCCTGGGCGGAAGAGTCCGGCTGATGGTGACAGGAGCCGC  
CCCGGTCTGCGCACTGTGCTGACCTTCTCAGAGCAGCCCTGGGCTGTGAGTTTATGA  
AGGATACGGACAGACAGAGTGCATGCCGGGTGCTGCTAACCATGCTGGAGACTGGAC  
CGCAGGCCATGTTGGGGCCCCGATGCGGTGCAATTTGATAAACTTGTGATGTGGGAAGA  
AATGAATTACATGGCTGCCGAGGGCGAGGCGAGGTGTGTGTAAGGCCCAAATGTATT  
TCACGGCTACTTGAAGGACCCAGCGAAAAACAGCAGAAGCTTTGGACAAAGACGGCTGGTT  
ACACACAGGGGACATGGGAAATGGTTACCAAATGGCACCTTGAAATTTATCGACCGGAA  
AAAGCACATATTTAAGCTGGCACAAGGAGAATACATAGCCCTGAAAAGATTGAAAATAT  
CTACATGCGAAGTGAAGCTGTGCTCAGGTGTTTGTCCACGGAGAAAGCCTGCAGGCATT  
TCTCAATTGCAATTTGTGTACCAAGTGTGAGACATTATGTTCTGGGCCCAAAAGAGAGG  
ATTTGAAGGGTCTTTGAGGAAGTGTGCAGAAATAAGGATGTCAAAAAGCTATCTCTGA  
AGATATGGTGAGACTTGGGAAGGATCTGCTGTAAGCAATTTGAACAGGTCAAAGGCAT  
CAGATTGCACCTTGAATTATTTCTATCGACAATGGCCTTCTGACTCCAAGCAATGAAGGC  
GAAAAGGCCAGAGCTCGGCAACTATTTAGGTGCGAGATAGATGACCTCTATTTCCACTAT  
CAAGGTTTATGTGAAGAAAGAGCTCAGAGGAAATGGCAGAGTTCCACAATCTTCTCTC  
CTGCTGATGGCCTTCACTGTTGTTAATTTGAATACAGCAAGTGTAGGGAAGGAAGCGTTC  
GTGTTTGACTTGTCCATTGCGGCTTCTTCTCATAGGAATGCTAGAGGAAACAGAACCCG  
CCTTACAGTCACCTCATGTGACAGCAATGTTTATGTAATACACACTTTCCAAATGAG  
CCTTAAAAATTTGAAGGGGATATATAAATGTGCTAAGTTATTTGAGACTTCTCAGTT  
TAAAAAGTGGGTTTTAAATCTTCTGCTTCCCTGTTTTCTAATCAAGGGGTAGGACTTT  
GCTATCTCTGAGATGTCTGCTACTTGTGCAATCTTGCAGCTGTCTGTGCTCTAAAGA  
GTACAGTGCCTAGAGGGAAGTGTCCCTTTAAAAATAAGAACACTGTCTTGGCTGGAG  
AATCTCACAAGCGGACAGAGATCTTTTAAATCCCTGCTACTGTCTCTTCTCAGAGCA  
TTCACAGAACCTTCTGATTGTAAGGGTTACGAAACTCATGTTCTTCTCAGTCCCCTG  
TGGTTTCTGTTGGAGCATAAGGTTTCCAGTAAGCGGAGGGCAGATCCAATCAGAAACCA  
TGCAGATAAGGAGCCTCTGGCAAAATGGGTGCTCATCAGAACCGGTGGATTCTCTTCATG  
GCAGAAATGCTCTTGGACTCGGTTCTCCAGGCCTGATTCCCGCACTCCATCTTTTTCAGG  
GTTATTTAAAAATCTGCTTAGATTCTATAGTGAAGACAGCATTTCAAGAAAGAGTTA  
CCTGGATCAGCCATGCTCAGCTGTGACGCTGAATAACTGTCTACTTTAICTTCACTGAA  
CCACTCACTCTGTGTAAGGGCCAAAGATTTTAAATGTGGTTTTTATATCAAAAGATCAT  
GTTGGGATTAATCTGCTTTTCCCAAATAAATACTCTCAGGCAAGCATTTCTTTAAA  
GCTATTAAGGGAGTATATACTTGAAGTATTATTGAAATGGACAGTAATAAGCAAATGTTT  
TTAATAATGCTACCTGATTCTATGAAATGTGTTGACAAGCCAAATTTTAGGATGTAGA  
AATCTGGAAGTTTCAATTTCTGGGATTCATTTCTCCAGGGATTTTAAAGTTAATTGG  
GAAATTAACAGCAGTTCATTTATGTGAGTCTTGGCACATTGACTGAATTGAGCTGT  
CATTTGTACATTTAAAGCAGCTGTTTGGGGTCTGTGAGAGTACATGTATTATATACAG  
CACAACAGGGCTTGCATTAAGAATGTGCTATTGTAATAACACTACTTGGTAGCCCTAAT  
CATATATGTATTCTAATTGCAAAAAAGTCAATAATTTGTACCTTGGGGTTTTGAATG  
TTTGCTTTAAGTGTGGCTAATTTCTATGTTTTATAAACCAAAACAAATTTCCAAAAACA

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ATGAAGGAAACCAAATAAATATTTCTGCATTTTCG

&gt;M\_1.0.0\_12599 Mus musculus L-amino acid oxidase 1 (Laol), mRNA cr: gi-21914876///

[Mouse\_jongleur\_201102.7471.C1] [SEQ ID NO: 29]

5 GTAGCATGGTGCACCAAGCCAGGGGAAGCAGGCATTCTGTATTGTGGGCAGTCAGGAGCT  
CTGGCTTGTGCTGGAAGTTCAGAGACCAGATGTCCACCCCAACCCTCATCCCTTCCCAGA  
GTGATTACAGCAAGTTCACAATGGCCCACTGTGCCATTCCCCTCTTGCTCCTTAGCAA  
CAGGAGGGCTGGGAGACCGGCTTTTCTAGAAGAGACTGTCAAGGGGAAAAGTGGATTGAAA  
GTGGGGGGAAGGTGAGGTGAGTTATTACTGTCTCATCTCACCTGACGGGTGAGGCTTGGTT  
10 CAGGCCCACTTGTCTGGCTGAGTCAATAGGGCCAGAGACCATTGGTGGGATAAGAGCC  
AAATATTGCCAGAGAGGTGCTGCTTCTTCATAAAGAGAAGAGCAGAGGCTCAGAGTTCCG  
CATGAGTTTCAGGACCATGGCCCAAGAGAGTGGAAATCCTTGTTTGGGGGATCCTGCTCTG  
CGTCTCCAGCTGCCTTGCCCTCTATGAGAACCTTGTCAAGTGTTCAGGATCCCATTGA  
TGAGGCTTCTCTCTCATAGCCAGAAATGGGCTCCATACCTCCCCACTGCTAAGCGTGT  
GGTGGTATGGGAGCTGGCATGGCAGGCCTAGTGGCAGCTAAGACCCTACAGGATGCTGG  
15 TCACGAGGTAACCATCTGGAGGCCAGCAACCACATCGGAGGTAGGGTGGTCACACTCAG  
AAACAAGGAAGAGGCTGTGACTTAGAACTTGGACCAATGCGAATCCCAAGAAAGCCACAA  
GCTAATCCACACCTATCTCCAGAAGCTTGGCCTGAAACTGAATAAGTTCAACAGTATGA  
TAGCAACACCTGGTACCTACTCAATGGACAACGCTATCGTGCCTCAGAAGTCATGGCTAA  
CCCAGGAATCTTTGGGCTACCCCTGAGGCCCTCAGAGAAGAACAAACTGTTCACAGACCT  
20 GTTCTACCAAGCCACTAAGATCAAGATCAAAACCATAGGAAGACATCCAAGTCCAGCCAGCT  
GCTCTCCCTTTATGACTCTTACTCCACCAAGGCTTACCTGATGAAGGAAGGAACGCTGAG  
CAAAAGGGGCCATCGACATGATCGGGGATATAATGAATGAGAATGCTGGATATTATAAGT  
CCCTCCTTGGAGTCTCTGAGGATTGCAAGCATCTTCTCCAAAGTGCCCAATTTTCAGAG  
25 ATCACCGGTGGCTTTGGCCAACTCCCCAATGGCCTCAGTGCTAGCTGAAGCCTGGCACC  
ATCCGCTCTGTGCTCCAAAGTAGAAAGAGTGGTGAGAGACGGGCCCAAGGTTAAGGTTATG  
TACCGCACAGATGGGCCCCTTCTGCACTGCACAACTCACTGCGGATTACGCCATCATC  
ACTGCTCAGCCCAAGGCCACTCGCCTCATCACCTTCCAGCCACCTCTGTCCCGAGAGAAA  
ACACATGCCCTGCGCTCCGTTTATTACACAGTGCCACCAAGGTGGTTTATGTGTCAAC  
GAACGCTTCTGGGAACAAGATGGCATCCGGGGCGGCTACTCCATCACTGACCGACCTCC  
30 CGCTTCATTATCTATCCCAAGCCACAGCCTGCCAGGCGGCAAGGGAGTCTGCTGGCTCT  
TTCACTGTGGGTGATGATTCTCTCTTTGCTGCCCTGAAGCCCAACAGGTGGTTCGAT  
GTTGTGCTGGATGACCTTGCGGCAGTGCCACCGCATACCAAGGAGGAGCTAAGCGCATG  
TGCCCAAAGTCAGCCAGGCTCAAGCACTGGTCTCTAGACCCCTCACCATTTGGCGCTTTACA  
GAGTTCACACCTACCTATTTGTAGACTATTGGAAGCAGCTCTCCAGCCAGAGGGCCGC  
35 ATCTACTTTGCTGGGGAGCATACCTGCCTGCCGCACAGCTGGATAGACACCGCCATCAAG  
TCGGGCATCCGGGCCCTCTGCAACATTCAAGCTGCAGTGGAACAAGGAGCCACTCGAGGA  
CATACGGCTCTTTAGAGGCCCTTTGCCAACAATCAGGATGCCACCACCAACCAAGA  
ACAATCTGTGGGAGAGTCTAAGAGAATAAATAGGCTAGAAGATGAAGGAAGCCGAGACC  
CAGGAGAGAAGTCACCACTGGTCCCTTGGTCTACAAGCAGAAGCCCACTGGGAAGCTAC  
40 AAGAGACACCAACCTGCTATTTCTGTCTCACTCCCTCTCTATGGGAAATCAGAGGCCAG  
GGCATACAAGGCAGGGAGTAGGGGGTAGCTGTCAAGGCTGGAGAATTCTAGAATCAGCC  
TTTAGCTTGAAGGAATTGTCTCTCTGCTACAAAACAATAACAAGCAAAAG

&gt;M\_1.0.0\_25869 Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN full-length

45 enriched library, clone:D730050C14:glycosylation dependent cell adhesion molecule 1, full insert  
sequence cr: gi-12862225/// /cds=(48,503) /gb=AK021358 /gi=12862225 /ug=Mm.219621 /len=626

[Mouse\_jongleur\_201102.19220.C1] [SEQ ID NO: 30]

50 GATTCTACTCTGCTTCCCAGGGAAGCTGACCTTGTTCAGTGCCACCATGAAATCTTC  
ACTTCTCTGCTATTTGTGAGTCTTGCTGCCACCTCTCTGCTCTCTGCTGGGTCCAAA  
GATGAACCTTCAATAGAGACTCAGCCACAGATGCCATTCAGTCCCGAGTCCATCCC  
ACCAGCTACACCACTGAGGAGAGTACTTCCAGTAAGGACCTTTCCAAGGAGCCTTCCATC  
TTCAGAGAAGAGCTGATTTCCAAAGATAATGTGGTGATAGAATCTACCAAGCCAGAGAAT  
CAAGAGCCCGCAGGATCGGCTCAGGAGCGGTCATCTCAGCTGGAAGAGACCACAAGACCC  
ACCACCTCAGCTGCAACCCACTCAGAGGAAAATCTGACCAAGTCAAGCCAGACAGTGGAG  
55 GAAGAAGTGGGTAAATAATGAAGGATTTGTAAGTGGTGAGAGACATAATCTCTGGT  
GCCAGTCGTATCAGGAAGTCATGAAGACAAAACACCTAACCACTAAGTCCCATTGCTAGG  
TGGTGCCTTCATCAGCCACATTCTGCTCATCTGACCACCACTCTCAGTCTGCCCCTTGA  
TGTCTTACATTAAAGTATTGCAACCGN

&gt;M\_1.0.0\_4293 Mus musculus peripheral myelin protein, 22 kDa (Pmp22), mRNA cr: gi-6679394///

[Mouse\_jongleur\_201102.1994.C1] [SEQ ID NO: 31]

60 AACACCGGGAGCCTCCACTGCCCCCTTGCTTTGCGCGCGGTGACCCGAGCACAGCTG  
TCTTTGGGGACGCCAGCAACCCAGTGGACGCACCGGAGTTTGTGCTGAGGCTAATCTGC  
TCTGAGATAGCTGTCTCCCTTTGAACTGAAACAGGCACCGCTCTCTGATCCCGAGCCGAAC  
TCCCAGCCACCATGCTCTACTCTTGTGTTGGGATCCTGTTCTGTCACATCGCGGTGCTAG  
65 TGTGCTCTTCTGCTCCACCATCGTCAGCCAATGGCTCGTGGGTAATGGACACACAGCTG  
ATCTGTGCAGAACTGTACCAACATCCGCTTGGGAGCCGTCACCACTGCTACTCTCTCAT  
CAGTGAGCGAATGGCTGCACTGTCCAGGCCACCATGATCTGTCTGTCATCTTCAGCG  
TCTTGGCTCTGTTCTGTTCTTCTGCCAGCTCTTCACTCTCACCAGGCGGCGGTTT  
ACATCACTGGATTCTTCAAATCCTTGTCTGCTGCTGCTGATGAGTGCAGCGGCCATCT  
ACACAGTGAGGCACAGTGAGTGGCATGTCAACACTGACTACTCCTATGGCTTGCCTACA  
70 TCCTGGCTTGGTGGCTTTCCCTAGCCCTCCTCAGTGGTATCATCTATGTGATCTCTGC  
GGAAACGCGAATGAGGCGCCGACGACGACCGTCCGCTCTAGGCTCTGAGCGCGCATAGG

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GTCCACAGGGAGGGAGGAAAGGAAACCCAGAGAACAAACCAACCAAAAAAGAGCTAG  
 CCCCCAACCCAAACGCAAGCCAAACCAACAGAACGCAGTTGAGTGGCGATTGCTGTTGA  
 TTGAAGATGTATATAATATCTATGGTTTATAAAACCTATTTATAACACTTTTACATATA  
 TGTACATAGGATGTTTTGCTTTTATGTTGACCGTCAGCCTCGTGTGAATCTTAAACA  
 5 ACTTTACATCCTAACACTATAACCAAGCTCAGTATCTTTGTTTTCGTTTTTTTTTT  
 TAATCTTTTGTTTTGGCTCAGACATAAAAACTCCACGTGGCCCCCTTTTCATCTGAAAGCA  
 GATACCTCCCTCCCACTCAACCTCATAGGATAACCAAAGTGTGGGGACAAACCCAGACA  
 GTTGAAGACCTTTACACTATGGGTGACCCAGTGCAATTTAGCAGGAGTATCCACTGCCGA  
 10 ATCCATGTGTGAAGCCCTAAGCACTCACAGACGAAAAGCCCTGACCGGAACCCCTCTGCAA  
 AAACAGTAATAGCTGGTGGCTCCTGAACACTTGACCCGTAGACGGAGTACTGGGGCCAC  
 ACGTTTAAATGAGAAGTCAGAGACAAGCAATCTGTGAATGGTGCTATAGATTACCATT  
 CCTTGTATTACTAATCGTTTAAACCACTCACTGGAACTCAATTAACAGTTTTATGCGA  
 TACAGCAGAATGGAGACCCGATACAAACGGTTCATACTGCTTTCATACCTAGCTAGGCT  
 GTTGTATTACTACAATAAAATAAATCTCAAAGCCTTCGTCAGTCCACAGTTTTCTCAGC  
 15 GTCGGAGCATCAGGACGAGCATCTAGACCCCTGGGACTAGCGAGTTCCTGGCTTTCTGG  
 GTCTAGAGTGTCTGTGCTCCAGGACTGTCTGGCGATGACTTGTATTGGCCACCAACT  
 GTAGATGTATATACGGTGTCTTCTGATGCTAAGACTCCAGACCTTCTTGTTTTGTCT  
 GCTTCTCTGATTTTATACCAACTGTGTGGACTAAGATGCATCAAAATAAACATCAGAGT  
 AACTC  
 20 >M\_1.0.0\_3000 Mus musculus ATP-binding cassette, sub-family B (MDR/TAP), member 1B (Abcb1b), mRNA  
 cr: gi-6755045/// [Mouse\_jongleur\_201102.1138.C3] [SEQ ID NO: 32]  
 GAGGCGCTGCTTCCATCTTCTGAGGTTCCGCTCAACTCAGAGCTACTTCCAAATTTCTACA  
 TCTTGGCTGACTTTGCGAAGGAAACCCGGAGGTGGCAGTGGTGGTGGTGGTGGTGGTGGT  
 25 AGAGAACCTTAAGGGAGAGAGCAGACAGAACTTCTCGAAGATGGGCAAAAGAGTAAAAA  
 GGAGAAGAAAGAAAGAAACCTGCTGTTGGCGTATTTGGGATGTTTCGCTATGCAGATTG  
 GCTGGACAAGCTGTGCATGATTCTGGGAACCTCTCGCTGCTATTATCCATGGAACATTACT  
 TCCCCTCTTGATGCTGGTGTGTTGGAAACATGACAGATAGTTTTACAAAGCAGAAGCCAG  
 TATTCTGCCAAGCATTACTAATCAAAGTGGACCCACAGTACTCTGATCATCAGCAACAG  
 CAGTCTGGAGGAAGAGATGGCCATATACGCCCTACTATTACACCGGGATTGGTGTCTGGTGT  
 30 GCTCATAGTTGCCATAGCATCCAGGTTTCACTTTGGTGGCTGGCAGCTGGAAGACAGATACA  
 CAAGATTAGGCAGAAGTTTTTCCATGCTATAATGAATCAGGAGATAGGCTGGTTGATGT  
 GCATGATGTTGGGGAGCTCAACACCCGGCTCACAGATGATGTCTCCAAATTAATGACGG  
 AATTGGTGACAAAATTGGGATGTTTTTTCAGTCCATAACCACTTTTAGCCGGTTTTAT  
 CATAGGATTTATAAGTGGTTGGAAGCTAACCTTGTCTATTTTGGCTGTGAGCCCTCTTAT  
 35 TGGATTGTCTCTGCTTTGTGGGCAAGGATTTGACTTCAATTAATAAGGAACTCCA  
 GGCTTATGCAAAAGCTGGAGCAGTTGCTGAAGAAGTCTTAGCAGCCATCAGAAGCTGTGAT  
 TGCCCTTTGGAGGACAAACAGAAAGGAACTTGAAGGTACAATAAAAAATTAGAAGAAGCTAA  
 AAATGTTGGCATAAAGAAAGCTATCACAGCCAGCATTTCGATAGGCATTGCCTACCTGTT  
 GGTCTATGCATCATATGCACATGGCATTCTGGTATGGGACATCCTTGGTCTCTCAAAATGA  
 40 ATATTCTATTGGAGAAAGTGTCTACTGTCTTCTTCTCTATTTTGTGGGGACTTTTAGTAT  
 TGGACACTTGGCCCCAAACATAGAAAGCCTTTGCAACCGCACAGGGGGCAGCCTTTGAAAT  
 CTTCAAGATAAATGTATAACGAGCCAGCATTGACAGCTTCTCAACAAAGGGCTACAAACC  
 AGACAGTATAAATGGGAACTTAGAGTTTAAAAATGTTCACTTCAACTACCCATCGAGAAG  
 45 CGAAGTTCAGATCTTGAAGGGCCTCAATCTGAAGGTGAAGAGCGGACAGACGGTGGCCCTT  
 GGTGGCAACAGTGGCTGTGGAAAGGCAACTGTCCAGCTGATGCAGAGGCTCTACGA  
 CCCCCGTGGAGGGCTGGTCTAGTATCGACGGACAAGACATCAGAACCATCAATGTGAGGTA  
 TCTGAGGGAGATCATTGGTGTGGTGAAGTCAAGAACCTGTGCTGTTTGGCCACACGATCGC  
 CGAGAACATTCGCTATGGCCGAGAAAGATGTCACCATGATGAGATTGAGAAGCTGTCAA  
 GGAAGCCAATGCTTATGACTTCATCATGAACTGCCCCACCAATTTGACACCTGGTTGG  
 50 TGAGAGAGGGGGCAGCTGAGTGGGGGACAGAAACAGAGAATCGCCATTGCCCGGGCCCT  
 GGTCCGCAATCCCAAGATCCTTTTGTGGACGAGGCCACCTCAGCCCTGGATACAGAAAG  
 TGAAGCTGTGGTGCAGGCCGCACTGGATAAGGCTAGAGAAGGCCGACCACTTGTGAT  
 AGCTCATCGTTTGTCTACAGTTTGTAAATGCTGACGCTCATTGCTGGTTTGTAGTGGTGT  
 55 CATTGTGGAGCAAGGAAATCATGATGAGCTCATGAGAGAAAAGGGCATTACTTCAAAC  
 TGTCTATGACACAGACTAGAGGAAATGAATTAAGCAGGAAATTAATGCTTATGGATCCCA  
 GAGTGACACTGATGCTTCTGAACCTGACTTCAGAAGAAATCCAAATCACTTTAATAAGGAG  
 ATCAATTTACAGAAGTGTCCACAGAAAGCAAGACCAAGAGAGAAGACTTAGTATGAAAGA  
 GGCTGTGGATGAAGATGTGCTCTGGTTTCCCTTTTGGCGGATCCTAAATCTAAATCTAAG  
 TGAATGGCCTTATTACTTGTGTTGGCTACTTTGCGCTGTTATAAATGGGTGCATACAACC  
 60 AGTGTTTGCCATAGTATTTTCAAGGATTGTAGGGGTTTTTCAAGAGATGATGACCATGA  
 AACTAAACGACAGAAATGTAATTTGTTTTCCCTGTCTTTCTGGTTATGGGGCTGATTTCT  
 TTTTGTACATATTCTTTTCAAGGCTTCACTTTGGCAAGCCGGAGAGATCCTCAACCA  
 GCGAGTCCGATACATGGTTTTCAATCCATGCTGAGACAGGATATAAGCTGGTTGATGA  
 CCATAAGAACAGCACTGGCTCACTGACCACCAGGCTCGCCAGTGATGCTTCTAGTGTAA  
 65 AGGGGCGATGGGCGCCAGGCTTGTGTAGTTACCCAGAATGTAGCAAACTCGGGACAGG  
 AGTCATCCTCTCCTTAGTCTATGGCTGGCAGCTGACACTTCTACTTGTAGTAATTATACC  
 GCTCATTGTATTGGGCGGAATATTGAAATGAAGCTGTTGTCTGGCCAAGCCTTGAAGGA  
 CAAGAAACAGCTTGAGATCTCTGGGAAGATTGCTACAGAAGCAATGAAAACCTTCCGCAC  
 TATTGTCTCTTTGACTCGGGAGCAGAAGTTTGAACCATGTATGCCAGAGCTTGCAGGT  
 70 ACCATACAGAAATGCGATGAAGAAAGCACAGTGTGTTGGGATCAGCTTCTCTTCAACCA  
 GGCCATGATGATTTTCTTATGCTGCTGTTTCCGCTTCGGTGCCCTACTTGGTGGCACA

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ACAACTCATGACTTTTGAAAATGTTATGTTGGTATTTTCTGCTGTTGCTTTGGTGCCAT  
GGCAGCTGGGAATACTAGTTTCATTGCTCCTGACTATGCGAAAGCCAAAGTATCAGCATC  
TCATATCATCAGGATCATTTGAGAAAACCCCTGAGATTGACAGCTACAGCACAGAGGGCTT  
GAAGCCTACTCTGTTAGAAGGAAATGTAATAATTAATGGAGTCCAGTTTAACTATCCAC  
5 CCGACCCAAACATCCCAGTGCTTCAGGGGCTGAGCCTCGAGGTGAAGAAGGCCAGACGTT  
GGCCCTGGTGGGAGCAGTGGCTGTGGGAAGAGCACAGTGGTCCAGCTGCTCGAGCGCTT  
CTACGACCCCATGGCTGGATCAGTGTCTTAGATGGCAAAGAAATAAAGCAACTGAATGT  
CCAGTGGCTCCGAGCTCACCTTGGCATTGTGTCCAGGAGCCCATTTCTTTGACTGCAG  
10 CATTGCAGAGAACATCGCCTATGGAGAACACAGCCGGGCCGTGTCTCATGAGGAGATTGT  
GAGGGCAGCCAAGGAGGCCAACATCCACACGTTTATCGACTCACTGCTGATAAATACAA  
CACCAGAGTAGGAGACAAAGGCACTCAGCTGTCCGGTGGGCAGAAGCAGCGCATCGCCAT  
CGCACGTGCCCTCGTCAGACAGCCTCACATTTACTTCTGGACGAAGCAACATCAGCTCT  
GGATACAGAAAGTGAAGAGTTGTCCAGGAAGCGCTGGACAAAGCCAGGGAAGGCCGCAC  
CTGCATTGTGATCGCTCACCGCCTGTCCACCATCCAGAACCGGAGCTTGATCGTGGTGAT  
15 TGAGAACGGCAAAGTCAAGGAGCACGGCACCCACCAGCAGCTGCTGGCGCAGAAGGGCAT  
CTACTTCTCAATGGTCCAGGCTGGAGCAAAGCGCTCATGAGCTGTGACTATCTGAGGTGC  
TAAGTCTTAAATATTGGTGTGTTAAACATGGCACCAACCAAAGTTAAAGGCAAGGGC  
TGTTAAAGGTAATCCATCAAGATGAGAAGCCTCCGAGACTTTGTAATTAAATGAACCA  
AAATCGGAACAAACAAACAAACAAACAAACAAACAGCCATAGTTAAACAGGGCCATGTTTTT  
20 AATTGCATTACGTGATTCATAAGAGACATATAGTTTTTAAATAAATGTATAATTTT  
GTTTCAGTTTTTAAATTTCTACCCCTACTTTCTTAAATGATTATAAAGATTGTAAGAAC  
TATTTCTTAAATGCCCTATAAAATTAATTTTTCATAT

>M\_1.0.0\_6080 Mus musculus retinol binding protein 2, cellular (Rbp2), mRNA cr: gi-6677686///

[Mouse\_jongleur\_201102.2997.C1] [SEQ ID NO: 33]

AGCTAAAGACAGGCCCTTTCTTTGTTTCACTGCTTATTTGACCTGCGTGCACCTTCAC  
25 TAAGCAATGGGCCCTCAAGAGACTAGGTTTCTGTCTGTTTCCCTTCTGTCTTATATC  
AGCACCAACAGCTCTTTCTCTCTATGCCCATTTACACCCAGGCTTCCTGCTCACCACAAT  
TAATAGCCCTTCTTATCTTCAGCCCCACCCACCAGGCCAGCTTTCCTTATATTCTTGCA  
TGCAAGGCCTGTGAGGTTTGGGGGAGCTGTTTAAAGTGCTTAAATCTGAATGTGGAAGG  
30 CAAGTGATGAATCCCCAAAGTCCCTTCTGTCCCATTTCTGCTGTCACAGGTACAGTTCA  
TTTTCCAGGTTCTGTCTTTTACAAGTCACCATTGGGCTTGATCATTTAACTTCCATGAGC  
CTTGACAGCTTGAGAGAGAGAGAGAGAGAGAGAGGGGGGGGGGAGAGAGAGAGAGAGA  
GAGAGAGAGAGAGAGAGAGAGAGAGAGTGAAGTCAAGTGAAGTGGGCTGTTAAATATAAC  
CCACAGAGCTTTTGTGAAGTGAAGCAAAATGAAGTTCAAGTGTGGCTTGGCACAAGAACA  
35 GTTCCTCAGATGTAAGAACCCACCATGAGCTTCACTGGCCAAATCAATGCTTCTTATGTG  
ATAGGCAGGCCTGGCTCCGTGTCTGCGAAGCCTGTGGGACAAATACTGAGTGTGTTGTT  
TTCTTTAGGAACGTGATGGAATGTTCTGTGTGAGGCCAGGACTGTGGGAGGCCAGTGAG  
CCTAAATGAGCTGCTCCAAGGCAGTGTGTCTATGGAGATCACAGGGACACGCAGACCTGG  
CAACGGCAGGACTTTGTGCTGGACTGCCACAGACCTGTTGAACCTTGAAGGCAAGG  
40 CAGTTTCTTTGAGCTGGGCTTATGACCTTTGACTCTATTATCTTTATATACCTGGTCCA  
CTAAGCTATAAAGCAGTAACATTTAGCATAGTCTCCCTACAGCCTGTTCCTTCACAGTC  
ACTGAACGTCCATATCAAAACAGAGGCCACCATCATGACGAAGGACCAAAATGGAACCTG  
GGAATGGAGAGTAATGGAAGCTTTGAAGGCTACATGAAGGCCCTAGATATTGATTGTTG  
45 CACCCGCAAGATCGCAGTGGCTGTGACTCAGACGAAGATCATCACTCAAGACGGTGATAA  
CTTCAAGACGAAACCAACAGCACGTTCCGCAACTACGACCTGGATTTACCGTCCGGGTG  
GGAGTTTGAGCAACACAAAGGGCTGGACGGCCGACATGTCAAGACCTGGTCAACCTG  
GGAAGGCAACACCTCGTGTGTGTGCAGAAAGGGGAGAAGGAGAACCTGGCTGGAAGCA  
GTGGGTGGAGGGAGACAAGCTGTACCTGGAGCTGACCTGCGGCGACAGGTGTGCCGACA  
50 AGTGTTCAAAAGAGTGATGGGCACGGGAAAGCCTGGAACATGTGCAGAGTTCTCTGCC  
AGTTCCCCAAAGCAGCATGGGGACTCCTCCCATTCCTGACAGAGCCCCCTTACATCATCT  
GCCTGGGTTTAACTGGAGTGATAAAAGGAACCTA

>M\_1.0.0\_10044 Mus musculus RIKEN cDNA 2010003F10 gene (2010003F10Rik), mRNA cr: gi-21312989///

[Mouse\_jongleur\_201102.5595.C1] [SEQ ID NO: 34]

AAGCCTCCCACCTGTTTAACTCCGGAGCCTGGCACTTCCTTCACTGCTCAGTTCACTCC  
55 GCTCCTGCCTGTTTGAAGCCTCAGACATGTGTACTGGAAAGTGTGCGCGCTGCCTGGGG  
CTCTCCCTCATCCCTCTCTCCCTGGTCTGCATCGTGGCCAACGCACTCCTGCTGGTACCT  
GATGGGAAGACCACCTGGACGGACGGCAACCTCAGCTTGCAAGTTTGGCTCATGGGTGGC  
TTCAATGGAGGGGCGCTGATGGTGTGTGTCCAGGAATTGCAGCGGTCCGGGCAGGGGGA  
AAGGGCTGCTGCGGTGCAGGTGCTGTGGCAACCGCTGCAGGATGCTGCGCTCCGTCTTC  
60 TCCTCCGCCCTTGGGGTGGCTTGGCGCCATCTACTGCTGTGAGTGGCGGGAGCTGGGCTC  
CGAATTGGACCCAAATGCTTAATAGACAACAAGTGGGACTACCACTTCCAAGAAACAGAA  
GGCGCTTACTTGGCAATTGACACTCTTTGGAATTGTGTGAGGCGCCACCTCAGTGGTA  
CCCTGGAATGTGACACTCTTCTCAATCCTGGTGGTGCATCAAGTCTGGAACCTGTGCTG  
TGTGGAATTCAGCTGGTGAATGCGACCTTGTGTGTGTGTGTGCGGATTGCAGGAAAAAG  
65 GAGGGTTTAGCTCACTGAGTACCATAGGCCACCCCTAATACCTCATTTCTGGAAGTCTGA  
GTGGTCAACCACTCCCTGGTTGGCTAGGGAAAAAAGAAAAAATGCACACTTTTAT  
CGTTACGGCTCTCCTTAGTGAATAAACCAACCTGAGCCCTTCCCCAGTTCTGGTTT  
AGCCTTTGGAAGAGTGATACGTGGGCCTTCAGAGATATGTGTCTAGACTTGGGGCTTCTA  
TATGTACCTCCCACTCTACCCACAACCCCCACCCCTCTGTGTATTCTTTAACAACAAC  
70 AACATAGTTATTGTTCTGGAATAAAATCTGTGCTCTCAAGG

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AATAAACTTATTGGGAAATTCACACGTGTAGACAATGGAAGGAGCTGATTGCTGTCCGA  
GAGGTTTCTGGTAATGAACATAATCCAGACCTACACATATGAAGGAGTTGAGGCCAAGCGA  
TTCTTTAAGAAGGAATAAGTCAACTTCTCAGAGCCTGGAGCAACGCTGAAGAGCTAAGCT  
GATGTGAGATTCTTTCTCCATCATGCTAATGCCAGGCTCATTCTGCATCCTATCAGCAC  
5 TGGTCTCCAGCCTTGTCAAAGCTAAAGAAGTAAAGCTAATTAAGAAGAACTTCATTGT  
TTATGGTCCCTTAAGCTATACATGAAC TAGTCTTTAAAGAAAATAAATCCTGTTCTCAC  
AC  
>M\_1.0.0\_7665 Mus musculus defensin related cryptdin 6 (Defcr6), mRNA cr: gi-13937346///  
[Mouse\_jongleur\_201102.3937.C10] [SEQ ID NO: 37,38,39,49]  
10 GACAGCTGCCTGCTCATCTAATCCATCCAGGTGACTCGCAGCCATGAAGACACTAGTCC  
TCCTCTCTGCCCTCGTCTGCTGGCCTTCCAGGTCCAGGCTGATCCTATCCAAAACACAG  
ATGAAGAGACTAAACTGAGGAGCAGCCAGGGGAAGAGGACCAGGCTGTGTCTGTCTCTT  
TTGGAGACCCAGAAGGCTCTTCTCTTCAAGAGGAATCGTTGAGAGATCTGGTATGCTATT  
GTAGATCAAGAGGCTGCAAGGGAAGAGAACGCATGAATGGGACCTGCAGAAAAGGGCTATT  
15 TATTGTACACGCTCTGCTGTGCTGAACATGGAGACCACAGAGGACAAGACGACCATGAG  
TACTGAGGCCACTGATGTGGTGCCTGATGACCATTCTCAATAAAITGTTGCAATATG  
AAAAAAA  
>M\_1.0.0\_7656 Mus musculus defensin related cryptdin, related sequence 10 (Defcr-rs10), mRNA cr: gi-  
6681162///  
20 [Mouse\_jongleur\_201102.3937.C1] [SEQ ID NO: 40,47]  
ACACATTGAGCCCTGCTCTCCAATCATCTAGGTGACTCGCAGCCATGAAGAACTTGTC  
CTCCTCTTTGCCCTTGCTGCTTGCAATCCAGGTCCAGGCTGATTCTATCCAAAACACA  
GATGAAGAGACTAAACTGAGGAGCAGCCAGGGGAAGAGGACCAGGCTGTGTCTGTCTCC  
TTTGGAGACCCACAAGGCTCTGCTCTTCAAGATGCAGCCCTAGGATGGGGTGGCGGTGC  
CCACCATGCCCCAGATGCCCGTCATGCCCATGGTGCCCAAGGTGCCGAGGTGCCGAGG  
25 TGCAAAATGCAATCCAAAATAAGCCTGCAATTGGCACCAGAAATCCAAATAAACAGCATAA  
ATTCTGCTGAGCTGAGCATGGAATCTGGGTCAAGATAACCATGTTCTTTGAACCTCAC  
TATCTGTCAAGACCTTGTTCTTAGCCTTGATTGCTCTTGCTTCCAAATAAATCCTTG  
CAGA  
>H\_1.0.0\_52731 Human RASFA PLA2 gene encoding synovial phospholipase, exons 2 through 5 si: gi-  
196885///  
30 [Human\_jongleur\_201102.cl.9676.single] [SEQ ID NO: 41]  
GAATTCCTGCTCATTCGCTGCCCTTGAGAGTGGCTGTGTTGTGCATGCATGTGCATGATT  
TGATATGTATGAGAGGGTGTGTGTGCATGAGTGTGTTGAGTGAGTATGTGAGTGTAGTGT  
AAGAGAGGATTTGGCACTATCAGGTAATTACGAGAGTGTGTATGTGGGCATAGGTGT  
35 GTTAACATGTATGCTCTTGGGAACTTGTGTATGTGGAAGGGGTTAGAAGGCCATAGAAGAG  
AGAGGTTGATGCTTTTCATCTGGAGGAAAATACTGAGGCCGAGCTCCATGGGTGCCCTTG  
GAGACTCCAAGCCTTGAATCCAGTGTGGGATATGCAAGCTATGTCTAGCGAGGGACACA  
TCCTCTGACCTCAGGAACCTCCCAGGTAGTTGGGAGGAACCTGGTTCCAACCTCCCAAGA  
ACTCTCAGTCTGATGACGGTACAGGGGAGGTCTCATTAGTGTATCATGGGGTTCTCCACA  
GGTCTGAGGGCCTGATGTGTGTGAAACCATTTCTGCAGAGCTGGGAACGGGTGAGGAGTG  
40 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCATTGCTGGAGGCACTCCTTGTGTGCTCTGA  
GTGTGACAGAGGAATCACCTGGACTTAGGTTGGATGGGAGAGCCATGTCTGTGTGTCT  
CAGAGCCACCAAGGAGGAGCAGGGGACCGACCGCGGGCAGAAATTGAGACCACCCAGC  
AGAGGAGCTAGGCCAGTCCATCTGCATTTGTACCCAGAACTCTTACCATGAAGACCTT  
CCTACTGTGGCAGTGATCATGATCTTTGGTAAGAGCTGACCCTGACCTCTGAGCATGGG  
45 GGACAGCCCCAGAAGGGAAGCACTCTTGTCCCCTAGTTTCTCTCCCATTTGCAGTGATCC  
TCTCTCAGGGGGGAAAAGAAGCCATTGGGAGGAAGGAGAGTAGCAGAGAGGGGACAGAG  
AGGAGGGGCACAGAACCCCATGCCCATCACAGACAACTCCCAATTTCTTCCAGGCC  
TACTGCAGGCCCATGGGAATTTGGTGAATTTCCACAGAAATGATCAAGTTGACGACAGGAA  
AGGAAGCCGCACCTCAGTTATGGCTTCTACGGCTGCCACTGTGGCTGGGTGGCAGAGGAT  
50 CCCCCAAGGATGCAACGGATCGGTGAGGCCACCTATCCCTCCCTACCTCCTAGACTCTG  
GCCAGGCAGGGCTGGGAGCTGCAAGACAGTGCCTGTTCTGATGGGCGCAGAGGTCTC  
AGGATGGCTGGCTGGGAAAGCAGCCGGCATGTTGGAACCTTCTGCTCTAGACTGTTGCAA  
AGTCACTGGGTCTCTGCCAGGGTCCAAGGGGTGAGACCACAGGCACAGGCCTCCTGG  
AGCTGTGGGACAAGAGCCCCAACAGGTGTCTCTCAGAGCTGTGTCACTCATGACTG  
55 TTGCTACAAAGCTCTGGAGAAACGTGGATGTGGCACCAAATTTCTGAGCTACAAGTTTAG  
CAACTCGGGGAGCAGAATCACCTGTGGTAAGAGTCTTACCTACCATCGAGTGGCCCTCA  
TTTGTTTAGACAGTGTCTGGGACTGTGCTGGGACCAAGATAGCACAGAGGGACACAGT  
TCCTGCTTCAGGAAGCTACGGTTGAGTGGGAAGCCAGGAAAGTGAATCCATGTAGT  
AAAGA CTCCAGTGGGAAGTAAACAAACAGATAAGGCATTAAACACAGCCTGAGGCTTGAGG  
60 AAGGCTCCTGGAAGGGGTGACCCCTAAGCTGAGTCTGAAAGGCTGTGCAGAGAGTCAAGG  
AAGAGGAGGGGAGCATTCCAGAGAGGACACAGCATGGTCAAGGCATTAAGGGCACTG  
TAAGCCATTCTGTACTGCCAGCAGAAACATGAGGAAGAGGAGCAGTGTCTGAGCCATGAT  
GCTGGAGACATAGGAAGGAGCTAGGTCAATCCGCCCTCCACTCCGGGCTGATTTAGGTT  
TTGCCCTTAAGCAATAGGATGCTATTAAGCAAGGAGCTACAGGGTCAGATTGCAATTT  
65 AGATGACTCACTGTGGGACAGGGTCGATGGAGACAAGTGAAGGGGGCAGAGAAAGCTA  
TTGCCATCATGCAGGCAAGAGGGAGTAACATCTTGACATAAAACAAATGGAGGTCAGGATG  
GGAAAGGTGGAGAAAATAAGATGCAATTTGAGATGGAATGAGCTGAACTGGTGGTACTG  
AGTTGGAGGGATGGGGAGAGGGAGTGTGTTGGATGGATATGTGGCTGCATGGATGGCACA  
ACTGTGATAAAGACCATGGGAGCAGGTGATGGTGGAGGGTGGGGAGGAGCAGTTCTATTT  
70 CCAGCATGTTAGGTTTAGGGGCTCCAGCACCCAGGGAGGGGTCCAGCAGGCAGCTGTCT  
ATACAAATGCAGCTCAGGGGAGAATTGAGACTGGGACACAGATTCAGAAGCCAGCAGCA

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GAGACCTGAGAGGTGGGTGTGATCACTCATTGCTGTTTAAAGGCCAGAAAGGAGACAG  
AGAAGGGATGGACAGAGAGGGAGAAGGGGAAGTGAAGGCGAGAGGTCAAGGAGTCAGTAAG  
GAAATGGTTAGCAAGGGCCAAGTGAACAGGGAGTCCTCCATGAAAAGGGCCAACAAGGCT  
CCCCTGGATGTTGAGGCAGAAACGCATGAGGGACTCAGGGAAGCTGTTTCCATGGAGTCG  
5 GGAGGGCAAGCCAGATTAGACCAGGTGGGGGCTGATGGGAAGGCCAAATAAGACAGGAG  
GCAAGACAAACATTCTGGAGAAAGTTTGGCCTGAAGGGAGGAGAGTGGTGGCACTGGAAG  
GCTTTGCTTGGTGTCCCCAGACAGCTGACTCATGAGTGGGATTTGGAAAAAGCGTGGACT  
CCTGCCCCATGGCCTGAGTCCTTTAAGATCAGAAATTATGTCTCCCATCATGGCCTCTCCA  
10 TAGAGGCATGTATCTTCAGCAGGCGTTAGGTCACAAGCCACATGATGCCAAGCTGCAGT  
GGCTTGCCATAATGGGGATATGTGACTGTGCGATAACTAGAATTCTGGAAGAGTGCAGTGC  
CAGGCTTGGGGCAGCTTTCAGCCATGTCATTAAGAATCCAGCCTTCTCTGGCCTCAG  
CTATGCCACGTGGCCAGTGTCTACACCTGGGATGTCAAGAGACAGGCTGCAGGTCCACCC  
TCCTGGCCTCATACTATGGAAGAGGCTTTCCTTTTGGGCATCTCTCTTTTGGAGGGAGG  
AAATAGATCGTTCAGAAAGCCCCAGCAGACTTCCCCTTGTGCTCATTGGTTGGAACA  
15 AGGTTACATGATACACAAAGACCAATCACTGCAAGGAAAAAGGGATGACCCTGCCTGGC  
TTACACCAATCACAATCTATTCCAGACCCCCGAGGCTAGGCTTGTGCTCCTGGACAC  
ATCTGTTAGCAAGAGGAAGAGATTATGGCTGTTAGGAAGGCTTTGAGAAAGTATCCAG  
TGCCCTGGCTGTGCTCCACAGGCTGGAGGCCAGCATCCCAAGGGCAAGAATTCTGTCTC  
CCCATTTGCTCAGAAATATCTGGAGCGCAGGTGTTGTCTCCAACTAGGAGCTTCTGGAGG  
20 ACAGGGCTGTGCTTCTACCCCAGGGTTCCACAAGAAGCCACTGAATATTAATAAAGTCC  
CATCTGTGTTTATTTCTTATGATTCAAAACAGGACTCCTGCAGAGTCAACTGTGTG  
AGTGTGATAAGGCTGTGTCACCTGTTTGTGTAGAAACAAGACGACCTACAATAAAAGT  
ACCACTACTATTCCAATAAACAAGTGCAGAGGGAGCACCCCTCGTTGCTGA  
>H\_1.0.0\_11184 Homo sapiens intelectin (ITLN), mRNA cr: gi-8923027///  
25 [Human\_jongleur\_201102.4257.C2] [SEQ ID NO: 42]  
AGGAGCGTTTGGAGAAAGCTGCACTCTGTTGAGCTCCAGGCGCAGTGGAGGGAGGGA  
GTGAAGGAGCTCTCTGTACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGA  
ACCAACTCAGCTTCTGCTGTTTCTCATAGCGACCCAGAGGATGGAGTACAGATGAGG  
CTAATACTTACTTCAAGGAATGGACCTGTTCTCTGCTCCATCTCTGCCZAGAAGCTGCA  
30 AGGAAATCAAAGACGAATGTCCTAGTGCATTGATGGCCTGTATTTCTCCGCACTGAGA  
ATGGTGTATCTACAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGG  
TGGCTCAGCGTGCATGAGATGACATGCGTGGGAAGTGCACGCTGGCGATCGCTGGTCCA  
GTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGGCCAACTACAACA  
CCTTTGGATCTGCAGAGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGACA  
35 TCCAGGCCAAGGACCTGGGCATCTGGCAGTGGCCAAAGTCCCCATGCGAGCACTGGA  
GAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCTCCAGACACTGGGACATA  
ATCTGTTTGGCATCTACAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTG  
ACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTT  
ATTACTCACCTATGGCCAGCGGGAATTCAGTCCGGGATTTGTTCAAGTTCAGGGTATTTA  
40 ATAACGAGAGAGCAGCCAACGCCCTTGTGTGCTGGAATGAGGGTCAACCGGATGTAACACTG  
AGCACCACTGCATTGGTGGAGGAGGATCTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAG  
ATTTTCTGGTTTGTAGTTGGAGTGGATATGGAACCTCATGTTGGTTACAGCAGCAGCCGTG  
AGATAACTGAGGAGCTGTGCTTCTATCTATCGTTGAGAGTTTTGTGGGAGGGAACCCA  
GACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGAA  
45 TGTAAATGGCAGAAGAAAAACATAAATCATATTGACTC  
>M\_1.0.0\_7658 Mus musculus defensin related cryptdin 5 (Defcr5), mRNA cr: gi-6681172///  
[Mouse\_jongleur\_201102.3937.C3] [SEQ ID NO: 43]  
ATGAAGACATTTGCTCCTCTCTGCGCTTGTCTGCTGGCCTTCCAGGTCCAGGCTGAT  
CCTATCCACAAAACAGATGAAGAGACTAATACTGAGGAGCAGCCAGGGGAAGAGGACCAG  
50 GCTGTGCTATCTCCTTTGGAGGCCAAGAAGGGTCTGCTCTTCATGAAGAATTGTCAAAA  
AAGCTGATAGCTATTGTAGAATAAGAGGCTGCAAAAGAGAGAACGCGTTTTTGGGACC  
TGCAGAAATCTTTTTTAACCTTTCGTATTCTGCTGTAGCTGA  
>H\_1.0.0\_23593 Highly similar to NEP\_HUMAN Neprilysin (Neutral endopeptidase) (NEP) (Enkephalinase)  
(Common acute lymphocytic leukemia antigen) (CALLA) (Neutral endopeptidase 24.11) (CD10) [H.sap cr:  
55 gi-8169687/// EST390530 Homo sapiens cDNA /gb=AW978421 /gi=8169687 /ug=Hs.307734 /len=675.  
[Human\_jongleur\_201102.11097.C4] [SEQ ID NO: 44]  
CCCTTTCTAGGACAACTAATGTTATCTGTATGTGATGGTGGCCCTCTCTGTTAATCACC  
CTAAGTCAGTACAGTGACCCCTAGGGCCCATTTTCTTTTCGATTAGAGAATTCCTCATTT  
CTGTGGTGTGGCAAGTCTAGCCAAGGGCTGCAATGCTTCTTTGAAGATCACCAACCC  
60 GGCACCTCTTTTCTGGATTATGTATGAATCTTTCGCGCAGTGAAAGGCTTCTGAAAACT  
CTGCAGAGTCTGCAAGTCCCAATAATCCTGAAATTCGCCAGGACTGTGCACATCTGTTT  
TAATGGAGTTAACCGCATACTCTGGCCATATAGGTTCCACACCACCTGTGCAAAGTTCA  
AGAAAAATAGTTGTTTGTGATTTAGGTCAAGTCCAGGAAGTAATTTTCTTCGCCATTCT  
TTTTAATAAATTTCTGATAGGCTCTGTATGCTTGACCAAGACCTCCATTATCAGCAATGT  
65 TTTCTCCCACTGTATTAATTCATTAAGGTGCTGTCACCTGCCAGGTCCCAGGAAAAAGT  
TTCCATCTGATACACCATGCATGGGATGCTCCTTAAAGTTACTTGCAGACTGTTGAG  
TCCACCACTCAACGAGGTCTCCATCTTTGTTAAAGTTTCTGCCATTGTCTCGAAGCCAT  
GGGTGATTTCTGTGCTATGACCATGCCGATGCCCCCATAGTTCAATGAGTTGGAGTGT  
GGGCACTAAAGAGGGGGGCTGCAGAAATGCCGGCTGGGAAGACTATCTGATTTCTCTCTG  
70 AAGAGTAAATGCATTGACTACAGCTGCTCCACTTATCCACTCATCTTTGCCACCTTTT  
CTCGGAGCTTCTCAGTTGTTTACTTTGGCTGAATTTCAAATTTTGAATTTATGTTCTCGA



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AGTATTTCATCTTCTTTGTAGTTCAAACGAGGTACTCATTATTTCAGTTTGTATCATTG  
AAACATGTGTCATCAGGATAGCCGATCCTTTCTTAAATGCTAAGGCCCTTTCTTCAGCTC  
TCTTTTTTGTCTCGGCATCCATCCAAGTGAGGTCACTAAAGTCTGAATAAAAACTTCTC  
GGATCTGTGCAATCAAATCCTCGACCACATGTTTACTCTCTCCAGCAAATGCTGCTCCA  
5 CATAAAGCCTCCCAACAGCATTTCATATTTCCATTGACATAGTTTGACAACGCTCTCC  
AAGTTGCTGTTTCTGAGGTTGTACCATAAAGGCCCTTGCGAAAGCATTCTCGGACTCCT  
TGTAGGTTGCGCTGAGGCTGCTTACAAGATCCATTATGAATCTCCAGGACATTAAATTT  
GAAGATCTCTGGCAGAATATTTGGTAAGAATGGGCTTAAGTTTGGTTAAATATTCTGGAG  
CATAAAACAACCATCTCTCCTCATTGTAAATACTAATATTACAGTTGACATGATTTTCAT  
10 TTGTGAAATTCACAGCTGAATGGCTTCCCATTGATCTCTAGTGAAAAGTTATTTTGGG  
TCTGGGCCAATGTCATCTGTATACAGAAGCATTGGATCATTTCGATCTTCAGGTTTAG  
CCGTAGCATTGGCAATTCTTTTTCCAATCCATAACTTTATTATTCCAAAGCAAGCT  
GGTTTTCATCGATGGGCAATCTTTCTCTGACGAATCAATCTGGCCACAGAAATCATAA  
AATCCACATATGCTGTACAAAGCCTCTTTATAGATTCCAGTGACATAGTAATCTCTAG  
15 AAGGGAGGCCAAGTCGAGGTTGGTCAATATGAATTACATGATTACAGAAATCTTATCAT  
CAGTGCCCAACAAACAAATTAATAAGGACTTTTTTCCCATATTTAGAATTTCAGTTGTGCAA  
TAGCTTTTTCAGCTGTCCAAAGAAGCACCATATTTTTGCTCCAGTTTCTGTTGCTACTG  
GCCACCCATATATGTCTGGTAACAGTTTGAGTAGAGGTTCTCCACCTCTGCTATCAATAG  
CAGATTCATTATACAGAGCCTGTACAATGCTTTGCTTTCTGCACTGCTACTATATCTT  
20 CAGTTTGGGTTCTTGAGGACATCTTTCAAACGACTTCTAGTTTCATCTCTTAAATGT  
CAAAGTTGCCGTAACGGGAGCTGGTCTCGGGAATGACATTACGTTTCAACAGCCTCCGC  
AAGCATATTGAAAAAGTCTGTACAAGGCTCAGTGGTGGCATCCATGTTTGGATCAGTC  
GAGCAGCTGATTTTATGTCAGTCTGATGACTTGCAAATACCATCATCGTAGTTGATAGA  
GTGCGATCATTTGTCACAGCTATGATGGTGAGGAGCAGGACAAGGACCGAGAGGCTGATCT  
25 CCAGTGGAGTCCATCGCTGTTTCTTCTTTGGCTTTGGAGTGTGATATCAGTTATATCCA  
TCTGACTTTCTGACTTGCCCATCACCTAAAATTCTTCAGTCCAGTAGCGGCTCCTTCC  
CAGGGCAGCGCTCCTCCACGGCCGAGGGTCTGGGCGCTCGGATCGCGTGGACCTTAG  
CTGCGGACCTTGCTCAGCGCACCTCCCGCAGCGCC

>H\_1.0.0\_2865 Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class)  
(GNAL1), mRNA cr: gi-4504036/// [Human\_jongleur\_201102.505.C2] [SEQ ID NO: 45]

TTCGGCCGGGCCGGGACGATGACTCTGGAATCCATGATGGCGTGTGCGCTGAGCGATGA  
GGTGAAGGAGTCCAAGCGGATCAACGCCGAGATCGAGAAGCAGCTGCGGCCGGGACAAGCG  
CGACGCCCGGCGCGAGCTCAAGCTGCTGCTGCTCGGCACGGGCGAGAGCGGGAAGAGCAC  
35 GTTCATCAAGCAGATGCGCATCATCCACGGCCCGGCTACTCGGAGGAGGACAAGCGCGG  
CTTCACCAAGCTCGTCTACCAGAACATCTTCACCGCCATGCGAGCCATGATCCGGGCCAT  
GGAGACGCTCAAGATCCCTCTACAAGTACGAGCAGAACAGGCCAATGCGCTCCTGATCCG  
GGAGGTGGAGTGGAGAAGGTGACCACCTTCGAGCATCAGTACGTCAGTGCATCAAGAC  
CCTGTGGGAGGACCCGGGCATCCAGGAATGCTACGACCGCAGGCGCGAGTACCAGCTCTC  
CGACTCTGCCAAGACTACCTGACCGACGTTGACCGCATCGCCACCTTGGGCTACCTGCC  
40 CACCAGCAGGACATGTGTCGGGTCCGCGTGCACACCGGCATCATCGATACCCCTTT  
CGACCTGGAGAACATCATCTTCCGGATGTTGGATGTGGGGGGCCAGCGGTGCGAGCGGAG  
GAAGTGGATCCATGCTTTGAGAAGTGCATCCATCATGTTTCTCGTCCGCTCAGCGA  
ATACGACAAGTCTGGTGGAGTCCGACAAACGAGAACCAGGATGGAGGAGAGCAAAGCCCT  
GTTCCGAGCATCATCACTACCCCTGGTTCAGAACTCCTCCGTCATCCTCTTCTCAA  
45 CAAAGAAGACCTGCTGGAGGACAAGATCCTGTACTCGCACCTGGTGGACTACTTCCCCGA  
GTTTCGATGGTCCCGACCGGACGCGCCAGGCGCGCGGAGTTCATCTGAAGATGTTCTGT  
GGACCTGAACCCGACAGCGACAAGATCATCTACTCACATTCACGTGTGCCACCGACAC  
GGAGAACATCCGCTTCGTGTTTCGCGGCGGTGAAGGACACCATCTGCAGCTCAACCTCAA  
GGAGTACAACCTGGTCTGAGCGCCCGAGGCCAGGAGACGGGATGGAGACACGGGGCAG  
50 GACCTTCTTCCACGGAGCCTGCGCTGCCGGGCGGGTGGCGCTGCCGAGTCCGGGCGGG  
GCCTGTCCGCGGGAGGAGATTTTTTTTTTTCATATTTTAAACAAATGGTTTTTATTTCA  
CAGTTATCAGGGGATGTACATCTCTCCCTCCGTACATTCGCGCACCTTCTCACCTTTG  
TCAACGGCAAAGGCGACCTTTTTCTGGCCTTGACTTATGGCTCGCTTTTTTCTAAAA

>H\_1.0.0\_25937 Homo sapiens guanylin mRNA, complete cds cr: gi-183414/// /cds=(8,355) /gb=M97496  
/gi=183414 /ug=Hs.778 /len=571 [Human\_jongleur\_201102.12385.C1] [SEQ ID NO: 46]

TCGCTGCCATGAATGCCCTTCTGCTCTTCGCACTGTGCTCTCTGGGGCTGGGCCGCT  
TGGCAGAGGGGTACCGTGCAGGATGGAATTTCTCCTTTTCTCTGGAGTCAGTGAAGA  
AGCTCAAAGACCTCCAGGAGCCCCAGGAGCCCAGGTTGGGAACTCAGGAACCTTGCAC  
CCATCCCTGGTGAACCTGTGGTTCCCATCCTCTGTAGCAACCCGAACCTTCCAGAAGAAC  
60 TCAAGCCTCTCTGCAAGGAGCCCAATGCCAGGAGATACTTCAGAGGCTGGAGGAAATCG  
CTGAGGACCCGGGCACATGTGAAATCTGTGCTTACGCTGCTGTACCGGATGCTAGGGGG  
GCTTGCCCATGCTGCTGCTCCCTCCCTCCGACAGGGAAGCTCTTTCTCTCAGAAAGG  
CCACCCATGATACTCCACTCCCAGCAGCTCAACCTACCTGGTCCAGTCCGGAGGAGCAG  
CCCGGGGAGGAACCTGGTGACTGGAGGCTCGCCCAACACTGTCTCTCCCTGCCACTTC  
65 AACCCCAAGCTAATAAACAGATTCCAGAT

>H\_1.0.0\_15482 Homo sapiens pancreatitis-associated protein (PAP), transcript variant 2, mRNA cr:  
gi-21070994/// [Human\_jongleur\_201102.6563.C1] [SEQ ID NO: 48]

GGGAGGTCCTTCTCTCAGGAGCACAGGAACCTGAGACTCAGCAAGGTTGCTCTGGGA  
GGGCTCGGGATGGAGAGTACACAGATTCACTCACTCAGAACTGTAGAAGATGATG  
70 GATGTGACCAAGATCACTTAGTCTAGGGGACTAGAGAAGGAAATGACATGAGGAGT  
GGGTATCTGTGTCTCTCCACTGACCACGCTTCTTTAGTGACTCTGATTGCTCTCT

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CAAGTCGCAGACACTATGCTGCCCTCCCATGGCCCTGCCAGTGTATCTTGGATGCTGCTT  
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60 ACTTGATATTTTGTACAAAACAGATTGTGTAAGATATATTTGAAGTTTCAGTGATTAAAC  
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65 GAATGCTTAGGCACGTGACAGTTATATATATCTTGGTTGTTGATTGTACCAGTGAAT  
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AATATATACATAAATGTAAAATACTTACAAAAGTGG  
>H\_1.0.0\_14531 Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA cr: gi-7869495///  
[Human\_jongleur\_201102.6032.C2] [SEQ ID NO: 57]  
CAGCTGCTGCCACACCGCTCGACGCCTTCACTGCCATCCCGCTGTCTTGGCGCCCC

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GCTAGCAAAGAGGATGAGACATGAACGTGCATAAAGGACTCAGCAACCAGCCAGGGACAG  
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5 GTTGAGACTTTTCAAATGGATTTTATGACCCACTACTGGGTTTGGATCCACAGTTTGAA  
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10 TGGGCCATAAGGCTGAGCAGAGTGAAGTTGATTAGTTGGTAGCTTTTAAAAATATAAT  
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15 GAGCAATGAG

>H\_1.0.0\_29063 Homo sapiens, Similar to uridine phosphorylase, clone MGC:42328 IMAGE:4818300, mRNA,  
complete cds cr: gi-23272324/// /cds=(216,1169) /gb=BC033529 /gi=23272324 /ug=Hs.128427 /len=2261  
[Human\_jongleur\_201102.15166.C1] [SEQ ID NO: 61]

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20 TGTGAGTTGGACCCAGCAAGAAGTGGTGAGGACAAGGCCTGAAGATGTGCTGCTTCC  
CATTCACCTTCCACCATGATGTGAAGTGTCTGAGGCCCTCCAGCCATGCTTCTGTACA  
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>H\_1.0.0\_17326 Homo sapiens mRNA for MCM10 homolog, complete cds cr: gi-11527601///  
[Human\_jongleur\_201102.7564.C2] [SEQ ID NO: 62]

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65 AAGAAGAAGTTCCCGCATCACAGTCAACTGAAAAATAGGGTCTCCTGCTCCTGCCCCCA  
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TGCAAAAAATCCCTGTAGAGAAGTCTCCCCGGCCACCTCTTAAGGAGAGGAGAGTTTCA  
70 GAATTCAGGATCAACATGCTTTTCTGCGAGCTTGATGTCCTCTGCGCTACCAAGAACCA  
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TGACAAGTGACCCCTCCCAACCCCTACAGACGATTCTCGGACAAACCTAGTGGGATAA

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CTAGAGGTCAAATTTGTGGGGACCCAGGAAGTTCTGGGGAAACGACTCAACCCATCTGTG  
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>H\_1.0.0\_23529 Homo sapiens cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide  
18 (CYP2C18), mRNA cr: gi-13699815// [Human\_jongleur 201102.11077.C7] [SEQ ID NO: 63]  
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>H\_1.0.0\_23524 Homo sapiens cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide  
20 C19 (CYP2C19), mRNA cr: gi-4503218/// [Human\_jongleur\_201102.11077.C2] [SEQ ID NO: 64]  
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50 AATAGGGAATTCT  
>H\_1.0.0\_11755 Homo sapiens solute carrier family 27 (fatty acid transporter), member 5 (SLC27A5),  
mRNA cr: gi-13325056/// [Human\_jongleur\_201102.4565.C1] [SEQ ID NO: 65]  
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70 GATGCTGTCTTATCTGGGGCCACAGCTGATGATGTGTTTACACGGTCTGCTCTGTGTA  
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TCTGGCCCCCAAGTTCCTACTTCTCTGCTTCTGGGATGACTGTGCGGCAGCATGGCGTGAC  
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15 CACCAGCAGCTTCAAACGTGATGAAGACCCGTTGGTGGCTGAGGGCTTCAATGTGGGGAT  
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25 TAAAT  
>gi|3743331|gb|AI192122.1|AI192122 qc95h03.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
IMAGE:1722005 3', mRNA sequence [SEQ ID NO: 67]  
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30 GAAACAACTGCCATGACAAAGTCAATGAGTAACAAGACTTGTAAATAAAAAGGCATAAAA  
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35 AGGTAACAGAGGAGAGGTGCTGCTGGGT  
>H\_1.0.0\_6007 Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA cr: gi-4885590///  
[Human\_jongleur\_201102.1857.C1] [SEQ ID NO: 68, 79].  
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40 CGGGAGGAACAGAGAGCCAGGACCAAAGCTTCCTTATGTAAGCAACCCCGAGCCTGGAGCA  
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50 AGCACCTTGGCAGCAGTGAAGCTTCAGAGAATCAGCAACCCAGGAGCACCAGTGTCTCTA  
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55 TCACCTGACAGTGTAAAGAAAACCTCCCATCTTTATGTAGCTGACAGGGACTTCGGGCAG  
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60 ATTTGTGCAACATGGAGAAATCTACTGAATTTGGCTTCCAGATTTTAAATTTTATGTCAT  
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70 GTCAATGATGGTTTAAATAGGTAACCAACCCCTATAAACCTGACCTCCTTTATGGTTAAT  
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AATAAAACCTTAAAGCTG

>H\_1.0.0\_25343 Homo sapiens selenium binding protein 1 (SELENBP1), mRNA cr: gi-16306549///  
[Human\_jongleur\_201102.12047.C1] [SEQ ID NO: 69]

5 CACACGACAGCAAAACCGCCGGGATCAAAGTGTACCAAGTCGGCAGCATGGCTACGAAAT  
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10 GTGATAGCACCAGTTCGCGCACCAAGCTGGTGTCTGCCAGTCTCATCTCCTCTGCATCT  
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15 CAGCTCCCAATGTCTTACGAGATGGCTTCAACCCCGCTGATGTGGAGGCTGGACTGTACG  
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TGCAGGTTGATGTAGACACAGTAAAGGAGGGGCTGAAGTTGAACCCCAACTTCTCTGGTGG  
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30 AGCATGTACCAACAGCCCAAGCTGAGACTGTGGCAATGTGTGAGTCATATACATTACT  
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>H\_1.0.0\_24583 Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A  
thiolase) (ACAA27), nuclear gene encoding mitochondrial protein, mRNA cr: gi-5174428///  
[Human\_jongleur\_201102.11645.C1] [SEQ ID NO: 70]

35 GTGTTTAGGGTGTGGCGGAGACAAAGGGGAAGAGTCATCGCCTGTCGGGGCTAGGATAT  
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40 CGCTGGGACCCCGCCCAAGGAGCCCCAGGAAGTAGGTGAAAGGGCAGGGGCGTGGCTCTCG  
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45 TGAACAGTTGACAGTGTGATTATGGGCAATGTCTCGAGAGTTCTTCAAGTGTATATA  
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50 ATGGGTATCATTAACAGATCAGCATGTCCAGCTCCCCATGGCAATGACTGCAGAGAATCT  
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60 TGCTTTGGGTACCCACTGGGAGGATCTGGATCAAGAATTACTGCACACCTGGTTACGA  
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>H\_1.0.0\_2171 Homo sapiens apolipoprotein A-I (APOA1), mRNA cr: gi-4557320///  
[Human\_jongleur\_201102.263.C2] [SEQ ID NO: 71]

70 NGAGAGACTGCCGAGAAGGAGGTCCCCACGGCCCTTCAGGATCAAAGCTGCGGTGCTGAC

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5 GCTCGGCCCTGTGACCCAGGAGTTCTGGGATAACCTGGAAAAAGGAGACAGAGGGCCTGAG  
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10 ACTGGCGGAGGAGATGCGCGACCGCGCGCGCCCATGTGGACGCGTGCGCACGCATCT  
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GTGAGGCGCCCGCGCTTCCCGTGTCTCAGAAATAACGTTTCCAAAGTGGG  
15 >H\_1.0.0\_15335 Homo sapiens L-kynurenine/alpha-aminoadipate aminotransferase (KATII), mRNA cr: gi-  
13518236/// [Human\_jongleur\_201102.6487.C1] [SEQ ID NO: 72]  
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50 GAAATCAAATAATCATGCTGCTCATGGATTTTCCAAATAAATTTCTGTTTGGCAGGA  
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>H\_1.0.0\_12049 Homo sapiens cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13  
(CYP2A13), mRNA cr: gi-19743563/// [Human\_jongleur\_201102.4706.C1] [SEQ ID NO: 73,74]  
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65 TTCAGCGGGCGAGGCGAGCAGGCCACCTTCGACTGGCTCTTCAAAGGCTATGGCGTGGCG  
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70 TTCTGTGCTGTTGCGCATGATGCTGGGAAGCTTCCAGTTACAGGCAACCTCCACGGGG  
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TTTAAGGAGCTGCAAGGGCTGGAGGACTTCATCGCCAAGAAGGTGGAGCACAAACAGCGC  
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>H\_1.0.0\_21557 Moderately similar to HEMI\_HUMAN 5-aminolevulinic acid synthase, nonspecific,  
mitochondrial precursor (Delta-aminolevulinate synthase) (D cr: gi-5850819/// ws61h08.x1 Homo  
20 sapiens cDNA 3' end /clone=IMAGE:2501727 /clone\_end=3' /gb=AW003903 /gi=5850819 /ug=Hs.407036  
/len=678. [Human\_jongleur\_201102.9885.C2] [SEQ ID NO: 75]  
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55 AGTGGACAATGCTCCGAGGGGCTGGCTTGGCCCCAACTTCCATCATCTTGGGGCAGTTTTG  
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60 CGTCCG

>H\_1.0.0\_5587 Homo sapiens carboxylesterase 3 (brain) (CES3), mRNA cr: gi-6912297///  
[Human\_jongleur\_201102.1674.C1] [SEQ ID NO: 76]  
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 >H\_1.0.0\_19636 Homo sapiens hydroxysteroid (11-beta) dehydrogenase 1 (HSD11B1), mRNA cr: gi-  
 5031764/// [Human\_jongleur\_201102.8752.C1] [SEQ ID NO: 77]  
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ACAAGTGGTACAGATGAAGGAGAAGATGGAGATGAACCAGATGACGGGAGCAATGATGTC  
GTTGATCTTTTCCGAGGACGGAGATCAGTGATAAAATCACTTCAGAGTTGGTATCTAAG  
ATTGGTGATAAGAATTTGAAGATTAGCAAGAAGGCCATAGATGAAGTGGCAGGTATTATT  
AATGACCCAAATTTATCCAACCGAATATAGGTGAATTTCCAACCTGCTTGAAGGTCGA  
15 CTCAATGATTCAAATAAAATCTTGTTACAGCAAAACGCTGAATATCCTGCAACAACTGGCA  
GTAGCCATGGGCCAAATATTAAAGCAACATGTAAAAAATTTAGGCATCCCTATCATCACA  
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AAGGAAATCCCTTTCTTTGAGGCAAGAGCTTTCTGGGCTGGCTGGCTGAGAACTACCTACT  
20 CTTGCTTCCACCCCTACAGACCTTATCCTTTGTGTTCTCTACTCTCTGCTGCTAGAA  
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AAAGCAACTTCTAAACCAATGGGAGGGTCCGCTCCAGCCAAATTCAGCCTGCAATCAGCA  
25 CTTGCTGAAGATTGTATTTCAGCAGTACAGAACCCAAACCTGATCCAAAAAGGCCAAA  
GCTCCAGGATTATCCTCTAAAGCAAGAGTGCACAAGGGAAGAAGATGCCAAGCAAAACC  
AGCTTAAAGGAGGATGAAGACAAATCCGGGCCCTATTTTATTGTGTGTTCCAAATGGAAAA  
GAGCAAGGATGAAGATCAAAAAGGATTGAAGGTGCTAAAGTGAATTTTACTACCCCA  
CGGGATGAATACATTGAGCAACTAAAGACTCAAATGCTAGCTGTGTGGCTAAATGGTTA  
30 CAAGATGAGATGTTTCACTCAGACTTTCAGCATCATAACAAAGCCCTGTGTGTTATGGTT  
GATCACITGGAGAGTGAAAAAGAGGAGTTATTGGTTGCCCTGGATCTTATCTTAAAGTGG  
CTTACCCTGAGGTTTTTTGACACCAATACAAGCGTCTGATGAAAGCACTAGAAATATTTA  
AAATTGCTCTTCACTTGCTAAGTGAAGAAGATATCATCTTACTGAGAATGAAGCATCT  
TCCTTCATCCCTATCTTGTGCTCAAGTTTGGAGAACCAGGATGTCATTCTGTAAGAT  
35 GTTCGTCGCCTCCTGAACCGGATGTGCCTTGTCTACCCAGCTAGCAAGATGTTTCCCTTT  
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GGATGTCTGTTGAGTCTTATGGCATGAATGTTTGCAACCAACCCAGGAAAGCCCTTA  
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40 ACCATTGTAACGGTGTACAATGTACATGGGGATCAGGTGTTCAAACGATTGGAATCTTT  
TCTGAAAGGATATGAGCATGCTCGAGGAGAGGATTAAGCGGTGAGCAAGAGACCCCTCT  
GCTGCACCAATAAACAGGTGGAAGAGAAACCTCAGCTGTCACAGAACATAAGCTCCAAT  
GCCAATGTTTACGCAAGGGACCAAGCTGAGGACATGCTTCCAAACTCAACCAAGCCCGA  
AGCATGAGTGGGCATCTCGAGGCAGCCAGATGCTCCGCCGAGAATTCAGCTGGATCTA  
GATGAGATTGAGATGACAATGGTACAGTCCGATGTGAATGCCAGAACTTGTTCAGCAC  
45 AAACCTGGATGACATTTTGGAGCCAGTCTTATTCCTGAACCAAGATCCGGGCTGTTTCT  
CCACACTTCGATGACATGCACAGTAATACAGCATCCCAATCAATTTCAATTATCTCCAA  
GTAGCCAGTGGTGACATCAACACAAGTATCCAAGCTCTGACACAGATCGATGAGGTCTTG  
AGACAGGAAGACAAAGCTGAAGCCATGTCGGGCCATATTGATCAGTTTCTGATAGCCACT  
TTTATGACGCTAAGACTCATCTACAACACACACATGTCAGATGAGAAATGGAGAAGGAC  
50 GAGATCATCAAGTTGTATAGCTGTATCATTGGCAACATGATTTGCTGTTTCAGATAGAG  
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AACCTCTTGGTGGTGAAGGTTCTGGAGAAGTCAGACCAACCAATCCTGAGTGCCCTA  
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55 GTTATGAAGTGTCTCTGGAGAATGGTTGACTGTTGCTGTATACCATCAATAGCATTAAAC  
CTAGACAGAATTTCTTGGATATCCACATTTTCATGAAGGTCTTCCCAAGAGAGAACTG  
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AAATTTAAAGGGCCCAAGATCTTGACCACTAACGATGATCGACAACAAAACAGAGTCT  
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60 TCTGATAAGGAAACAGAAAAGGGAGCATCTCGAATAGATGAAAAATCATCAAGGCCAAA  
GTGAATGATTTCTTAGCTGAGATTTTAAAGAAGATTGGCTCTAAAGAAAACATAAAGAG  
GGACTAGCAGAGTTATATGAATATAAGAAGAAATACTCAGATGCTGACATTGAACCATTT  
CTGAAAAATTTCTCACAGTTCTTCCAGAGCTATGTGAAAGAGGCCTTCGGGTGATTGAG  
ATGGAGAGGGGCAAGGTCGATTTTCCACTTCAACAGGCATCTCCCTCAGATGGAA  
65 GTCAATGTGTGCCACGCCCCACAAGCACAGTGTCTCCATAGGTAACACAAATGGGGAA  
GAAGTGGGGCCATCTGTCTACTTGGAAGGCTAAAGATCTCCGACAGCGATGTGGTCTG  
GACAAACAAAGCAAGATGACCGACCTCTTTGACCTCTTTGCTCTCCAAACAGCAGTT  
CCTACTGTGCGCTCTTCCACAGACATGCTCCACAGCAAACTCTCTCAGCTCCGGGAGTCA  
CGGGAGCAGCAGCAGCATTCAGACCTGGATTCTAACAGACTCACTCTCAGGAACTGTG  
70 ACCTCTCTCTCTCCACAGCTAACATAGACGACTTGAAGAAAGACTGGAGAGAATAAAG  
AGCAGTCGCAATGAAGCTGCCCCACTCCCCCGCACCTTAGTTTACTAAAC

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TAGAAGTCTCATAGTTTAAATGGCCTCAGCAGGCCTAGTGATACAACTGGTTGTAT  
GTATCATGCCGTGGAGCTAGGGGAGGAGTCATTGTGGCACAAGTATTTGTACATACTCT  
GCTTCTCTCTGTGAGCGTCTGTGCTCTAGAAAGCTGTCCGTGGATGAGTTTAGTGATAC  
AGACTTGTAAACAGCTGCCCTCTCTGCTCAGTCTAGTTCCCAGATCCTTTCTTTTAA  
ATTGCTCATTGTAAATTTGCTTAATCTTTCTAGCTTTTAAATAGTTAATATTAGAAA  
CTCTTTAATAGTTTTCCTTTTCTAGTTTGTGAGCTCTTCTGTGCGCCCTGAAGGGTCACTG  
TATTCTGTATGAATGCATGGCATGATACAACTAATTTAAGAGTCTTTTATAAATAAAGTT  
TGCATTAACTATACCTG

>H\_1.0.0\_134944 Homo sapiens, Similar to KIAA1001 protein., clone MGC:8996 IMAGE:3882163, mRNA,  
complete cds as: gi-15214501/// [gi|15214501|gb|BC012375.1|BC012375] [SEQ ID NO: 87]

GCCGTCGCTCCAGACAAATCGGAATCCTGCCTTACCACCATGGGCTGGCTTTTCTAAAG  
GTTTTGTGGCGGGAGTGAGTTTCTCAGGATTCTTTATCCTCTGTGGATTTTGCAATC  
AGTGGGAAAACAAGAGGACAGAAGCCAACTTTGTGATTATTTGGCCGATGACATGGGG  
TGGGGTGACCTGGGAGCAAACCTGGGCAGAAACAAAGGACACTGCCAACCTTGATAAGATG  
GCTTCGGAGGGAATGAGGTTTGTGGATTTCATGTCAGCTGCTCCACCTGCTCACCTCC  
CGGGCTTCTTGTCTCACCGGCCGGCTTGGCCTTCGCAATGGAGTCACACGCAACTTTGCA  
TGCACCTTCTGTGGGAGGCCCTTCCGCTCAACGAGACCACTTGGCAGAGGTGCTGCAGCAG  
GCCGGTTACGTCACTGGGATAATAGGCAAATGGCATCTTGGACACCACGGCTCTTATCAC  
CCCAACTTCCGTGGTTTGTATTACTTCTTGGAAATCCCATATAGCCATGATATGGGCTGT  
ACTGATACTCCAGGCTACAACCACTTCTTGTCCAGCGTGTCCAAGGGTGATGGACCA  
TCAAGGAACCTTCAAGAGACTGTACACTGACGTGGCCCTCCCTCTTTATGAAAACCTC  
AACATTGTGGAGCAGCCGGTGAACCTTGAGCAGCTTGGCCAGAGTATGCTGAGAAAGCA  
ACCCAGTTTCTCAGCGTGAAGCAAGCAGCGGGAGGCCCTTCTGCTCTATGTGGCTCTG  
GCCACATGCACGTGCCCTTACCTGTGACTCAGCTACCAGCAGCGCCACGGGGCAGAAGC  
CTGTATGGTGAGGGCTCTGGGAGATGGACAGTCTGGTGGGCCAGATCAAGGACAAAGTT  
GACCAACAGTGAAGGAAAACACATTCCTTGTGTTTACAGGAGACAATGGCCCGTGGGCT  
CAGAAGTGTGAGCTAGCGGGCAGTGTGGGTCCCTTCACTGGATTTTGGCAAACCTCGTCAA  
GGGGGAAGTCCAGCCAAGCAGACGACCTGGGAAGGAGGGCACCGGGTCCCAGCACTGGCT  
TACTGGCCTGGCAGAGTTCCAGTTAATGTACCAGCACTGCCTTGTAAAGCGTGTGGAC  
ATTTTTCCAACTGTGGTAGCCCTGGCCAGGCCAGCTTACCTCAAGGACGGCGCTTGTAT  
GGTGTGGACGTCTCCGAGGTGCTCTTGGCCGGTCAACAGCTGGGCACAGGGTGTCTGTT  
CACCCCAACAGCGGGGACAGCTGGAGAGTTTGGAGCCCTGCAGACTGTCCGCTGGAGCGT  
TACAAGGCCCTTCTACATTACCGGTGGAGCCAGGGCGTGTGATGGGAGCAGGGGCTGAG  
CTGCAGCATAAGTTTCTCTGATTTCACCTGGAAGACGATACCGCAGAAGCTGTGCC  
CTAGAAAGAGGTGGTGGGAGTACCAGGCTGTGCTGCCGAGGTGAGAAAGTTCTTGCA  
GACGTCTTCCAAGCAATGGCAACGACACATCTCCAGCGCAGATTACACTCAGGACCTT  
TCAGTAACTCCCTGCTGTAACTCCCTACCAAAATGCTGCGCTGTCAAGCCGCATAACAG  
ACCAATTTTTATTCCACGAGGAGGAGTACCTGGAATTTAGGCAAGTTTGTCTCCAAATTT  
CATTTTTTACCTCTTTTACAAACACACGCTTTAGTTTGTGAGTTTGTCTTGGAGTT  
TAGCCTTGCATATCCCTTCTGTATCCTGTCCCTCCTCCACGCCGACCCGAGAGCAGCTGA  
GCTGCGCTGCTCTGGGAGGAGTGTGCTTAAATGGGAAGCACAAGGGCTTTGGAGTCA  
GGCACAGGTGCGCAGCTCCAGCTTTTGAACCTGGGCAATTGTTTAACTAACCTGCAAGTT  
GATTTTGGGGTTAAATAAAGGCATACATGAAATGCTGGCAAATTACCTGACACAGAG  
CAGACATTCAATCATTTTAGTTTCTGTGTTTNNNNNNNNNNNNNNNN

>H\_1.0.0\_14660 Homo sapiens KIAA0102 gene product (KIAA0102), mRNA cr: gi-7661907///  
[Human\_jongleur\_201102.6112.C1] [SEQ ID NO: 88]

GGGGCACACATTTTATATACAGACCTCTGAGAAACCTCTCAGCAGAAAACCTGCAGGAAG  
GAAGTCTTCAGTTAACTAAAGAGAGTTAATGCTCCTAGAAAGATATTCTAGGCAGAGATT  
ACAGCAAAATGCAAAAGCTCTCAAGTGGGAGAGTACTTGGGGTGTTGAGGACTATCAAGG  
ATTGAAGAGGCTGTGTGGCTGCAGGGACAGGGCGAGTGAGGATTGCTGAGAGGTGAGG  
TCAGAGTGCAAGGGCCTTAGGGCTGGGCGAGGTGCTCACGCTGTAATCCAGCACTTT  
NAGACGCAGAGGCGGACAAGATGGCGGCGGAGCTGTACAGGCGGGAGAAGCGTGGTA  
GCCGAGGCTGTAGTGGGGCTGGTGGTCTTCCAACTGCGGACAGGAAGTGGCCGTAGCG  
GCTTGTGGGATAAGTGAAGATAGATGATAAGCCTGTAAAAATTGACAAGTGGGATGGAT  
CAGCTGTGAAAAACTCTTTGGATGATTCTGCCAAAAGGTACTTCTGAAAAATACAAAT  
ATGTGGAGAATTTTGGTCTAATGTATGGTCCCTCACCATCTGTACAATCTCCTGTTTCT  
TTGCCATAGTGGCTTTGATTTGGGATTATATGCACCCCTTCCAGAGTCCAAACCGTTT  
TGGCTTTGTGTGTCTATCTTATTTTGTGATGATGGGATTCTGACCAATTTATACCTEAT  
ATAAGGAGAAGAGCATCTTTCTCGTGGCCACAGGAAAGATCCTACAGGAATGGATCCTG  
ATGATATTTGGCAGCTGTCTCCAGTCTTAAAGGTTTGTATGACAAATACACCTTGAAGC  
TGACCTTCTCAGTGGGAGAACAAAGCAGCAGCGGGGAAGCCGAGTTTCAAAAGTCCATTG  
CTAAGTTTGTGACCAAGTGGGACACTGGTCAATGATGCAATAGAGCTGAAATATCCA  
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TCTTTCTCCTGGATCTTGTCTGAATAGTGGCTTGGGGGTGGGGGAGATAAAAGAACTT  
AAAAAGGGTAAAGTAAAGAAATGTTAAAGTCCCTGTTTGTCTGAAATTTTGTCTAT  
TCTGGGTAAATAGGATTTTCTGACACAGATATGAGAAGTTGTAGCTCTGATGTCTAGCTG  
TAGTCTCCTTGTATCTGTGATTGCAATATTTAATTTGCTTTTCTGGGAAGCAGTTTTG  
CTAAAGCTGTACAGACTTTTCTTTTGTACCTAGCAGTACTTTATATAGTATAGCTTTG  
GGCCATGTAGCATTTTAAAGTCAATTTTAAAAAATTTAATCTGTGCTGACTCTTAA  
TCTCTATTTCAATATGTGTTTCTTGAAGAAATTCAGGATACAACCTTCTGTGTATGACAG  
CTTTCTTTCACACATAATTTTGTGGGTGTATATATCTGATTGGGAAGAAATTTAAAT

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AACACATAGCTTTTAAATTGTTTGAACAGACTTICTGCCTGTTACATTTTGGCTTTTA  
ACCAATTAAAGAAGCCAATGGCATTTTAGTTTTATATTGTGTTTTCCACTAGTATATCCC  
TGTTGATTGTGTGTCCTTTTATTAAGTCCATTTCTAAAATTTTTTCAATAAAAGG  
AAGGAAGATGTG

5 >gi|4505154|ref|NM|002402.1| Homo sapiens mesoderm specific transcript homolog (mouse) (MEST), mRNA  
[SEQ ID NO: 89]

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GCGCACGCGGAGTGGCTGTAGCTGCCTCGGCGCGGCTGCGGCCCTGCGCGGGCTGTGGG  
CTGCGGGCTGCGCCCCGCTGCTGGCCAGCTCTGCACGGCTGCGGGCTCTGCGGCGCCCC  
10 GTGCTCTGCAACGCTGCGGCGGCGGCATGGGATAACGCGGCCATGGTGCGCCGAGATCG  
CCTCCGAGGATGAGGGAGTGGTGGGTCCAGGTGGGGCTGCTGGCCGTGCCCTGTCTTG  
TGCGTACCTGCACATCCACCCCTCAGCTCTCCCTGCCCCTCACTCATGGAAGTCTTC  
AGGCAAGTTTTTCACTTACAAGGACTGCGTATCTTCTACCAAGACTCTGTGGGTGTGGT  
TGGAGTCCAGAGATAGTTGTGCTTTTACACGGTTTTTCAACATCCAGCTACGACTGGTA  
15 CAAGATTTGGAAGGGTCTGACCTTGAGGTTTCATCGGGTGATTGCCCTTGATTCTTAGG  
CTTTGGCTTCACTGACAAACCGAGACCACATCACTATTCATATTTGAGCAGGCCAGCAT  
CGTGAAGCGCTTTTGGCGCATCTGGGCTCCAGAACCGCAGAATCAACCTTCTTTCTCA  
TGACTATGGAGATATTGTTGCTCAGGAGCTTCTCTACAGGTACAAGCAGAATCGATCTGG  
TCGGCATACCATAAAGAGTCTCTGTCTGTCAAATGGAGGTATCTTCTCGAGACTCACCG  
20 TCCACTCCTTCTCCAAAGCTACTCAAAGATGGAGGTGTGCTGTCAACCATCTCTCACAG  
ACTGATGAACCTCTTTGTATTCTCTCGAGGTCTCACCCAGTCTTTGGGCGGTATACTCG  
GCCCTCTGAGAGTGAGCTGTGGGACATGTGGGCAGGGATCCGCAACAATGACGGGAACCT  
AGTCATTGACAGTCTCTTACAGTACATCAATCAGAGGAAGAAGTTCAGAAGCGCTGGGT  
GGGAGCTCTTGCCCTCTGTAACTATCCCCATTCATTTATCTATGGGCAATTGGATCTGT  
25 AAATCCCTATCCAGAGTTTTTGGAGCTGTACAGGAAACGCTGCCGCGGTCCACAGTGTC  
GATTCTGGATGACCACATTAGCCACTATCCACAGCTAGAGGATCCCATGGGCTTCTTGAA  
TGATATATGGGCTTTCATCAACTCCTTCTGAGCTGGAAAGAGTAGCTTCCCTGTATTACC  
TCCCCTACTCCCTTATGTGTGTGTATTCCACTTAGGAAGAAATGCCCAAAGAGGTCT  
GGCCATCAAAACATAATTCTCTCAAAAGTCCACTTTACTCAAATTTGGTGAACAGTGTATA  
30 GGAAGAAGCCAGCAGGAGCTCTGACTAAGGTTGACATAATAGTCCACCTCCCATTACTTT  
GATATCTGATCAAATGTATAGACTTGGCTTTGTTTTTGTGCTATTAGGAAATCTGATG  
AGCATTACTATTCACTGATGACAGAAAGCGTTCTTTTGATATAAAGACTTTTTTTAAACA  
CTTTGGACTTCTCTGAAATATTTAGAAGTGCTAATTTCTGGCCCAACCCCAACAGGAATT  
CTATAGTAAGGAGGAGGAGAAGGGGGCTCCTTCCCTCTCCTCGAATGACGTTATGGGCA  
35 CATGCCTTTTAAAGTTCTTTAAGCAACACAGAGCTGAGTCCCTTTTGTATACCTTTGG  
ATTTAGTGTTTCATCAGCTGTTTTAGTTATAAACATTTTGTTAAATAGATATTGGTTT  
AAATGATACAGTATTTTAGGTATGATTTAAGACTATGATTTACCTATACATTATATATAT  
TTTATAAAGATACTAAACCAGCATACCCTTACTCTGCCAGAGTAGTGAAGCTAATTAAC  
ACGTTTGGTTTTCTGAATAAATGAACTAAATCCAACTATTTCTAAAATCACAGGACAT  
40 TAAGGACCAATAGCATCTGTGCCAGAGATGTACTGTTATTAGCTGGGAAGACCAATTCTA  
ACAGCAAATAACAGTCTGAGACTCCTCATACCTCAGTGGTTAGAAGCATGTCTCTCTTGA  
CTACAGTAGAGGGGAAGGGATGTTGTGTAGTCAAGTCAACATGCTGAATGTACACTGA  
TTCTTTATGATGACTGTCTTAACTCCCACTGCTGTCCAGAGAGGCTTTCCAATGTAG  
CTCAGTAATTCCTGTTACTTTACAGACAGGAAAGTCCAGAACTTTAAGAACAACTCT  
45 GAAAGACCTATGAGCAATGTGTGTAATACTTTTTTTTAAAGCCACATTTTATTGTCT  
TAGTCAAAGCAGGATTATTAAAGTGATTATTAAATTCGTTTTTTTAAATTAGCAACTCT  
AAGTATAACAACTTTGAAACTGGAATAAGTGTATTATTTCTATTAATAAAATGAATTGT  
GACAAAAAAAACCG

50 >M\_1.0.0\_5828 Mus musculus 11 kDa secreted protein precursor, mRNA, complete cds cr: gi-8926323///  
/cds=(23,361) /gb=AF272844 /gi=8926323 /ug=Mm.71887 /len=524 [Mouse\_jongleur\_201102.2852.C4] [SEQ ID  
NO: 90]

GAATGCATTTAGCACTCTTCACCATGAAGGGGACACTTCTTCTGCTGGGCTTGCTGGTGA  
CTGGGAAGCTGAGCTTCCAGACAACAGAGCATGTGTTCCTTCTCGAAGGCTATGCAA  
55 GTGTTCTCTCGAAGTAGGGTGTGGATGTATCAAGAACTCCAGGCATTCAATGCTACTG  
CAGAGGAAAAGGTGGCCTTGGAATAAATCCAGGACTGCTACAGAGAGGAAAGATTAAGAA  
CCGTATTTCTGGAACCCAAAATTATGGAAGCCATGGTCTCCAGCCAAGAAATGCCGTGGCAT  
TTTATACTACTGAAAACATATTGAACATTTTCGACCTTTTAGCTGGTTAATTAGAAGAAT  
AGATATTAAATGTGTTTTGGGCAACCCATCTTTGCAACATGTGTGATCCAGTACTATCTT  
GCTGTCTCTCTTTTCTCTCTGGAAGATGAATTCTGTATCTGTTTATTCTGCTATTCACT  
60 CTCTTAGACTGATTCTAATAAAGGCTTGCAAGCTCTGTCTCTGTG

>gi|16442925|gb|BB513945.2|BB513945 BB513945 RIKEN full-length enriched, 10 days lactation, adult  
female mammary gland Mus musculus cDNA clone D730048K19, mRNA sequence [SEQ ID NO: 91]

TTCCGACTTTGGCATGATTTTAAAGGCATCACCAAGTGCAAGCTTAAATGCCAAAGAAA  
65 GCAACACTGGATTTTAAATTTAGTAAATCCAATAAATAAGATCAAAGCAAGTCACAGAT  
TTTAAATTTGCTTGATGGTCTGCTGAAAAGTTAAAGGAAAACCAAAACATTGATCTT  
TGAGCAATTTAATTGATCATTTGAATCAGATAAATGTTTTTGTTTTATTCTGCTTAIAA  
CACATCATCCATAATTGATACAATTGGAGTTGATATAATTGACAGAAATTTGTACGCT  
ATATTTTAAAACTGGCTGCTATGGTTTGGGTAAGTGTCTCAACGGCCTGTGTATTGAA  
70 GGTGTGCTGTTTCTTCATCTGTGGTGTCTCTGGGAAGCAGGGAATACTGGAATGTGGA  
GTCTTCCCTTCAGGGTGTGTCTGTCTTTGTTTACACCACCAAGCAAGCAGCTTCC  
TTGGTCTCATATTTCCACCACAAAATATTCTGTCTGCCACAGGCCAGTGGAATGATC

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ACAGGCTGAAACTTCTAAATCGAGAGCCAAATAAACCTTTCTGCTTTTAAAGTTGATT  
TGCTCTCAAGTACTTGTTACAGAAACGAGGATGAAATGCAAAGATTTATGTGAATGTAAA  
TAGCTAATGAGATT

>M\_1.0.0\_6038 Mus musculus retinoic acid early transcript 1, alpha (Raet1a), mRNA cr: gi-6679616///  
[Mouse\_jongleur\_201102.2973.C1] [SEQ ID NO: 92]

GCGCCGCTTGCCCGGGCCGCTGTAGTCAGTTACCTGCTCCGCGGGCGAACACGTGCGGG  
GGCAGACAGACACTCCAGCTTGCAGGAGGCGGGCGCCCTGCACCGCAGGTGCAGCTCA  
CAGCTGGACCCACAGACCAATGACACATAAGCAACTACTTGAAAACAGCTGGGAGCACT  
CTAGCAAGAAGCTCAAAGACAGAGAAGTGTGTGCAGAGGTCAGAAACCTGCCTGGAATC  
CCCTGGAGCAGCAGCTCAGAGAAGGTTGTGAGCTGCTCGATTTCAGAGGCTGCAGTTCAAG  
ACACCAACTTTTTCTTTCTTCACCTTCTCTGACACTATTGCCAATAGTCCCTGAGGGCG  
CAGCTGTTGCCACAGTCACATCTGTGAGAAGAAACCATGGCCAAGGCAGCAGTGACCAAG  
CGCCATCATTTTATGATTTCAGAAGCTGTTAATCTACTGAGCTATGGATACACCAACGGG  
CTGGATGATGCACACTCTCTTAGGTGCAACTTGACCATCAAGGATCCTACCCAGCAGAT  
CCTCTCTGGTATGAAGCGAAGTGCTTAGTGGATGAAATACCTTATCCTCCATTAAAGTAAC  
ATAAACAAGACCATGACTTCAGGTGACCCAGGGAGACAGCAAATGCCATGAAGTGGGG  
GAATGTTTGACACAACCTCTGAAAGATTGTGCCAGAAGTTGAGGGACAAGGTGTCTAAC  
ACCAAAGTGGACACTCACAAGACCAATGGTTACCCACATTACAAAGTCACCATGATTTAT  
CCGCAAGCCAGGGCCAAACTCCTAGTGCCACCTGGGAATTCACATCAGTGACAGTTAC  
TTCTTCACCTTCTACACAGAGAATATGAGCTGGAGATCAGCTAATGATGAATCAGGGGTT  
ATCATGAATAAATGGAAAGATGATGGGAATTGTGAAACAATTGAAATCTTGATACCC  
GAATGCAGACAGAAAATGATGAATCTTAAAGCAGTCCAAGGAAAAGCCAAAGATCAACC  
TCAAGGTCCCCAGTATACCCAGCTTACATCAACTTCCCGCTTCCACCTCCCAGCCAC  
TCTACTTCTAAGAAGAGTATTTATCTCTGTGGGACTCATCTCATATCTTTATTATTGCA  
TTTGCAATTTGCGATGTGAAGAGGAAATATTATACCCAAGGAGAGGCCAGAGAGGGCATC  
GGATCCTGTGGAACTGGAGTTACAGTTGGTTTCCAATACTGGGAACCTGAATCCAGGACCT  
CTCCAAGAACAGCAAGTCTCTTGTCTACTGAGCCTTATCTCCCTCCTTAATACATTTT  
TTAATAAGAGAATATAGTTTGAATATTATTAAACCCAGGGCAAGTCCACAGTAAGCTTC  
ACATAAAGTTGATTGTTTTCAGAAATCAAAAAGGAAAACACATTTTAAATGACTGTCTAG  
GCCAGTTATCACATCGTTTGTAGCAATGTATGATGGAGGACGTCAGGTCCGTCTAAAAA  
AATGCCAGGCAATACAGCAACATCTAAGAAAACCTGGTAAATTTAAA

>M\_1.0.0\_4198 Mus musculus peroxisomal biogenesis factor 11a (Pex11a), mRNA cr: gi-6755033///  
[Mouse\_jongleur\_201102.1926.C1] [SEQ ID NO: 93]

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ACTCAGCACGCATGCATGTTGCTTAGATATTTGTTAGAGTCAAAAGCTGACAAAGAGGCC  
GTGGTACTGAAGCTCAAGAGGCTGGAGACCAGTGTGAGCACTGGCCGTAAATGGTTCAGA  
CTGGGCAACGTGTTCCATGCCATCCAGGCAACTGAGCAGAGCATCCAAGCCGCTGACCTC  
GCGCCCGCTTATGCTGACATTAGCCAACTCAACCGCGTGGTTTATTACATCTGTGAC  
ACTGTCTCTGGGCGAAGAGTGTGGGTCTTACCTCTGGAGTCAACAGAGAGAAATGGCAA  
AGGTGGGCGGCTCGCCATTACTACTTCTCTTGTGAGCCTGGTCCGGGATCTGTAT  
GAGATCTTGCTGACAGTGGGACAAGTTGCACGTGACAGAGCAAAGAGAGAGAAATCCTCT  
CGGGACCTCTCTAAGTACAGCGTGGCTAATGAAGAGACTGAATGGCTCCAGTCCTTCTC  
CTCCTCTATTCCAGTCTCTAAAGCGACATCTCCCTTGCTCCTGGACACCGTGAAGAAC  
TTCTGTGACATCTGATCCCTCTGAACCAGCTTGGGATCTACAAGTCCAATCTCGGCGTG  
GTAGGACTTGGAGGTCTCATATCCTCTTGGGCTGGTCTCCTCACGGTAGTGTATCCTCAG  
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>M\_1.0.0\_15194 Mus musculus ATP-binding cassette, sub-family A (ABC1), member 8b (Abca8b), mRNA cr:  
gi-23956075///  
[Mouse\_jongleur\_201102.9242.C5] [SEQ ID NO: 94]

GGTGTGTTGGCAAGACCAACCCAGAGCTGAGATCATAAACTCCCGCTGAGAGCAGCTTICA  
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AGTCCCTGCTTGSCATTTCCCGAAAGGCAACATGATCAAGAGAGAGATAAGTGTGCGCCA  
ACAAACTTGTGCTTTATTACAGAAGAACCTTCTTAAGAAATGGAGACTGAAAGGGAGTCT  
CTTGATGGAGTGGGTGAGCTCCTTGCTCCTTCTGCTTTTCTGTATTGGTATCCCCATGG  
TCATGGAGCTACTGACCTGTCTTCTAGTGCCCAAGGATCTGGGACGAGTCGATTCTTT  
CAGACAAATCTGGGTTTCATGATAGGGTACACGCCTGTCAACAGCATGACACACAGATAAT  
GGAGAAGGTAGCTGCAACCCCTTTCAATGGCAGATAAAAAAGTCTTGGGACTGTTGGATGA  
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CACATTTCTATACCACTGAAATTCAGTTTGATCAGAGAATCCAAAGTCCGAGGGAAC  
CAGAGACCATAATGCTCATTGTGATGGACTGTATGAAGATGTCAACTGCTCTGATAGCCAT  
ATTCTGGAAGGAAGGATTGTGGCTCTTCAAGCTGCCATCAATGCTGCCATCATAGAAAC  
CACAAACAAACCATTCAGTGATGGAGGAACCTGCTATCAGTGTGAGGGAATTCATGAAGAT  
CCATCCTTTTGTCCGTCAAGAAGGAATCTGACTGATTTCTTTATTTTCACTGCAATCAT  
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 >H\_1.0.0\_124998 zm73a01.s1 Homo sapiens cDNA 3' end as: gi-1578801/// /clone=IMAGE:531240  
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>M\_1.0.0\_20499 Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library,  
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/gb=AK020029 /gi=12860486 /ug=Mm.45194 /len=1349 [Mouse\_jongleur\_201102.13747.C1] [SEQ ID NO: 97]  
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70 TCAGTCAAGAGGAGGTGAACCTGAGGATGGTCCAGAGGAGGTGAGCCTGAGGGTGGTCCA  
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>H\_1.0.0\_45987 Homo sapiens mutant guanine nucleotide-binding protein G(s), alpha subunit mRNA,  
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25 ATTCTTCAATCAACCCCGACCACTTGTCTTATTTCCACTTGTGGGGCGGATCATGGGGC  
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GCACATGCACTCCTAGAACCTTCAGTTTCTACGATGGTTTGGTTGGTCCCTTTTGAACCACC  
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60 AAATAAAGTGACCTCGTTCTAGCACCAGG  
>H\_1.0.0\_23668 Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 1 (BNIP1), transcript  
variant BNIP1, mRNA cr: gi-4502440///  
[Human\_jongleur\_201102.11130.C4] [SEQ ID NO: 114]  
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65 GTGATTGTTTCAGGACCTTAAAGTGCTTACTGAACTGAATACTAAAGTAAAGAGAGAAAT  
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TGGATGCAAAATGAAGAATTTAAGTCCATGTCGGGCACCATCCAGCTGGGCCGGAAGCTTA  
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>H\_1.0.0\_12581 Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA cr:  
gi-20070168/// [Human\_jongleur\_201102.4957.CB3] [SEQ ID NO: 115]  
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G  
40 >H\_1.0.0\_37314 Homo sapiens cDNA FLJ38286 fis, clone FCBFF3008153, highly similar to ALPHA-AMYLASE  
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70 AATTAAATCATATGCTGGAATGCTGTGAGTGCAGGAACAAGCAGTACCTGTGGGAAGTTA  
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>H\_1.0.0\_10016 Homo sapiens hypothetical protein FLJ10563 (FLJ10563), mRNA cr: gi-8922518///  
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>H\_1.0.0\_72558 qc96g08.x1 Homo sapiens cDNA 3' end as: gi-3743449/// /clone=IMAGE:1722110  
/clone\_end=3' /gb=AI192240 /gi=3743449 /ug=Hs.147175 /len=410 [gnl|UG|Hs#S1124018] [SEQ ID NO: 121]

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>H\_1.0.0\_17761 Homo sapiens KIAA1576 protein (KIAA1576), mRNA cr: gi-24308256///  
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35 TATGTTTACATAAAAAATAAATAAAGTATTACGATAGCAAAACCTC  
>H 1.0.0.11371 Homo sapiens similar to intermediate filament-like protein MGC:2625, isoform 2; HOM-  
TES-103 tumor antigen-like; similar to CG15021 gene product (LOC126917), mRNA cr: gi-22041886//  
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70 GGGAGAGAGGCCGGGGTAGGGTGTCTGTGTGGCAGCACTGACTGGGTAGTGTGGGTTT  
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5 AAAAAATACATTTAATGTTTTTCATTGATGGACAAAGTTCCCTAATGGTATAGAGCCAATGT  
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70 AAAGATAGTTGATTATTTGCAATCAGATGGCATTCAAACTTAACTGGAGCATATACA  
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40 >M\_1.0.0\_48237 v122a05.r1 Mus musculus cDNA, 5' end as: gi-2504317/// /clone=IMAGE:904496  
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70 CTTTGGATACCTTGAATCCCTCAGTGTAGTAATATTTTCAGACGTTTCCCAATAAGTGTGT  
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[Mouse jongleur 201102.12200.C1] [SEQ ID NO: 132]

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 GTCTCAATGTTTTTCTTACGCCCTCATTTTAAATTTAATGAAGGTAATAATTAATGAT  
 TTTACCAGCTTTCTTTTCACTTTTATCTGTGAGCTCTGACACATCTGAAAAGTAAT  
 CTGATGTGCAAAATATAATTTAAATATGTTAATTTTTTGTCTTCTAAATTTGCTTTTCA  
 15 TCATTAATAATGTCAAGTTCAGGTGATATGTGCTAATATCACTTGGATGTTGGTGGGTTT  
 TTGAATTTTTGGGTGGTTAATCAGTTATTTGAAAAGACGTAATGTAATAGTTACAGCAT  
 ATGTTTGAACAGGAAGTAGGAACATGCATACACGAAGAAATGCTAACGGAAGGATTGTT  
 ATGTTTAGGATCTTCCCTTGGAACTAAAAATAGAATATTAATGACATTACTGTTGTAG  
 AATGACATATGACAGATTTTCTCATAGCAGTCTATGTTGTTGCCAGTAATGTTTGAAGA  
 20 CATGTAAGTTGAAAGTTTGTCTAAATTTAAAGCTCTTTAATTCGTGGTTTGTGATTT  
 CTTATTCTCTGTCTTTTCTAAATGTTAAACAAATATATCTTAACAGATTACATGAAAT  
 TAGGAATTTATTAAGTTTACATTAGCTCTAAATTAAGATTCCGATGCTTTATTTATA  
 GTAACTGAAGCTAATAATGTTTATGTTTGTGATTTTGAATTTAATTTGTAGAAGTCA  
 TGCTTCTGAGTTTCAAATAGATAACACCTTTAATATTACATGCTTATAATACTAAT  
 25 GTTTACAGATATGTTTCTGTTTATAACCATATAATACATTGGCTTTGTCATATTAGTTT  
 TTTTGCAAGTAGTTATGTAAGAGATAGATAATAAATATTAATAACNNNNNNNNNNNN  
 NNNNN

>H\_1.0.0\_140359 Homo sapiens similar to Gliacolin (LOC222404), mRNA as: gi-20473752///  
 [gi|20473752|ref|XM\_169005.1|] [SEQ ID NO: 148]

ATGCTGTCCAACTGTACATGAGCTGATGTGTGGGAACAGCTTCTACATTACCGTGGAG  
 30 CAAATGGGCTTTAATAGCCGATCCGAGAGTCTCAAAATCAGGAAGAGAACTCTGATCGG  
 CCCATGTTGGGACAAGGGTTCACCTGGTCAAATGTGGCTGGTGAATAATGTGGCAACTGGG  
 TCTCAAGGACAGAGGACAGCATGGCTACCGGTGCGCCATCCAGTGTCTTCCCAATGAT  
 CCTGGAGAACGAGGAGTCTACTCTGAGTGGGACCACAACTCCATAAGGATCCAGGTGCTG  
 35 GCAGCAAACTCTACCATTTTGTCTCCAAAGGAAGGTGACTTTTAAGAAGCAATCCAGA  
 AGGTGTGTTAGGAACCGCAGCCTCCGCGGGGGAGCAGGAGTCCGCGAGCGCGGCCGCG  
 GCACGCAAGCCAGGGGAGTTGGGGTTGCGAGGGGGTTGTTTTCGGCTCTGAAGAGGTCC  
 CCGCCCAACCTTCAAATTTCTGTCCAAAGCAGACAGAGGATCGCCCCGCGCTGAGCCG  
 GCTGGTGGGAGCAGGAGGCGCTGATCGCGCGGGGGCGCTGGGGGTGGTGTGGTGTCT  
 40 GCTGCTGGTGATCTCTATCCCGGTGCTGGTGAGCTCGGCGGACAGTGGGCGCACTACGA  
 GATGCTGGGCACTTGCCTCATGGTCTGCGACCCCTACGGGGGACCAAGGCGCCAGCAC  
 CGCTGCCACGCGGACCGCGGCTCATGCACTCCCTGCCACCTTCACTCCAGGGGCCCAA  
 AGGCGAGGCGCGGAGGCGCGGGAAGGCGGACAGGTGCCAAGATCGCTTCTACGCGGCG  
 45 CTCAAGCGGAGCATGAAGGCTACGAGGTGCTCAAGTTCGACGAGCGGTGCTACCAACCTC  
 GGAACCACTACGACCCACACCGGCAAGTTTCACTGCTCCATCCCGGGCATCTACTTC  
 TTCACTTACCACTGCTCTGATGCGCGGAGGGGACGGCACAGGATGCTGGGTGATCTCTG  
 AAAACCAACAGGTGCGTGCTAGTGCAATTTGCCAAGATGCTGATCAGAATTACGACTAT  
 GCCAGTAAAGTGTGGTCTTCAATTGGAGCCGGGAGATGAAGTCTATCAAAATTAGAT  
 50 GCGGGGAAGCCCATGGAGGAACAACAACAAATACAGCACGCTTTCTGGATTATTATT  
 TATGCTGACTGA

>H\_1.0.0\_66547 nf70b01.x5 Homo sapiens cDNA 3' end as: gi-5053451/// /clone=IMAGE:925225  
 /clone\_end=3' /gb=AI732338 /gi=5053451 /ug=Hs.105621 /len=558 [gnl|UG|Hs#S1425572] [SEQ ID NO: 149]

NNNNNNNNNNNNNNNNNNNNNNAACACTGAAAATTCATTATGTTTGTATTTCAAAG  
 55 AAAACGTAAACTTGTAAATAACAATAGTTCTTTGTAAATCTGCATGACACTTTTATTA  
 GCTAGGGGAAGCGGGAGGTTTGGTTAAACAGGAATCCATGTGAATATTGGGGGAAGAAA  
 GCTAGAGCTGAACAACATATGATTTAAAAAATAATAATCATGTTGGGTTTGTCAAACCA  
 CCTGTACCTTGTGATCCCAAAAAATGTAAAGAACAGTCTCATGGATGAGTGAATAAT  
 TTTCTCTGCTAGATAAGGAGAAGGTCAAAAGACGACAGCTTAGCTGTGAGTCCCACC  
 60 AGCAGATTGCTTTTCAAGGCTCAGTGTGGACCTGACAAAAGCTATTTACAGCTTTTGA  
 ACTGGCAAGGTTTATTTGTTGAGTACAACTCTTGTCTTAAAGATAAGGAACCCACGTTG  
 AGGTACAGTAATAGACACGAAAGATGTTCTGTGCTCATTTGGACACCCCTCTGAGCCTT  
 TATTTTGAGAGTCCGCCAA

>M\_1.0.0\_48261 vm50h11.y1 Mus musculus cDNA, 5' end as: gi-4597033/// /clone=IMAGE:1001733  
 /clone\_end=5' /gb=AI587986 /gi=4597033 /ug=Mm.31187 /len=330 [gnl|UG|Mm#S464186] [SEQ ID NO: 150]

CTTAGAAATGAAGCCCTGAATCCACTGAGCCAAGATTGTTGTTTACGGCTTCTCAGTTC  
 65 ACTAAGTGAATTAAGACAGCTCATTGTCATAGCTTCAATATATTATATCTGGTTCAA  
 TGAACACAAAAACGCTTCCAGCTTTCTAACAAATGAAATTTGTTGGCAAGAAATTTAAA  
 GGGCACCCCGTTATGTACACACCAAGCCAGAGTTACAGTTTATCTTGGGGTCAATC  
 70 ATTTAGTGGCTAGGTAAGTTCCCCCCCCAAAAAATTTTAATTTGAAAAATACGAAGAAC  
 ACTTGTAAACACAGTTAACTAGATGGTTT

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>M\_1.0.0\_7537 Mus musculus leukemia/lymphoma related factor (Lrf), mRNA cr: gi-6754571///  
[Mouse\_jongleur\_201102.3863.C1] [SEQ ID NO: 151]

TTGCTGTCGCACGGTCGCGGCGCGCGCGCGCGCGAAGGAGGTGTCGCGGAAGAT  
GGCTGGCGGCGTGGACGGCCCCATCGGGATCCCGTTCCCGGACCAAGCAGCGACATCCT  
5 GAGCGGCGCTGAACGAGCAGCGGACTCAGGGGCTGCTTTGCGACGTGGTGATTCTTGTTGA  
AGGACGTGAGTTCCCCACGCACCGCTCGGTGCTGGCGGCTGCAGCCAGTACTTCAAGAA  
GCTGTTACGTCGCGGAGCTGTAGTGGACACAGACGAGTACGAGATCGACTTCGTGAG  
TGCCGAGGCACTGACGCGCTCATGGACTTCGCTTACCCGACGCTCAGGTCAGCAC  
GGCCAATGTGGGCGACATCCTGAGTGCAGCAGGCTGCTGGAGATCCCGGCCGTGAGCCA  
10 CGTGTGCGCCGACCTGCTGGAGCGTCAGATTCTGGCGGTGATGATGTGGCGCAGCGGAG  
CCAGCCCGACGGGGCGGGCCCCACTGACCAGCGCAACCTGCTGCGTGCCAAAGGAGTACCT  
GGAGTTCTTCCCGAGTAACCCCATGAATAGCCTGCCCCCACTGCGCTTCCCATGGTCTGG  
CTTCGGTGCCCCGACGACGACCTGGACGCCACCAAGGAGGCTGTGGCCGCGCTGTGGC  
CGCTGTGGCCCGCAGGCGACTGCAATGGCTTGGACTTCTATGGCCAGGGCCCCCGGCTGA  
15 TCGGCCCCCAGCGCGCGATGGAGATGAGGGTGACAGTACCCAGGGCTGTGGCCTGAGAG  
AGATGAAGATGCCCCGCGGAGGGCTCTTCCCACTCCTACTGCCCCACCGGCCACCAC  
ACAGAACCGCCACTATGGCGTGACGGGGCTGGCACCGGTGAAGAAGAACGCGCGGCTCT  
CTCTGAGGCGCTCCAGAGCCGGGCGACTCCCCGGGCTTCTGTGAGGCGCTGACAGGGG  
CGAGGATGGGGACGCGCTGATGTGGATGGCTAGCGGCCAGCACGCTGCTACAGCAGAT  
20 GATGTCTATCGGTGGGCGGGCGGGGACAGTGATGAGGAGTCCGCAACCGACGCAAGGG  
CGTCTATGGACTACTACCTGAAGTACTTCAGTGGAGCCACGAGGGGATGTGTACCCAGC  
CTGGTCACAGAAGGGTGAGAAGAAATCCGGGCCAAGGCCTTCCAGAAGTGTCCCATCTG  
CGAGAAGGTGATTTCAGGCTGCGCGCAAGCTGCCCCGTACATCCGACGACACGCGCGGA  
GAAGCCCTACGAGTGTAACTCTGTAAAGTTCGATTACCAGACAGGACAGCTGAAGGT  
25 GCACATGCGGAAGCACACGGGTGAGAAGCCGTACCTGTGCCACAGTGCAGCGCGCCCTT  
CGCGCACAACTACGACCTGAAGAACCACATGCGGTGCACACGGGGCTGCGGCCATACCA  
GTGCGATAGCTGTGCAAGACCTTTGTGCGCTCCGACCATCTGCACAGACACCTCAAGAA  
GGACGCGTGCAATGGGGTCCCTCGCGCGCGCGCGCAAGCCCGTGTGCGGGTGTGCC  
ACCCGATGTCCCTGCGCGGGCGGGCGCACCCCCCGGGCTCCCGGACGCCCCGCGCAATGG  
30 CCAGGAGAAGCACTTTAAGGACGAGGAGGAGGCCAGCCCGGACGGCTCAGGCGCGCTGAA  
TGTAGCGGGCAGCGGAGGAGACGATGGTGACGGTGGCCCGCGGTGGCCACCGCCGAGGG  
TAACTTCGCAACCTGACTCGTATTAAACAACCAAAACAACCAAAACAAACAAACTAA  
GAACAGAGAGAAACACCCACCCACCCAGCACCCAGGATGAAGCAGTCTCTGTCCAGAC  
GCCCTCCATCCACTCGCCTGCGCGGACGTGTGTGCTGTATATACCATGGCCGCGGGCGCTGC  
35 CTTTCTCAGATCCTTAGGATGTGGCCCCATCTGCTCCTGTGCTCCCTCGTCCCATCCACCA  
AGGGGTCCCAACGACGGGGCCAGCCTGCTCTTGGCTAAAGCGAGGGTGATGGGACCCCA  
GGACAGGCGCCCGGCTCCTTGTGCTGTTGTTTAGGGGCTTTAGACAGACCTTAAATGC  
TCTGTCCACTATGAGTGGACGTTAAATGGTCCCCACCCCTCCTTCTCAGGGCACTTACT  
AAAGAGGGGGGTGTCCCTCGGCTCCCTCCCGGCTGTGGCCTCCGCATCTCTGCACAT  
40 CCACCCTGGCCACCACTGACATACAAATCTATTATTCCCAAGCCTGGATGGCCAGAGCG  
GGGATTGGGGGGGGCGGCTGCGGGTCCCGGCCACCTCCTTACCGGCACITACACCTGAC  
GGGGCCCTCGGGGCGCACTGCTCAGGCGACCCCCCCCCAACCTTCCCATCTCTGCTTGG  
CCATGCCCCCCACCCGTTTTCAGAGATTGAAATTTGTGCTCACCCCACTCCCCACTTTT  
TAAGGCACTTTTATAGATCGAATTCCCTTTGACTCCTTAAAGACAGTTTATATAGAGATA  
45 TATATAGAGAGATATATAAAATATTCTTTCTCAGAGAGCCGGCAGCAGTTTGGG  
TGGACATAGCCAAGATCAGAGGTAACCCAGGGACTCAGGCAGAGACAGCAAGGGAGTG  
AGAGAGGCCACAGCTTAATGTACAAAAACAGCAATAAAACCCCAAGATTTTGAATAACAC  
GAAGGCAGAACATTTTAAAAAATCAGCAAAAGCGGTGACAGCCAGTGGGGATCTTGG  
CACTTTGTAACAGACGGGTACTTTTCACTTCTTAACCTTGAGAAATGTTTACAAGTTGCAC  
50 CCAGCTTCTATGAAAAATTGAAGAGAGAGAGAGTGGGAAGTAACCTAAGTCAATTTATTT  
TGTATAAAATAAAGAACCCCAACCCACC

>M\_1.0.0\_28460 BB404618 Mus musculus cDNA, '3' end cr: gi-9224014/// /clone=C330037B05 /clone\_end=3'

/gp=BB404618 /gi=9224014 /ug=Mm.230612 /len=313 [Mouse\_jongleur\_201102.22092.C1] [SEQ ID NO: 152]

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55 TGTGTGTGTGTGTGTACATCTGCAGTCTACTGTTGTTACTACACAGGGTCTTAAAG  
TCICAACTTTTCTCTATATTCTCCAAAAAGGTCAATTCATTTAATTGGAAATGGCTA  
ATAATGTTCCAATTAAAGTGAGTGATGAAGAGGGACATAGATAGATAGATTCTTACTAAA  
TGCCAGTCTCATGCTTAATAGCCCTACTAATTATGCTTTTAAATGATTGTTCTTGT  
GTTTATTTGGATTTTTCATACAAATATTTTGACTTTTATTCTTTTACACGATTCCGTACC  
60 CCAACTCTTCTATATATCTCCTTCCCTCCACCTCCACCCATCCAACTTCAAGCTC  
TATCTTTTCAAGGGGAAAAAGAAATCCGTGCATTTGAATCAGTCTTTTTCCTTAATCTC  
AGGCATCTTACATCTTTTCTTACCTTTCCCTTAAAGGACTCTTTATTACAAAGACATG  
TTCAAAATCAAAAAATTTATTTATCTCTCTACCCGTGTAAACCCCATTTCCCATTTATC  
ACCCCAATTAATTAATGGCTCCTTCCACTT  
65 >H\_1.0.0\_38087 Homo sapiens similar to RNA polymerase I transcription factor RRN3 (LOC94431), mRNA  
si: gi-22067165/// [Human\_jongleur\_201102.c1.56.single]. [SEQ ID NO: 153]  
CGCGTCGCGTTAGTTCGGCCCAATGGCGGCACGCTGCTTACACGTTGTTTGTGCGGGAG  
ATCGGGCGGCTTCGCTCTGAGTCAAGACGCTGGCGCGCTCGAGGACTGGGATTTCAA  
ATATGCGTGCAATAGAGAATGAATTTTCAATTTCTCCCCAAGAAAACTGTTTCGTTTG  
70 GTGGAACGTGCACAGAACTCTTGCTGAAGTACAAAAGGGTGAAACCAATGACTTTGAGT  
TGTTGAAGAACCAGCTGTTAGATCCAGACATAAAGGATGACCAGATCATCAACTGGCTGC

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TAGAATTCGGTTCTTCTGTCTACTTGACAAAAGACTTTGAGCAACTIATCAGTATTA  
TATTGAGATTGCCCTTGGTTGAATAGAAGTCAAACAGTAGTGGAAAGATATTGGCTTTTC  
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CCCATTTTGTGCCCTCCCTGAGTGATCATTAAAGGAAGGCGATGTAGATGTTTCAGATTCTG  
5 ATGATGAAGATGATAATCTTCTCTGCAAAATTTTGACACATATCACAGAGCCTTGCAAAATA  
TAGCAAGATATGTACCATCGGCACCGTGGTTTCTCATGCCAATACTGGTSGAAAAATTTTC  
CATTTTCTCGAAAAATCAGAGAGAACTGGAATGTTACGTTTCATAACTTACTAAGGATTA  
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10 AGCTGGATGTGAATGCATCCCGGCAGGGTATTGAAGATGCTGAAGAAAAGCAAAATCAAA  
CTTGTGGTGGGACAGATTCACCGAAGGATTGTTTAAATAGNNNNNNNNNNNNNNNNNNNN  
NN  
NN  
15 NNN  
NN  
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NN  
CAAGTAATCTGCCATCATCAGGCAGGCTGCTGGAATTTATTTGGAAGCTTTTGGCAA  
GAGCTAAATTTATTCTCTTATTACTGTAAACCATGCTAGATCTTTTGGTTAACTGGC  
20 TGCACATATACCTTAATAACCAAGGATTGCGGAACAAGGCATTCTGCGATGTTGCTCTCC  
ATGGACCATTTTACTCAGCCTGCCAAGCTGTGTTCTACACCTTTGTTTGTAGACACAAGC  
CTTTTGTAGCGGAAACCTGAAAGAGGTTTGAGTATCTCTCAGAGTCTGAATTTTGAGC  
GGATAGTGATGAGCCAGCTAAATCCCTGAAGATTGCTGCTCAGTGGTTAACTTTT  
TTGCTGCAATCACAAAGTAAGT

>H\_1.0.0.27490 Homo sapiens cDNA FLJ90378 fis, clone NT2RP2004847, weakly similar to ZINC FINGER  
PROTEIN 135 cr: gi-22760577// /cds=(5,976) /gb=AK074859 /gi=22760577 /ug=Hs.53996 /len=1987  
25 [Human\_jongleur\_201102.13667.C1] [SEQ ID NO: 154]  
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GATCCAGGAGCCATGGACCTGGTCTTGGTCCCTGATGACTGCCGGCCTGGCACACCCC  
CGAGTGACCTCATCGAGATCCAGGTGGTGAAGGTGACGGACACCAAGCTGGTCCCTGAGC  
CCCGGAGCCAGGTTCTTTCCACTGTGCTTGTGCCCTGCTGCTCCCGGCTGGTTCCG  
30 AGCTGCTGTTCCACGAACATGGCCACTTGGCTGGGGCCGAGGGAGGCGGGCAGGGTGGGG  
ACCGAGCCCGTGGCCAGTGTGCGGCCACAGCTGCCGGGCCCCCGCCAGCCTGCGCGCGC  
ACTACAGCTTGACACCGGGGAGCGGCCCTACCGCTGCGCGCTCTGCCCCCGCGCTTCA  
AGGCCTTGGCGCCCTGCTCCGCGACACAGCCAGCGGGTGGAGCCGGGCACCTCTC  
GGAGGCTCTCGGACACAGCGCGCTGACAGAACAGAGGCCCGGGGTGGCCCCGGAGAGGG  
35 CGGAGGTGGTGGTGGCGCGCGCGCGGGCGCGAGCGGTGGGAAGCCTTTGCTGCA  
GGTTCTGCGCAAGCCCTTCCGCGCTCCTCAGACATGCGAGAACACAGCGCGCTGCACA  
CTGGCGAGCGGCCATACCATTTGCGGCATCTGCGGCAAGGGCTTCAACAGTCTCTGGTGC  
TTAGCGGCCACGCCCCATCCACACTGGCGAGCGCCGTTCCGCTGCACGCTCTGCGACC  
GCACCTTCAACAACTCTCTCCAACTTCCGCAAGCACAGCGCACCCACTTCCACGGGCCGG  
40 GGCCGGGCTGGGAGACTCTGGAGGCCAGCTGGGCTCGTGGCGGCTGAGGGTCTGGGGA  
CGGGGTGTGGGTAGGGGACCTTGGGAGGAGGGGCGGGGGGAGCCCGCAAGGTGAAGG  
TGGAGGCCAGCAGTAGGCTGCAGACAGGGACATGGGTTAGTTAAGCGCGAGGTACGAG  
GCCGACCCGGGAGGGGGACGGGGTGGGGAACGGAGGCAGGGGACAGAGAGGGGAGAT  
45 TGGGGAGAGATGACAGCTGCGAGGGATGTTGTGAGCGCTAGTGTGGAGAGCAGAGGG  
AGAGGGCCAGGCTCCAGACTCCACACGCCACACAGCACCTCTGCCAGGCCCTAGGAGAG  
GACAGGTGCAGCTCTTGACGCTCTGCGGGTGTGCGGCCAAAGGCAAGGCCACGGGCTGG  
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50 CCACCATAGTCTTCTGCTCTGTTCTTCCACGGGTGGACAGGATGGTGTCTTGTGCTTAC  
CTCACTGCATTGCACTGGACCTGGGATGCCATCACCTCAAAGCCAGAGGGTCCCAAGTCA  
CGCTGAGAGCACTTGAGCCTCAAGGATGTAAGCCTGACCATAGGACCTTGACTCCAACA  
CGGCAACCCCCACCCCATTTGGTCCGTCCTTAACCCATCCACTCTTCTTGGAGGCA  
55 ACTGAGAACACATAAAGCAAGCAGCTACCTAGCATCCCTCTCTAAAGCTTTAGACTCAG  
AGCCAGGGTCCCCACAAAGCCTCAAGGTAGCCTCAGGTTTCTCTAATTTCTTCCACTCC  
CAGTTTCAAGCAACAGCTTACTGCTAGTCCCCGCCAATCCCAAGGGCGGGCTGGCTGA  
TGGCAGCATGGTGGCTGGCTGGGTGTGGAGTGAAAGAGTCACTGGTGGGGGCGAGA  
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60 GAAGGGCN

>M\_1.0.0.56987 BB667377 Mus musculus cDNA, 3' end as: gi-16398826// /clone=C730006J15 /clone\_end=3'  
/gb=BB667377 /gi=16398826 /ug=Mm.105955 /len=706 [gnl|UG|Mm#S2255490] [SEQ ID NO: 155]  
AGACAAGGTCTCATTACATAGTCCAGGCTGCATCTCCCTCAGCCCTCCAAAGCTGCAAT  
65 GTCAGGGGTGAGGCGAGGCACATCCAGTTTCAAGGCTTTCAGGCTTTTCTTCTGGTGGT  
TTTCTTATAAAACCTGAGCTAGAATGGGTTAATATATGTAAAGTGCTTAGAATCTGAC  
TGGCTAGGCTTAAACAGTATGTTCTTAGCTATTATAGTAATTTGGAAGATGCTGTATAT  
AAAACACTTCATCTTACTAGCAACTTACCTATCTTCTGCCATTGAAAGAACCTGTAAACAC  
CTGGCATTGCCTTACTAGCAACTTACCTATCTTCTGCCATTGAAAGAACCTGTAAACAC  
AAGCTGATTTACCACAAAATAAAATTTCCAATCAATGGGGTAATATTTCTTCAATTT  
70 GAAAACCTGGCTGGTGGTGGGAGAATACTTGCCTAGCATTCCTAGCTCTGATCTGTTT  
AGCAGACTCGGGGCGAGGAGTACAGTAACATACAGAGCATGTTCAAGGAAAAACAAAGC  
CTGAAAAATATATAGATAGGTTTACACTTAAGGCAGCTGAATCTCCAACCTGGGCAAT

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ACTAGAATAACCTGGGAATAGTCAAGAATATTGTCATCTGGATCCCATTTAATTTATGGA  
ATNCTTTATGGTCAAACTCTTTAAGATGGGCTCAGGCATAAACT  
>gi|388764|gb|L11702.1|HUMPHOSDP Human phospholipase D mRNA, complete cds [SEQ ID NO: 156]  
5 ATGCTCTGCTTTTCAAGTTTGGGCTGGCCTGCTGATCATGTTGGGTCTCTCTGCCATAGA  
GGTTCACCGTGTGGCCTTTCAACACACGTAGAAATAGGACACAGAGCTCTGGAGTTTCTT  
CAGCTTCACAATGGGCGTGTAACTACAGAGAGCTGTTACTAGAACACCAGGATGCGTAT  
CAGGCTGGAATCGTGTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAATTC  
10 CATGATGTGTCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATC  
CGAGAGAACTATCCCCTTCCCTGGGAGAAGGACACAGAGAACTGGTAGCTTTCTTGTTT  
GGAATTACTTTCACATGGCGGCAGATGTCAAGTGGCATAGTCTGGGCTTGAACAAGGA  
TTCTCTTAGGACCATGGGAGCTATTGATTTTACGGCTCCTATTGAGGCTCATTGCGCT  
GGTGATTTTGGAGGAGATGTGTTGAGCCAGTTTGAATTTAATTTAATTACCTTGACCGA  
CGCTGGTATGTGCCAGTCAAAGATCTACTGGGAATTTATGAGAACTGTATGGTGGAAAA  
15 GTCATCACGAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAATGTATGGT  
GAGATGTAGCTGTTTCCAAGTTATATCCCACTTACTCTCAAAGTCCCGTTTTTGGTG  
GAACAATTCGAAGAGTATTCTTGGAGGAGTGGATGATATGGCATTCTGGTCCACTAAT  
ATTTACCATCTAACAATCTTCACTGTTGAGAAATGGGACCACTGACTGCAACCTGCTGAG  
AACCTCTGTTTCACTGATGTGGCGGCCAGCAAAACACACCCAGGGCTCAAAATGCGAG  
AAAAATGATTTTACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAATATA  
20 AACTATACTGAAAGAGGAGTGTCTTTAGTGTAATTCCTGGACCCCGGATTCATGTCC  
TTTATCTACAAAGGCTTTGGAAAGGAACATAAGGACAATGTTATAGGTGGCTCTCAGTTG  
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CTTGGCTGGGCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTG  
GGCGCACAGGCTACAGCCGCCCGGCCACATCCATCGGGCGCGTGTACCTCATCTAC  
25 GGCAATGACCTGGGCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCACAGGATC  
CTTGAAGGCTTCCAGCCCTCAGGTCGGTTGGCTCGGCTTGGCTGTGTTGGACTTTAAC  
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TACAAAGGTGCCGTGTATGTCTACTTTGGTTCCAAACAAGGAGGAATGCTCTTCTCCCT  
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30 GATGTGAATGGAGACAGTGAACCCGATCTGGTCTATCGGCTCCCTTTTGCACCAAGTGGGA  
GGGAAGCAGAAAGGAATTTGGCTGCGTTTATTTGGCCCCAGCCTGAGCGACAAAGAA  
AAACTGAACGTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCTGGTTT  
GGATATTTCCCTTACCGGTGTCACTGTGGACAACAGAACCTTGCTGTTGGTTGGGAGCCCG  
35 AACTGGAAGAAATGCCAGTGGGCTGGGCCATTTGTTACATCCGAGATGAGAAAAGAGC  
CTTGGGAGGGTGTATGGCTACTTCCCACCAACCGCCAAAGCTGGTTTACCATTCTTGGGA  
GACAAGGCAATGGGAACTGGGTACTTCCCTTTCCAGTGGCCACGTAATGATGAATGGG  
ACTCTGAAACAAGTGTCTGCTGGTTGGAGCCCTACGTAAGATGACGTGCTAAGGTGGCA  
TTCTTGACCGTGACCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATCTGAC  
40 GCGCAGCTCTGCTGCTCAGCACCTTACGCGGAGACCGCGCTTCTCCCGATTTGGTGGC  
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CTGAGGATAGCAGATTAACCTCTGGACTGATTTGGGGAGAAAGACGGCCGAGTATATGTA  
TATAATGGCAAAGAGACACACCTTGGTGACATGACTGGCAATGCAAACTCATGGATAACT  
CCATGTCCAGAAGAAAGGCCCAATATGATTGATTTCTCTGAAAGCCAGCTCAAGGTTT  
45 GGGAGCTCCCTCATCACGTTGAGTCCAAGGCAAGAACCAAGTCGTCATTGCTGCTGGA  
AGGAGTTCTTTGGGAGCCGACTCTCCGGGCACTTCACTGCTATAGCCTTGGCTCAGAT  
TGAAGATTTCACTGCATTTCCCCACTCTGCCACCTCTCTCATGCTGAATCACATCCATG  
GTGAGCATTTTGTAGGACAAAGTGGCACATCCAGTGGAGCGGTGGTAGATCTGTATAGAC  
ATGGGGCTCTGGGAGTAGAGAGACACACTAACAGCCACACCTCTGGAATCTGTATACA  
50 GTAAATATATGACTGCACCAAGAAATATGTAAATAGCAGACATTTGCTTACTCATGTCT  
CTTCCACAGTTTACTTCTCTGCTCCCTTTGATCTAAACCTTTCTTCTTTCCCACTTA  
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TGGCTGGAAGGTCCTCTGCTGTTATCTGTTAGAACAGTCTGTACACAATTTCTCTCT  
55 AAAAAACATCTTTTAAAAAAGAAATGTTTCAAGCATAAAGAAAGAACAAAGATCATGCC  
CTTTGACGGGACATGGATGGAGCTGGAGGCCATTATCTTCATAAACTATTGACAGGAACA  
GAAACCAAACTCCATATTCTCACTGTAAAGTGGGAGCTAAGTGAGAACACGTGGACA  
CATAGAGGGAACACACACACTGGGGCTATGAGAGGGCGGAAGGTGGGAGGAGGAGA  
GATCAGGAAAAATACTAATGGATACTTAGGGTGATGAAATAATCTGTGTAAACAAACCC  
CATGACACACCTTTATGTATGTAACAAACAGCACTTCTGCGCATGTACCCCTGAACCTT  
60 AAAAGTTAAAAAAGTGAACCTAAAAATAACAGATTGGCCCATGCCAATCAAAGTATA  
ATAGAAAGCATAGTATAC  
>M\_1.0.0\_19077 v70h06.x1 Mus musculus cDNA, 3' end cr: gi=4613514/// /clone=IMAGE:1227803  
/clone\_end=3' /gb=AI604347 /gi=4613514 /ug=Mm.32372 /len=421 [Mouse\_jcngleur\_201102.12391.C1] [SEQ  
ID NO: 157]  
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65 CACAATACATGAGGACAGAAAGCATCTTGAGTAGGCAAGAGCCCAAGATGCGGCAAGC  
AGTTCTCAGTGTACTGGCAACAGAGACAATTCCTTTCTCTGTGCAGGAGGTCTTAC  
TGGGACCACTAGGAGGCTGGAACCTTTTGTAGATTCTCCGAAGCATAAGCAAGTGGTCT  
TGGCAGTGTGAGTGAAACAAGATTCTAGCTATGTTGTAATGAGCTGTGCATGGAGCTTCT  
CTGGTTCTCTCTGGCTTTTGAATCTTGTGTGACAGAAATTTGGTGTGAGCTGGAGCTGGCTC  
70 AGCGGTGACAGGCTTGTGGCTGAGGCTGTGGGGCTGAGCCTCACGGGTGATGGGGC  
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GTGTCGAGTCAGCGCAGTCAGGCTGACTGGAAGTTGGCTTTTGTCTATCACACTTATCGT  
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AGGTCGGGCGGCGTAGTATGGAATAGCAGGAGCGTAGCAGGCTGGGCGGTAAGTGATGG  
5 ATGTCACATATGGCTGCCTGAAGGTGATGGGTCAGAACAGATGGGGCGCAAAATGGGGC  
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GGGCAGACAGGTTGGCAGATGCTGGAGACACAGCATGAGGAGTCTTGGCAGCTGCTAGAG  
ACACATGGTGGCTCACAGGGGCCCAGAGCCATACAGGCAGATGGCTGACAAGCACTGGCC  
TCTGAGCAAGGTGGCTCGCAGGGAAGTGGTTTACAGCCGACTGGCTGGCAGCTACTGGCA  
10 CAGGCTCACAGATCATTGGTTGGCAGGAAGCAGGCACAGCGCAGACAGCTGAGCAGCAGC  
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CAGGCAAGCAGAGGACAGGCTGGCAGGATGAGGTCTCACAAACACAGGGCTGGCAGCTGC  
TCACAGAACAAGAAGGCTGGCACAT  
>H\_1.0.0\_30299 602849886F1 Homo sapiens cDNA 5' end cr: gi-14504763/// /clone=IMAGE:4991396  
/clone\_end=5' /gb=BI086433 /gi=14504763 /ug=Hs.169061 /len=855.Weakly similar to kinase suppressor  
15 of ras [Mus musculus] [M.musculus] [Human\_jongleur 201102.16424:C1] [SEQ ID NO: 158]  
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TGTAACTGCAGAAAGTTTCAGATGGCAAGGGAGCCCTTAAGTGAGATTAGGTTGC  
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GTCAGTCTGGGTTTGTCTTTCTCGTGAGCATCACAGTTAAAGAACGCTCATTGAGGAA  
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CCTGCTCTTAAGGAACTGATGACCTGGTGGGGCCCTGTTGCTTCAAGGAACCCAGAAGC  
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45 TGAAGCCCTGCTGCTTTAAACCACAGAGCCGAGCCCTTGGGTTTCTGTCTAACTCGA  
AGTCTTGAATCCTAGCTAGTATGGGGTTGTGAGCAGTGTGTAGCAAAGTTGATCTCTCCA  
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50 CATCAGCGTGCAAACTAGCATCTTCTGTGGCCACAAGCCACACACTTGTCTTTTGTGAA  
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TGAATAAAGTTATACCAAGGTG  
55 >M\_1.0.0\_47487 ub51g06.r1 Mus musculus cDNA, 5' end as: gi-2861340/// /clone=IMAGE:1382266  
/clone\_end=5' /gb=AA798385 /gi=2861340 /ug=Mm.25607 /len=473 [gsl|UG|Mm#S323719] [SEQ ID NO: 159]  
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60 CTCAGGCAATCAGTTCTCTGCTAGATATGTGCCACAGGCTTGAATAAGCCCATGTATG  
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TCTTCATGTGGGGTAGCTCCTTTCATCCCTTCACTTCTGATCTTTCTCTCTAACTCT  
TCAATAGGGGCTCTTGACCTTAGTCCAAATTATCTGTAATGTAATTTNNNNNNNNNNNNNN  
NN  
65 >gi|15689855|gb|B1714150.1|B1714160 ie33g03.x1 Kaestner ngn3 wt.Mus musculus cDNA 3', mRNA sequence  
[SEQ ID NO: 160]  
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AACACAAAGTTCCGCCCTGTGGCCTGTACCAGCCACACTCATCCAGCGGAAAGAACG  
70 TTATCAAGGCATGAAGCAACATCAAGAAGCATAGTAACGCACCTTGTATCTTAAACAAA  
ACTGTGGGGCAAGTATAGTCTGAGCATGTCTTTAACCAGTGTCTGTGAAACTACGAAG



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TCAAGATAACTAATGTCCAGGAAGGAGAAAGTGACAATTCCTTAAAGAAAGCACTCCCGTT  
AGGATCGCCTGGAGCTGTTCTTCATTCCCTGCTGTGGTGCTAGTGATGCTATACTGTCA  
ATATAAGCTTAGGAATTTATGGCACCAGAACTTGCTTCCTCTCACTTGGCTCGGGGGCTT  
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>H\_1.0.0\_2912 Homo sapiens interleukin 13 (IL13), mRNA cr: gi-4504644///  
[Human\_jongleur\_201102.525.C1] [SEQ ID NO: 161]

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ACCAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTGGCA  
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TGGTGGGACAGGGACCCACTTCACACACAGGCAACTGAGGCAGACAGCAGCTCAGGCACA  
CTTCTTCTTGGTCTTATTATTATTGTGTGTTATTAAATGAGTGTGTTGTACCCGTTG  
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>M\_1.0.0\_7164 Mus musculus killer cell lectin-like receptor subfamily A, member 21 (Klra21), mRNA  
cr: gi-21361215/// [Mouse\_jongleur\_201102.3652.C9] [SEQ ID NO: 162]

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CCACCACCATAACTGCAGCAACATGCAAAGGGATTTCACTTAAAGGAAGAAATGTTGAC  
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ATTCCCTGATTAACTTTCCAACCAAGAGTTAAAGAACATAGTCTGCTGTGAAGAGAAACAA  
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TATCCTGTGGAGAGAGGACGCATCTACTCGGGTGAATGTGCACGCTTTCGCCATAAGCC  
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CTAAATAAC

>H\_1.0.0\_14332 Homo sapiens step II splicing factor SLU7 (SLU7), mRNA cr: gi-20127500///  
[Human\_jongleur\_201102.5919.C1] [SEQ ID NO: 163]

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GAAGAAGGAAAGACATCAACCCCATATTCTCTCAGTATATTCTCTCAGTGCCATGGTAT  
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GCCTATGACAAGGGATCTGAAGTGCACTACAGGCAGATCCTACAAAGCTAGAGCTGTTG  
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>H\_1.0.0\_9637 Homo sapiens nuclear phosphoprotein similar to *S. cerevisiae* PWP1 (PWP1), mRNA cr: gi-  
5902033/// [Human\_jongleur\_201102.3438.C1] [SEQ ID NO: 164]  
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>M\_1.0.0\_48190 BB032870 Mus musculus cDNA, 3' end as: gi-15403607/// /clone=5830473M12 /clone\_end=3'  
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[Human\_jongleur\_201102.12659.C1] [SEQ ID NO: 166]  
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65 GCTTGTTCCTCAGACTGTAAATAATACAAACCCCTAGAAATGGTGCCTTAATTCTCAGGT  
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70 GTAAAGCAATCAACCAATGAGTATCTTATAAAGGCAAACTTTATGGCTAATAGGAAG  
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CCTGTAA  
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35 ID NO: 188]  
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25 GCGGGGAACCCGCGTTAAGCCTCTCTAACAAGCCCTGGAGCAGGAACGAGGGAGCGTG  
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TGCGACGGCAACCGCGGTACGGTACCTGGTGGGACCTATGTGTGCACTCGTTAATTTGGGA  
TGACGAACGATCCGTGCTGTGGCGGGTTGACATATCGTGTAGTGACACACACTGCGGCC  
30 GCGAGGGGACGCGCGCGGAGATTCCCGCACTGGGCACGGGCCACTGAGCGCGTGGGCGA  
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AGCTGCGCGACGCGCAAGAGGCGATCAGCGCAGAGCTCACACCGTCNCAACACGACGCGA  
35 CGATAAAGACGACTACGTCAGTGGACACCCCTTAGACACNTCTAGATGGACTCGACAGC  
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40 >gi|15335166|gb|BI495822.1|BI495822 df121a08.w1 Morton Fetal Cochlea Homo sapiens cDNA clone  
IMAGE:2540054 3', mRNA sequence [SEQ ID NO: 191]  
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45 TGAAATGGTGAAATTTTCTTACAAATTTTACATCAAGGTAGTAGCCAACTCATTGA  
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CATCCTTAGAAAGGAGGAGGAGAAACACAAGACCTGTAAACATCAGTTGCTTTGGGAACA  
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50 TAGAAAAATTTAAACATACCTCTTGGTATCAATACAGTTTAAATATTTTGTAGTATTC  
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>gi|2201613|gb|AA473386.1|AA473386 vd64f01.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
clone IMAGE:805369 5', mRNA sequence [SEQ ID NO: 192]  
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60 >H\_1.0.0\_35549 Homo sapiens mRNA for YEA4 protein (YEA4 gene) cr: gi-20387030///  
[Human\_jongleur\_201102.22053.C1] [SEQ ID NO: 193]  
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65 CGCTGGGCGTGGTGTTCGACGGCTGCTGCACTAACGTGATCTTCTTAGAGCTCTGGCCC  
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70 TGGTGTCTGTGGGGATATTTATTGCACTTTATGTGAGCAAAGCAGGTGACTTCCAGT  
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CATTGACTTTTGCTCTTCTGATGT CAGCAAGGATGGGGATATTCCAAGAGACTCTCTACA  
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5 ACATCATCACTCAGTACGTGTGCATCCGGGGTGTGTTTATCCTCACCACGGAATGCGCCT  
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10 GGGACCTGTGAAGGTCTGACCACCGTTTCGCTTTTGTTAATGCCGAGCTACCCGCACTG  
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15 TGTCCTTCTCTGTCTTCTAATGCATCTCTGTACAGCAGTCATTGTCTCCTGTGAC  
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GGGCTGGAATTCCTCCAGCGTTTGGGAAGGAAAGAGATGTTCCCTGAGCTGATTCECA  
GTGACAGTGACAGCAAGACTAGTGGGACTCCTCTTTC

20 >H.1.0.0\_9281 Homo sapiens DKFZP566H073 protein (DKFZP566H073), mRNA cr: gi-14149701///  
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50 CTAATAAAATGTTTCTTTGTGGCCTN

>H.1.0.0\_13591 Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)  
(HNRPU), transcript variant 1, mRNA cr: gi-14141162/// [Human\_jongleur\_201102.5470 C3] [SEQ ID NO:  
195]

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60 AGTGTCTCCGTACAGCGAGGGGCGGGCGCTATATTACGTGCGGGCGCGGCTCTGTC  
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65 AGTTCTCGCTGTTAATGTAAAAAGCTGAAGGTGTGCGAGCTGAAGAGGAGCTCAAG  
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70 GACCAAGATGGAGTAGAGAGGAGAACGGGGCGCGGGGGCGGCGGCTCGGGCCGATG  
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>H\_1.0.0\_10796 Homo sapiens growth factor, augments of liver regeneration (ERV1 homolog, S.  
40 cerevisiae) (GFER), mRNA cr: gi-4885264/// [Human\_jongleur 201102.4053.C3] [SEQ ID NO: 196]  
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70 AGCCAGAGAACTCATGGGTGAGGATGGAGTCCAGGAGAGCTGTGGGAGCCGCCGTGTG  
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5 GCTTCTGTAGAGGCTGCCAGAGGGGCCAGGTGGCACAAATAAGAGAGGGGAGATGGGGG  
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10 >H\_1.0.0\_579 Homo sapiens hypothetical protein MGC26914 (MGC26914), mRNA cr: gi-21699059///  
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45 >H\_1.0.0\_22812 Homo sapiens hypothetical protein MGC18216 (MGC18216), mRNA cr: gi-22748948///  
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35 >M\_1.0.0\_18917 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library,  
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AAGTATAATATAAGCCACATGTATAAATAAAATTTCTACTAGCTACC  
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 65 >H\_1.0.0\_58925 Homo sapiens cDNA FLJ34661 fis, clone KIDNE2018989, weakly similar to Homo sapiens  
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70 GTTTCATTTGAACTGCATAAAGAAATGGGCAAGGCTTCCAGCATCTCAAGCAGATGGCCA  
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5 >H\_1.0.0\_24040 Human cathepsin L gene, complete cds cr: gi-809235///  
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[Mouse\_jongleur\_201102.3553.C2] [SEQ ID NO: 216]  
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65 ATGGTGACCTGACTCCTGTGGAGAGTCYGCNGTTACTGCNNTNTGGGGCAAGGTGAAC  
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70 CCTGAGAACTTCAGCTCCTGGGCACAGTGTCTGGTGTGTGTGGCCCCATCACTTTGGC  
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GCCTTGGCCCCACAAGTATCACTAAGCTCGCITTCTTGTGTCCAAATTTCTATTAAAGGTT  
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GGATTCTGC

5 >M\_1.0.0\_62347 Moderately similar to F261 MOUSE 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase  
1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-  
biphosphatase ] [M.musculus] as: gi-15714162/// 603360763F1 Mus musculus cDNA, 5' end  
/clone=IMAGE:5368118 /clone\_end=5' /gb=BI737149 /gi=15714162 /ug=Mm.132391 /len=896.  
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25 >H\_1.0.0\_25516 Homo sapiens septin 3 (SEPT3), transcript variant A, mRNA cr: gi-22035571///  
[Human\_jongleur\_201102.12125.C2] [SEQ ID NO: 221]  
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65 >H\_1.0.0\_33714 Homo sapiens mRNA; cDNA DKFZp761J0720 (from clone DKFZp761J0720) /gb=AL833252  
/gi=21733885 /ug=Hs.349845 /len=3602. Highly similar to KPC1 HUMAN Protein kinase C, beta-1 type  
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>H\_1.0.0\_125034 Moderately similar to CLUS\_HUMAN Clusterin precursor (Complement-associated protein  
SP-40,40) (Complement cytolysis inhibitor) (CLI) (NA1 and NA2) (Apolipoprotein J) (Apo-J) (TRPM-2)  
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TGTCTTTTAATGGTATGTTTTAAACAGCTGACATTTTAAATTTTGATGAAATCCAGTTTA  
TTCGTTTGTCTTTTATGCTTTGGGTGTTGCATCCGAGAAATCTTTCCCATCCCAAGAT  
CACAAATTTTTTTTCCCTTTTACTTCTAGAGTGTATAATTTTAAAGCTTTATACTTTGGT  
CTATGACCCGTTTTTTTTTTTGTGTTTTGTTTTTTCGTTGTTTCTTTGTTTTTCAGA  
TGGAGCCTGGGTGATAGAGTGAGACACTGTCTTGCCNNNNNNNNNNNNNNNNNNNNNNNN  
N

>H\_1.0.0\_4048 Homo sapiens zuotin related factor 1 (ZRF1), mRNA cr: gi-22049761///  
[Human\_jongleur\_201102.987.C3] [SEQ ID NO: 230]

GTGAGACTGGCCTCCACACCAGAAAGATCCATCCCGAAGTGCTTACTGGTCTCTCCA  
TGCGCCGGTTCCTGGGGCTCTTAGAGCCAAGGCGCGAGGCTCGGAGTGAGAGGTAGAGCT  
GGAGGGGACCCTAAGCGCCCTCCGCCCGGGACGTGAGCCGCTGCGCCACCGGGCTAGAC  
CCGGCGCCATCATGTGCTTCTGCCAAGCGCGCGGACGGCCGGGCGCCATCACCC  
ACGCTCTGACCTCTGCCCTCTACACTCTGTCAAGTTGAACCTGTGGGAAGATGTTTGAAG  
CTTTTGTAAAGAGGAGAAACAGAAATGCTTCTGCCCTTTTCAGGAAGTGGAGGATAAGA  
AAGAGTTATCCGAGGAATCAGAAGATGAAGAATTGCAGTTGGAAGAGTTTCCATGCTGA  
AAACACTTGATCCCAAAGACTGGAAGAACCAGATCATTATGCAGTTCTTGGACTTGGCC  
ATGTGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAGCAATGGTTTTAA  
AACATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAGGAGATAATGACT  
ACTTCACTTGATTAACCTAAAGCTTATGAAATGTTATCTGATCCAGTGAAGAAGACGAGCAT  
TTAACAGTGTAGATCCTACTTTTGATAACTCAGTTCCCTTCTAAAGTGAAGCAAAGGATA  
ATTTCTTCGAAGTGTTTACCCAGTGTGTTGAAGGAATTCAGATGGTCAATATAAAAAA  
ATGTTCTCTAACTTGGTGATATGAATTCATCATTGAAGATGTAGATATATTTTATTCTT  
TCTGTATATAATTTTGAATTTCTTGGAGAGATTTCTTATTATAGATGAAGAAGAAAAAGAA  
AAGCAGAAATGTCGTATGAGAGGAGATGGATTGAAAAGCAGAACAGAGCAACAGAGCAC  
AAAGAAAAAAGAAGAAATGAACAGAATAAGAACATTAGTTGACAAATGCATACAGCTGTG  
ATCCAAGGATAAAAAAGTTCAAGGAAGAAGAAAAAGCCAAAGAAGAAAGCAGAAAGAAAG  
CAAAAGCAGAAGCTAAACGGAAGGAGCAAGAAGCTAAAGAAAAACAAGACAAGCTGAAT  
TACAAGCTGCTCGGTTAGCTAAGGAGAAAGAGAGGAGGAAGTCAGACAGCAAGCATTGC  
TGGCAAGAAGGAAAAAGATATCCAGAAAAAGCCATTAAAGAAGGAAGGCAAAAAACTTC  
GAAACTCATGCAAGACCTGGAATCATTCTTCTGATAATGAGGCAGAGCGGGTTAAATGA  
TGGAGAAGGTGGAAGAACTTTGTGATCGGCTTGAACCTGGAAGCTTACAGTCTTGAATG  
AAACATCATCATCTGCAACAAAGAGTGAAGAAAGGCTGCTTTGGAAGAAACAGATAGAAG  
AAATAAATGAGCAAAATCAGAAAGAGAAAGAGGAAGCTGAGGCTCGTATGCGACAAGCAT  
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AIGATCTACAATTACTAATTAAGAGCTGTGAATCTGTTCCCTGCTGGAACAAATTCAGAT  
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AAGATGTTATTGGCAAGCAAGAGTCTCCAAAACCTTGACCTTCATCAAAAGATGACA  
TAAATAAAAGGCATTGATAAGTTCAAAAAGAACATGGAGTGGTACCTCAAGCAGACA  
ACGCAACGCGCTTCAGAACGATTGAAAGGTCATATACAGACTTCAACCTTGGACAACAG  
AAGAACAGAAGCTTTGGAACAAGCTTTGAAAACATACCCAGTAAATACACCTGAAAGAT  
GGGAAAAATAGCAGAAGCGGTGCCCTGGCAGGACAAAGAAGGACTGCATGAACAGTACA  
AGGAACTTGTGAGATGGTAAAGCAAGAAAGCTGCTCAAGAACAAGTGTGAATGCAAG  
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CTGTAACATTTTCAATCTTAAATATATACTCATGGTAATAATTGAAAGT

>H\_1.0.0\_61535 Homo sapiens cDNA FLJ36226 fis, clone THYMU2001018, moderately similar to MOB1  
PROTEIN si: gi-21752445/// [Human\_jongleur\_201102.cl.22024.single] [SEQ ID NO: 231]

ACTTCGCCCCCTCCGCTGCCATTGGAAGTCTGAGCCGAAGTGTGCGCCACCCGA  
GCAGCCGGCTCTCGGCACCTCTCTCCGCTCCCTGTCTCTGTTCCATTGCTCTTTCC  
TCTTCTTTCTGGCCCAACGCGCTCCGAGGCTCGCGACCGCGAGCTGCAGCTGCCCC  
CGCGGCAACATGAGCTTCTGTTTGGTAGTCTCTTCTAAAACCTTTTAAACCAAGAA  
GAACATTCAGAGGGTTCTCACCAGTATGAGCTCTTAAACACGCAAGCCACATTGG  
CAGTGGCAACCTTCGGAAGGCTGTGATGCTTCTGGAAGGGGAAGATCTCAATGAATGGGT  
TGCAAGTTAAGCTGTGATTTCTTCAATCAGATCAACATGCTTTATGGAACATACAGAG  
CTTCTGTACAGAAGAGAGTTGTCAGTGTGTCAGCTGGCCCAAAATATGAGTATCATTG  
GCGAGATGGAACGAACATAAGAAACCTATTAAGTGTCTGCACCAAGATATATTGATTA  
CTTGATGACTTGGGTTCAGGACAGTTGGATGATGAGACGTTATTTCCATCAAAATTTGG  
TATAATTAATTTTGAAGGGGGATCCATCATGATTTATCTTTTATATGTTTATAGAATT  
TTCCTCCCTCTTCCCATATATCTAGTCGAGAGTTCTTTATGGCTGTGTTGATATATGT  
ATATGTTACGCAAGTTCCTCAAGAGAGGCACAAAAGTTTGTAAACCCAGTGGTAAAATAAG  
CAAGTGATCCTGTGTGAATTGAGCTTTCCCTTTAACTTAGTGCTTTTAAATGCTTAAT

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TAGCTGAAAGTATAGGTTTATTAGAAAAATAAATGATCTCCCTCTCTTAAGGTAATTATTT  
TTGATGATATCTAGATTAAGTATCACTGAGTTTATTTTCAGACAATGATAGCATTTTT  
TAACACTTTAAAAAATATGATCATCATTGAGAATAAACTTACTTCCCTGAAGTAAGGG  
AAAGGCTTAAGAAGCCCTTT CAGTAGAAGTTCTAGATGGAGGGTTATTCCTATCTAGG  
AACCATGGTAAATACCATACATAACATATATTTTAACTTTATGCACTTACAGGTGTTT  
TATGTTTTTCATACCAAATTTATCATGAACATTAAGGTAAACCTCTATTTTATTTTATTT  
TATTTTAACTCTAAATTTTTCATTTTGGGAGACAAGAGTATCTCTGTATTGCCAGGCT  
GGAGTGCAGTGGCGTGATCTTGGCTCACTGCAGCCTCCACCTCCCGGTTCAAGTGATTC  
TCTTGCTCAGCATCTTAAGTAACCTGGGACTACAGACGCGTGCCACCACGCCAGCTAAT  
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CTGACCTCAAGTGATCTACCCACCTCGGCTCCCAAAGTACTGGGAACCTCTCTATAAT  
TTTAAATGATGAGATCAGTATATCTAGGATAGTAACAAAATCTGGCCCAAAAAACAGAAT  
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TTTATGACCCCAATATGAATCTTACAGATTAGATATTAAAGCTTTGTGAGAAGAAAAACA  
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AGGGCAGACTTATCAAGTAGAAATGTTTACGTTTAGATAGTCAATGTTTTCCTTCTCA  
AACTTCTGACAACCTGATTTGCTCAAAAAGCTAAGAACTCTGCTCTGTAATGTTAGAACTT  
TTTGACATTTACGATTTTTTTTGAATAAATATGACACAAATATAAATAGTTGTTGT  
TATGGAGTACTTTAAACATATTTTATGAAATGCAATTAACCACTTGGAACTTTTTTAATAAA  
AGAGCAATTTTCAAG

>H\_1.0.0\_113724 Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]  
as: gi-20265192/// UI-E-EJ1-aka-c-14-0-UI.r1 Homo sapiens cDNA 5' end /clone=UI-E-EJ1-aka-c-14-0-UI  
/clone\_end=5' /gb=BQ189641 /gi=20365192 /ug=Hs.373409 /len=566. [gnl|UG|Hs#S4404983] [SEQ ID NO:  
232]

AAGATGATGTTACTCCAAATATGCAGATGACCTCATCAGGGCAGCCATCCAACATGGACAC  
GTGCACAATGGCCACTCAAGAGCTCCTAGGACCTCTCCAATGCTGAGATACTTGATGGA  
TGTGCACCAAGAAGGCCCACTCTGCAACCGGAATGCCACATACTTGGGATTCATGAAG  
GGAGGAAGTCTCAGTTTATGTCATGTGAACAGGAAATCTTGGGTGGCGAGATGGCTCAA  
CGGCTAAGAACACTTATTGCTCTCTGAAGGCCCTGAGTTCAAATCCCAGCAATCAGATG  
GTGGCTCACAAACCTTATAATGAGATCTGATGCCCTCTCTCGGTGTCTGAACTCAGC  
TACAGGGTACTTATGTTTAAATAAATAAAATCTTTGAGCCAGAGTGAGCAAGTTTGACC  
AAAGCGAGCGGGCGGAGTGGAGCTAGTAAAGGTCTTAAATTTCAATTCCGAACAACCA  
CATGAAGGCCCAACCATCTGTACAGCTACAGTGTACTCACATAAAATAAGAAATCTT  
TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

>H\_1.0.0\_5968 Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,  
pigment epithelium derived factor), member 1 (SERPINF1), mRNA cr: gi-4505708///  
[Human\_jongleur\_201102.1833.C1] [SEQ ID NO: 233]

GGAGCCCCCTCAGTGTGCGAGGCTTAGAGGGACTAGGCTGGGTGTGAGCTGCAGCGTATC  
CACAGGCCCCAGGATGCGAGGCCCTGGTGCTACTCTCTGCAATTGGAGCCCTCCTCGGGCA  
CAGCAGCTGCGCAGAACCTGCGAGCCCCCGGAGGAGGGCTCCCCAGACCCCGACAGCAC  
AGGGCGCTGCTGGTGGAGGAGGAGATCCTTCTTCAAAGTCCCCGTGAACAAGCTGGCAGC  
GGCTGTCTCCAACCTCGGCTATGACCTGTACCGGGTTCGATCCAGCATGAGCCCCACGAC  
CAACGTGCTCCTGTCTCTCTCAGTGTGCGCCAGGCCCTCTCGGCCCTCTCGCTGGGAGC  
GGAGCAGCGAACAAGATCCATCATTCACCGGCTCTCTACTATGACTTGATCAGCAGCCC  
AGACATCCATGGTACCTATAAGGAGCTCCTTGACACGGTCACTGCCCCCAGAAGAACCT  
CAAGAGTGCTTCCCGGATCGTCTTTGAGAAGAGCTGCGCATAAATCCAGCTTTGTGGC  
ACCTCTGGAAAAGTCATATGGGACCAGGCCCAGAGTCTTGACGGGCAACCTCTGCTTGG  
CCTGCAAGAGATCAACAACCTGGGTGCAAGGCGAGATGAAAGGGAAGCTCGCCAGGTCCAC  
AAAGGAAATTTCCGATGAGATCAGCATTCTCTTCTCGGTGTGGCGCACTTCAAGGGGCA  
GTGGGTAAACAAGTTTGACTCCAGAAAGACTTCCCTCGAGGATTTCTACTTGGATGAAGA  
GAGGACCGTGAGGTCTCCCATGATGTGCGACCTAAGGCTGTTTACGCTATGGCTTGG  
TTGAGATCTCAGTGCAGATTGCGCAGCTGCCCTTGACCGGAAGCATGACTATCATCTT  
CTTCCTGCCCCGTGAAAGTGACCCAGAATTTGACCTTGATAGAGGAGAGCTCACCTCCGA  
GTTTATTATGACATAGACCGAGAACTGAAGACCGTGCAGGCGGTCTCTCACTGTCCCCAA  
GCTGAAGCTGAGTTACGAAGGCGAAGTCAACAAGTCCCTGCGAGGAGATGAAGCTGCAATC  
CTTGTTTGAATTCACAGACTTTAGCAAGATCACAGGCAAAACCCATCAAGCTGACTCAGGT  
GGAACACCGGGCTGGCTTTGAGTGGAACGAGGATGGGGCGGGAACCAACCCAGCCAGG  
GCTGCGCCTGCCACCTCACCTTCCCCGCTGGACTATCACCTTAACAGCCTTTCATCTT  
CGTACTGAGGGACACAGACAGGGGCCCTTCTCTTATTGGCAAGATTCTGGACCCAG  
GGGCCCTAATATCCAGTTTAAATATTTCAATACCTTAGAAGAAACCCGAGGGACAGCA  
GATTTCCACAGGACACGAAGGCTGCCCTGTAAAGTTTCAATGCATACAATAAAGAGCTT  
TATCCCT

>H\_1.0.0\_21590 Homo sapiens, similar to sphingosine kinase, clone MGC:40267 IMAGE:5213270, mRNA,  
complete cds cr: gi-22539642/// [Human\_jongleur\_201102.9905.C4] [SEQ ID NO: 234]

GAAAGATTGAGGCGGAGGAGCGAGGCCGGGGAGTCCGCTCCAGCGGGCGCTCCAGT  
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CGGCGGTGGGCTCTCCCGAGCAACCGGACCGACTGGGTAGGGCCGCCACCTGCTTCT  
GCGCGCTCGTGCTCTGTGCGGCCGCCCTCGCGGGGCCCGGGAACCTGGCCACTTG  
TCGCTTGGGCGAGAGCGGCGGAGCTGTTGGCCGCTTGGGCTTGGCGCGAC  
CCGGGAGCGGCTCCACAGCGCCGCGCGCTCGCAACGGAGCGGGGCCCTGAGAGCGC

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GCGCGCGGCTCCACCGCTCTGGAGCTCCGGGCAGGGGACACGGCAACCTGGATGGCTG  
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 TTACGCAGCTGGACTCCCTCCCTGGCAGCCCGAGGGGTCCAGCCCGCAGGGAAT  
 5 GACGCCGTGTCTCTACAGCCACGGCTCCGGGCGGGGAAGCGAGCCCCACAGCCGGCC  
 TGCAGACGCCCGCTGGGCAGCACCGATAAGGAGCTGAAGGCAGGAGCCGCCACGGGC  
 AGCGCCCCACAGCGCCAGGGACCCCTGGCAGCGGAGCCGCGGGTCGAGGTTATGGAT  
 CCAGCGGGCGGGCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGTGGTGTCTGAAC  
 CCGCGCGGCGGCAAGGGCAAGGCCCTTGACGCTCTTCCGAGTACGTCGAGCCCTTTTG  
 10 GCTGAGGCTGAAATCTCCTTACGCTGATGCTCACTGAGCGCGGAACACGCGCGGAG  
 CTGGTGCAGCTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCTATGCTGGAGACGGG  
 CTGATGCACGAGTGGTGAAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCCATCCAG  
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 15 TGCGCGGGCTGTCTGACCCATGAACCTGTCTCTGCACACGGCTTCGGGGCTGCGC  
 CTCTTCTCTGTGCTCAGCTGGCCTGGGGCTTATTGCTGATGTGGACCTAGAGAGTGAG  
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 CTGCGCACCTACCGCGCGGACTGGCTACCTCCCTGTAGGAAGAGTGGGTTCAAGACA  
 CCTGCCTCCCCCTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCACTGGAG  
 20 GAGCCAGTGCCCTCTCACTGGACAGTGGTGCCTGACGAGGACTTGTGCTAGTCTTGGCA  
 CTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGTGCAACCATGGGCGCTGTGCACT  
 GGGCTCATGCTCTGTCTTCTACGTGCGGGCGGAGTGTCTCGTGCCATGCTGTGCGCTC  
 TTCTTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCTACTTGTATATGTG  
 CCCGTGGTGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTGCACTGGATGGG  
 25 GAATTGATGGTTAGCGAGGCCCTGTCAGGGCCAGGTGCACCCAACTACTTCTGGATGGTC  
 AGCGGTTGCGTGGAGCCCCCGCCAGCTGGAAGCCCGCAGCAGATGCCACCGCCAGAAG  
 CCTTATGACCCCTGGGCGCGCTGTGCCCTAGTGTCTACTTGCAGGACCTTCTCTCTT  
 CCTAGGGCTGCAGGCCCTGTCCACAGCTCTGTGGGGTGGAGGAGACTCCTCTGGAGA  
 AGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGACAGGCCAGAATGAAGTCTGGGTGAG  
 30 GAGCCAGCTGCTGGGCCAGCTGCCCTATGTAAGGCCCTTCTAGTTTGTCTGAGACCC  
 CACCCACGAACAATCCAAATAAAGTGACATTCCC  
 >H\_1.0.0\_15972 Homo sapiens proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), mRNA  
 cr: gi-5803122/// [Human\_jongleur\_201102.6827.C1] [SEQ ID NO: 235]  
 ATTCGCGGCGCTGCAAGAACCAGCGCAASAGGGAAGCGGAGTTATAGCTACCCCGGCCG  
 35 CGGAGCCGGCTCACTGCACTACCCCGCCCCCTTCTTCTCCAGACGCGAAGTCCCGG  
 GCGCTCATGGCGGGCTTGAGGTACTGTTCCGATCGGCAGCGCCGCCATCACTGCAGG  
 CAGGACGCGCTCGTCTGCTTCTTGCAATGGGAAGTGGTGACACACGGTTACTGCGGCTT  
 GGTGTGCTGTGACGAGCCGGGTCCCAATGATAAGAAGTCAGAACTGCTGCCAGCTGGTGG  
 40 AACAAATAAAGACCTGTATGTCCTCCGGTATGAGTATAAGGATGGGTCCAGAAAGCTC  
 CTTGTGAAGCCATCACCGTGGAGAGCAGCATGATCCTCAATGTGCTGGAATATGGCTCA  
 CAGCAAGTGGCAGACTTGACCTGAACTTGGATGATTATATTGATGCAAGACACCTGGGT  
 GACTTCCACAGGACCTACAAGAACAGTGAGGAGCTTCGGTCTCGTATTGTGCTGGAATC  
 ATCACACCTATCCATGAGCAGTGGGAAAAGGCTAATGTAAGCAGTCCCCACCGGAGTTC  
 45 CCCCTGCTACCGCCAGAGAGGTGGACCCACTCCGGATTCTCCACACCCACACACC  
 AGTCGGCAGCCTCCCTGGTGTGATCCCTGGGCGCGTTTGTGTGCGGGGAGAAGACTTA  
 GACCTTTTGGGCCTCGGAGAGGTGGCATGATTGTGGATCCCTGAGATCTGGCTTCCCA  
 AGAGCACTTATTGACCTTCTCAGGCCCTCCGAACCGACTTCTCCAGGCGCTGTGCC  
 CCAGAGCTCGCTTTGACCCCTTTGGACCCATTGGGACCAGCCACCCGACCTAACCCCA  
 50 GACCATCTCCCCCGCGGGCTACGATGACATGTACCTGTGAAGGCCTCAAGAATGTAAC  
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 55 CCCAAGAGAAATCAGTGTGTCTCTTCAACCATCAGCTCTCCCTTTTACCACACAGCTC  
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 CAGTGCTATAAGAACAGAACGCATTTTGGATGTTATTATTAAGAACCAATGTCAATACA  
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 60 ATGGGTCCCTTCTGCTGCTGATGAATGGAATGAGTGACTGGAAATCCCATAGGCCACAA  
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 65 AAATTGGAGGTGCTTCTGCTCTAAAGCATTTTGTATGCTCTCATCTGTGTTTGGTAAC  
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 GAGCATGGGCTGCTCTGAGTGTGGTGTGAACTTCGGGAGGAGCAGGGAGCCCTGCAAC  
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 70 CAGACGCGGGCAGTGATGAGCCCTGTCTGGAGTGGAAAGAGCAGGATAGAGCACAGGC  
 TAAGAGGCAGGATCAGGCGGTAGTCACTTCCGCTCTGAGCTAGCATTTTCAACCAT  
 TGTGGATCCTTTCACTTCTCAGCTCCCTGGATTCTTCCCTAAATAGGACCTATTATT  
 TACCTGTAGGTAAGCAGCTACTGTAGCTCTCTGAGGTATCTCCAGGCTGTTTCTGT

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AGCCTCAGATTGCTTATCTGCTTAGCCTGAGAACAGGTAGATGAAAACCTAACTGATGCC  
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CTCCCTGGGTATTTCTGTCACTCCCATGGCAAGCAGTGATTAGTAAACACCCAGAG  
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5 GATCAGGCAGAGGTGCAGATTCAATCATTACTCATAACCTTTGAGAGATGTACATGGGA  
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TTTGCTCATAAAGACATCCTTTATTATAAAGGAAGTATTTATAGGATGATAGAGACCAT  
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10 ATACAACATTTCTGTTTTCTGATAACAACCTGTGATTACCTTCAGAATTGGCCATTTTTTT  
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CTGGGCCACTTCCCTCCCTCCAGTCATGAGTAATCATCAAGGAGCAAGTTGGAGTGTTC  
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15 GCGAATTC

>H\_1.0.0\_4691 Homo sapiens, hypothetical protein similar to CG7943, clone IMAGE:4827650, mRNA cr:  
gi-19913535/// [Human\_jongleur\_201102.1275.C6] [SEQ ID NO: 236]

AGCGGAGAATCAGTCTGAGCCTCCTCGCCTCCCGGCTCTCCCGCTGTTGCGGGTGT  
20 ATCCGGCTGCTGGGGGACCTTTCCCGGAAGGAGGCTGCTTTCATTCGGTCAACGCCCC  
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TGCTGAGCTCCGGAGGGAGCAGAGCTGGCACCCGCGCAAGGCCCTGCTCCTCCGGGAGA  
CTGGGATTTCTGGCCTCCTCACCTCGGGACCGCTGACTGTGGAGTGTCAAAGACGGAACA  
GGGTTTAGTGATCTTGTCCAACCCCTCCCGCTTTTACAGACTGGGGAAATGGAGCGCC  
25 TGGAGAACGGAATCCAGTTATCAAATGACTCCAGAAGAGAGAACCTAACAGAACAT  
AACAAATGGAAGAAATGGGAATATTATCAAAAAGCTATCATTCTGTTAAACTCCAGGCTT  
GGATGGTGTACAGGTTTAAAAAAGAAAGTCTTTCATGAAAAAGAGAA  
CTTAAGCAACATGATGGATTGAGAAGCTCATGGAAGAGACCACCAATACTAACATCTTC  
GAAACAAGATATGTACCTCATATTACAGATTTAGTGAAATGAAGCATTAATTGTGTGGC  
30 TGCTGTGCAGCCTTCAACAACGTCGCAATCACATTTCCCATTCAGAAGGTCTCTTTCCA  
CAACAGCTGTATGGCATCAAAACGGGGGATGCAATACCTCAGTTGAGAACGGATGGATTT  
CGAACTTGTATCGGGGAATCTTTCCCGATTGATGCAAGAGACAACTACACTTGCACTT  
ACGTTTGGTCTGTATGAGGATTATCCTACCTTCTCCACAAGCATGTGAGTGCTCCAGAG  
TTTGCAACCTGTGGCGTGGCAGCAGTGCTTGAGGGACAACGGAAGCAATTTTCACTTCA  
35 GACATTGCTTCAAGACCACAAGCACCATGACAAATTTGCCAACATTTATCAGGCTTTCAA  
GGCACTGAAATGTATGGAATTTGAGAGTTTATCGAGGGTTGGTGCCATTCTTTTCCA  
GAATGGACTCAGCAATGTCTTTTTCGGGCTTCAGGTCACGTTAAGGAGCATCTG  
CCTACCGCGACGACTCACAAATCTCATTTGGTCAATGATTTTATCGGTGGAGGTCTATTG  
GGTGCCATGTTGGGATTCCTGTTTTCTCCAATTAATGTTGAAAACTCGCATACAGTCT  
40 CAGATTGTTGGGGAATTTCACTCTTTCCCAAGGTTTCCAAAAAATCTGGCTGGAAACGG  
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CAAGTTGGTGTATAACTCCAGGCCACACTTTGAAGACCAGACTGCAAAATATATTACCA  
GGGATGGTTTGTGTGTCTCAGACTTCTTAAATTTGATAAAATTCAGCGGAACCTG  
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>H\_1.0.0\_28568 603077615F1 Homo sapiens cDNA 5' end cr: gi-15943675/// /clone=IMAGE:5169579  
/clone\_end=5' /gb=BI832125 /gi=15943675 /ug=Hs.116415 /len=717 [Human\_jongleur\_201102.14663.C1] [SEQ  
ID NO: 237]

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50 GTGAAAGAAAGTCTTCAATTTAGAGACCACAAGGTCCGGAGCGCTGCGGAGGCTTCTG  
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TACGAGAGCATCATCTTTGAGTGGGCAAGGCTTCCCATGGGTGGAGGTGSCCAGGTG  
GTCAAGTTTACAGAAGAGCTGCTAAGGGAACCAAGGTTTCACTCCAGGAGTCCACACAG  
55 CCCACCACTGTGTAGGAATGCCAGCAGAGGCTGATGATGGCAATGACGGTGACAAATGG  
CATTACTTATTGAGTGTCTTACTGTGTACCAGGCACGTGGAAGACACCACATATGCAATGC  
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ACTGAGGCTGTGACGATCCTGGGGAACAAGCTTAGAGATTACCGGGGCCATTTCAACACC  
ACCCACCTGTGTGGCCTCTGTGACTACTTCCACCACACCTTCATCCGCCACTACAACTC  
60 TACCAGTATGCTTGGGCCAGGACCAGCAGGTGACCTGACCGTTGCCACCTGGAGGTG  
TGCAATGCCACCCCATCCCTTCCGCTGGCCGAGGGCATGACAGGGGACTTGTGATCCAC  
GAGCAGCAGGTGGCCACACTGACGGAGGCCGAGGCACAGAAGCGCGCCGACGTGCTGCTC  
CTGAAAGAGGCGCTGCGCTGGAGCGGGAGAACTCGCTGCAGAAGGCGTTCGCTGCGCGCC  
CGCCTGCGCAGCCGCGCCAGGTCCTGGAGAGACAGCAGTTGGAGAGCCTCATCTGCCAG  
65 GCAGTCCACACCCAGATGGAGCTCCTGCAGGAGCTGCTGCAGCGCCAGATCCAGAAACACA  
TTCCGCAATCTTGGACTGAGCTTTCAGAAGAAGACTCTGAACCTCAACGCCCCACCCCT  
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>H\_1.0.0\_40132 Homo sapiens golgin-245 mRNA, complete cds si: gi-1173564///  
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20 >H\_1.0.0\_36669 Human phosphoglycerate mutase 2 (muscle specific isozyme) (PGAM2) gene, 5'; end si:  
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CAAAGGGAATCTTTGTTCTCAAAGAAACCAAAACCCACACACTATATTCAGCTATGATT  
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10 >H\_1.0.0\_4005 Homo sapiens serine/threonine kinase 12 (STK12), mRNA cr: gi-4759177///  
[Human\_jongleur\_201102.967.C1] [SEQ ID NO: 267]  
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30 CGGAGGGTGTCTCCCTCTGCCCCCTCAATCTGTGCGCTGATGGTCCCTGTCAATCACT  
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C  
>H\_1.0.0\_20190 Homo sapiens hypothetical protein CL25022 (CL25022), mRNA cr: gi-7661547///  
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>H\_1.0.0\_13832 Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA cr: gi-  
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CGTCATTGTGTAATTATCTCTAGA

>H\_1.0.0\_6694 Homo sapiens mRNA for period (Drosophila) homolog 3 hPER3, complete cds cr: gi-13160924/// [Human\_jongleur\_201102.2143.C5] [SEQ ID NO: 275]

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 >H\_1.0.0\_11336 Homo sapiens deoxyguanosine kinase (DGUOK). transcript variant 1, nuclear gene  
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5 G C C C G G C C A G C C G C C C C G T C C G G G A G G T T A G G G G C G C C T C T G C C C G G C C G C C C T A C T G G  
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15 > H\_1.0.0\_24134 Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA cr: gi-  
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G G G G A T G C A C A T T T C G A T G A G G A C G A A T T C T G G A C T A C A C A T T C A G G A G G C A C A A A C T T G  
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>H\_1.0.0\_99143 p07c08.x1 Homo sapiens cDNA 3'.end as: gi-11448929/// /clone=IMAGE:3644943  
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30 dehydrogenase (EC 1.1.1.27) chain X - human [H.sapiens] [gnl|UG|Hs#S2910008] [SEQ ID NO: 294]  
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35 CCTCCCTCCTCAGCGGTGATGTTGACTTTCACAAAGTCTGTATACCACTTTGTCCCAAG  
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>gi|21452365|gb|BQ551479.1|BQ551479 H4009E10-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone  
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50 TCTCCATCTGTGACTTGTCAAGATAAATTTGAGGGGATGTTTTTATTGTTTGGTGCCTT  
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55 >H\_1.0.0\_310 Homo sapiens cell-type T-cell immunoglobulin gamma chain, V region (IGHV@) mRNA,  
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65 >H\_1.0.0\_19016 Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA cr: gi-4504612///  
[Human\_jongleur\_201102.8413 C2] [SEQ ID NO: 297]  
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ACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGC  
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>H\_1.0.0\_7743 Homo sapiens eosinophil chemotactic cytokine (TSA1902), mRNA cr: gi-11141866///  
[Human\_jongleur\_201102.2578.C2] [SEQ ID NO: 298]  
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70 GACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGACACCCACCTGGGTGGGAGGAC  
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 >H\_1.0.0\_19194 Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA cr: gi-5579469///  
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TACTGCCATCTTACGACTATTTCTTCTTTTAATACACTTAACTCAGGCCATTTTAAAG  
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10 >H\_1.0.0.18527 Homo sapiens D-lactate dehydrogenase (LDHD), mRNA cr: gi-23821028///  
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[Human\_jongleur\_201102.3990.C6] [SEQ ID NO: 310]  
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5 AGGAGTTGGAGTTGACATTAACAAGGCTCTTCTTGCCAAGAGAAAGAGACTAGAAATGTA  
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 >H\_1.0.0\_23435 Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2  
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